EURO EVO DEVO

26-29 July 2016 | Uppsala, Sweden

Previous Meetings

2006 Prague

2008 Ghent

2010 Paris

2012 Lisbon

2014 Vienna

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Society Committees

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Ronald Jenner – Natural History Museum, London
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Peter Olson – Natural History Museum, London
Michael Schubert – Laboratoire de Biologie du Développement de Villefranche-sur-Mer
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Program Committee

Frietson Galis (Chair) – Naturalis Biodiversity Center, NLD
Graham Budd – Dept of Earth Sciences, Uppsala University
Charlie Scutt – Ecole Normale Supérieure de Lyon

Welcome from the President

On behalf of EED, the European Society for Evolutionary Developmental Biology, I extend a cordial welcome to all participants of our 6th biennial conference. In concert with the previous meetings in the Czech Republic, Belgium, France, Portugal, and Austria, this year's Swedish venue reflects the European dimension of the society. It is wonderful to join our colleagues in Uppsala for several days of scientific exchange. With close to 500 participants, we are looking forward to a rich meeting. The key note lectures, symposia, contributed sessions, and posters cover a representative variety of current themes in the developmental evolution of plants and animals. It is very rewarding to see that the society is able to keep to its declared goal of promoting EvoDevo in a comprehensive organismal sense. Besides the genetic, genomic, and organ system contributions, there will be sessions on the genotype-phenotype relation, life cycle evolution, reproductive medicine, domestication, and other subjects not usually found in similar meetings. With the quantitative, bioinformatic, and philosophical approaches also present, the theoretical content of the EvoDevo enterprise will be kept in focus. This way the EED meetings provide a valuable interface between developmental and evolutionary biology.

As with previous conferences, two associated meetings, the Tribolium satellite meeting and the Amphioxus satellite meeting, will be held a day prior to our conference. Welcome to the participants of these meetings who stay on to particpate in and enrich the EED conference.

The EED is grateful to all sponsors who have provided support for symposia and other activities, in particular the Company of Biologists and Nature Ecology and Evolution, and to the conference management team of the University of Uppsala for their professional organization. We would also like to thank the members of several committees who assisted in the planning stages, and we are most grateful to the local organizing team headed by Graham Budd for the excellent preparation of the meeting.

Ha det så trevligt i Uppsala!

Gerd B. Müller
President EED

Welcome from the local committee

A warm welcome to „ungdomens stad“ (the „city of youth“): home to Linnaeus, Hörstadius, Jägersten and the North‘s oldest university (founded 1477). We hope that you will find time to enjoy the beautiful long Swedish summer days as well as the many sites of cultural interest in and around Uppsala. Above all though, we wish you a stimulating and productive EED2016!

Graham Budd (chair, local committee)

General Information

Dates & Venue

Tuesday 26th to Friday 29th July 2016

Uppsala Konsert och Kongress

Vaksala torg 1, 753 31 Uppsala

The venue opens at 08.00 each day.

Registration

The registration desk is at the Venue. If you have registered previously, it will be possible to pay the registration fee on-site on Tuesday evening. Registration will take place on the ground floor on Tuesday evening, and on the help desk on Floor Six on the following days.

Fees include:

- Access to all sessions
- Welcome Reception at the venue
- Delegates‘ documents (printed program booklet, pdf of abstracts on USB stick)
- Certificate of attendance
- Lunches
- Coffee breaks

Badges and security

Please wear your name badge at all times whilst at the congress venue and during the social events, as well as during the breaks. It is the official entrance pass to the scientific sessions, the welcome reception.

Coat/Bag check

The coat/bag check is open on 26 July from 13.00 and all day on 29 July

There is a self-service coat hanger and small storage units on the lower level if needed during the other days (coin operated).

Conference locations

All sessions take place on level 3 and 6. There are signs with the EED logo directing you to the various sessions.

Lunches

Please wear your badge!

Lunch is provided in the downstairs restaurant at the conference locality, Uppsala Konsert och Kongress. It consists of a seated meal with coffee, non-alcoholic drink and salad included.

Vegetarian options are available for those who indicated this at registration. All registered participants who registered for special dietary need, will have a red ticket in the registration pack to show the staff in the restaurant.

Wednesday 27 July
Oven baked chicken with lentils, tomato and herbs, served with mango salad, corn sauce and bacon crust

Thursday 28 July

Ground meat steaks with cabbage tureen and crushed potato, veal gravy, cucumber salad and lingon berries

Friday 29 July
Hazelnuts baked pork with dill flavoured turnip, pickled beetroots, green peas puree and gravy, topped with sweet potato chips

Social Events

Welcome Reception

The welcome reception will be held on Tuesday 26th July, at 19:00, on Floor Six of the conference locality. The reception is free, but you will need to wear your badge to have access.

Conference Dinner

The conference dinner will take place on 29 July, 19.15, in the historic Uppsala Castle (for directions refer to the map at the end of the booklet). There will be a cash bar open afterwards until 01.00

Technical Information

WiFi Access

All registered participants can log onto the conference centre wireness network:

User name: UKK

Password: Uppsala1

Eduroam is not available at the venue.

Oral Presentations

Speakers are asked to transfer their presentation (Powerpoint or pdf) from a USB stick onto the Macs/PCs in the lecture rooms before their session starts: between 8.30 and 8.55 for the morning sessions, or during the breaks immediately preceding their session.
Speakers may use their own laptop computer if they prefer. In this case, they should also come to the lecture room before the start of their session, in order to check whether the projection is working. It is best to have a copy of your presentation on a USB stick, in case of a problem. We kindly ask chairs to be present 15 minutes prior to the start of their session.

The maximum duration of symposia talks is 25 minutes (including 5 minutes for questions) and 15 minutes for contributed talks (including 3 minutes for questions).

We ask speakers to keep closely to the time schedule and session chairs to be very strict in not allowing speakers to go over the allotted times.

Poster Presentations

The poster boards are suitable for posters of the A0 format (1.2 m height x 1.0 m width). All posters can remain posted throughout the meeting. Presenters should put up their posters on Tuesday evening or Wednesday morning. Please be present at your poster during the poster sessions on Wednesday (even numbers) and Thursday (odd numbers). Materials for the fixing of the posters will be available. Posters should be removed before the end of the meeting, i.e., at the latest during the coffee break on Friday afternoon.

Poster Prize Competition

Doctoral or Master's students presenting a first-author poster will take part in the poster competition if they indicated their participation upon submission of their abstract.
The Student Poster Competition at EED-2016 is generously sponsored by Elsevier, New Phytologist and Springer. We are offering two-equal first prizes of iPad-mini tablet computers, and two equal-second prizes of 150 euros (each) of Springer book vouchers.These prizes will be awarded to the four best posters, as decided by a panel of judges, on any evo-devo subject. Posters will be judged during the two poster sessions, so presenting authors should make sure they are available to speak informally about their work during their allotted session, on either the Wednesday or Thursday evening. Poster prizes will be awarded on the last day of the Congress, and the four main winners will be invited to say a few words about their work, in full plenary session during the prize-giving ceremony (around 1700 on Friday in Stora Salen).

Programme at a Glance

Preconference Meetings

Monday, July 25th

	SAL C		K3/K4
13.00 – 18.00	Satellite Meeting Amphioxus	1300 – 18.00	Satellite Meeting Tribolium

Tuesday, July 26th

	STORA SALEN		SAL C
09.00 – 12.00	Satellite Meeting Amphioxus	09.00 – 12.00	Satellite Meeting Tribolium
13.30 – 17.00	Satellite Meeting Amphioxus	13.30 – 17.00	Satellite Meeting Tribolium

EURO EVO DEVO 2016

Tuesday, July 26th

	STORA SALEN
18.00 – 18.20	EURO EVO DEVO 2016 Opening
18.20 – 19.00	Keynote Lecture (K1) Per Erik Ahlberg
19.00 – 21.00	Welcome Reception at the Venue

Wednesday, July 27th

	STORA SALEN	SAL B	SAL C	K3/K4
09.00 – 10.40	Symposium S1 Evolution of sensory cell types	Symposium S2 Epigenetics and inheritance	Symposium S3 Morphological diversification	Symposium S4 Theoretical perspectives in EvoDevo
10.40 – 11.10	Coffee break			
11.10 – 12.25	Contributed C1 Evolution of sensory cell types I	Contributed C2 Regulatory capacity in early embryos	Contributed C3 Morphological diversification	Contributed C4 Theoretical and process perspectives in Evodevo
12.25 – 14.00	Lunch break			
14.00 – 15.40	Symposium S5 Regulatory capacity in early embryos	Symposium S6 Cranial sense organs in vertebrates	Symposium S7 Life cycle evolution	Symposium S8 Developmental complexity in plants and animals
15.40 – 16.10	Coffee break			
16.10 – 17.10	Contributed C5 Evolution of sensory cell types II	Contributed C6 Epigenetics and inheritance	Contributed C7 Life cycle evolution	Contributed C8 Palaeobiology and deep time
17.10 – 17.20	Break			
17.20 – 18.00 STORA SALEN	Keynote Lecture (K2) Kirsten ten Tusscher			

18.00 – 20.00	Poster Session 1 (even numbers) Floor Six

Program at a Glance

EURO EVO DEVO 2016

Thursday, July 28th

	STORA SALEN	SAL B	SAL C	K3/K4
09.00 – 10.40	Symposium S9 Phenotypic plasticity and evolution	Symposium S10 Old questions, young approaches	Symposium S11 Ancestral proteins, genomes and networks	Symposium S12 Process thinking for EvoDevo
10.40 – 11.10	Coffee break			
11.10 – 12.50	Contributed C9 Phenotypic plasticity and evolution	Contributed C10 Old questions, young approaches	Contributed C11 Ancestral proteins, genomes and networks	Contributed C12 Genotype-Phenotype map and EvoDevo
12.50 – 14.00	Lunch break			
14.00 – 15.40	Symposium S13 Genotype-Phenotype map and EvoDevo	Symposium S14 Animal phylogeny and animal organ evolution	Symposium S15 EvoDevo of domestication	Symposium S16 Branching across the tree of life
15.40 – 16.10	Coffee break			
16.10 – 17.10	Contributed C13 Biomimetics	Contributed C14 Animal phylogeny and animal organ evolution	Contributed C15 Contributions to Evodevo	Contributed C16 Branching across the tree of life
17.10 –17.20	Break			
17.20 – 18.00 (STORA SALEN)	Keynote Lecture (K3) Beverley Glover			
18.00 – 20.00 (FLOOR 6)	Poster Session 2 (odd numbers)			

Friday, July 29th

	STORA SALEN	SAL B	SAL C	K3/K4
09.00 – 10.40	Symposium S17 Evolutionary developmental genomics	Symposium S18 Serial homology and segmentation	Symposium S19 Evolution of plant epidermis patterns	Symposium S20 Micro-evo-devo
10.40 – 11.10	Coffee break			
11.10 – 12.25	Contributed C17 Evolutionary developmental genomics	Contributed C18 Serial homology and segmentation	Contributed C19 Evolution of plant and animal epidermis patterns	Contributed C20 Gene regulatory networks and origin of novelties I
12.25 – 13.50 NB	Lunch break			
13.50 – 15.30	Symposium S21 Gene regulatory networks and origin of novelties	Symposium S22 Vertebrate limb as evolving dynamic system	Symposium S23 Developmental evolution and reproductive medicine	Symposium S24 Symmetry in plants and animals
15.30 – 16.00	Coffee break			
16.00 – 17.00	Contributed C21 Gene regulatory networks and origin of novelties II	Contributed C22 Vertebrate limb as evolving dynamic system	Contributed C23 Developmental evolution and reproductive medicine	Contributed C24 Micro-evo-devo
17.00 – 17.05	Break			
17.05 – 17.20 (STORA SALEN)	Student Poster Prizes			
17.20 – 18.00 (STORA SALEN)	Keynote Lecture (K4) Ehab Abouheif			
17.20 – 18.05 (STORA SALEN)	Close of meeting			
18.10-18.40 (STORA SALEN)	Business meeting			

19.15	Conference Dinner (see map)

Notes

Detailed Programme

Detailed Programme

Tuesday, July 26th

14.00 – 18.00 Registration

18.00 – 18.20 Opening
STORA SALEN
Welcome addresses by Graham E. Budd (chair, local organisers) and Gerd Müller (President, EED)

18.20 – 19.00 Keynote Lecture (K1)
Fossils, embryos and the origin of the vertebrate jawed head
STORA SALEN
Per Erik Ahlberg
(Evolutionary Biology Centre, Uppsala University, SWE)
Chair: Gerd B. Müller

19.00 – 21.00 Welcome Reception at the Venue

Wednesday, July 27th

09.00 – 10.40 Symposium S1:
Development and evolution of sensory cells and organs I: Evolution of sensory cell types

STORA SALEN

Organizers: Detlev Arendt and Jacob Musser
Chair: Jacob Musser

S1-01 From nerve net to centralized nervous system: the evolution of sensory cell types
Arendt, Detlev (European Molecular Biology Laboratory, Heidelberg, DEU)

S1-02 Evolution of the sensory nervous system: From protoneurons to elementary receptors to complex sensory arrays
Hartenstein, Volker (UCLA, USA)

S1-03 Is the evolution of sensory structures phylogenetic tree-like?
Oakley, Todd (University of California, Santa Barbara, USA)

S1-04 Antibody-based sorting for cell type profiling in Evo-Devo: example from placode derived cell types and technical advances in various species
Patthey, Cedric (Umeå University, SWE)

09.00 – 10.40 Symposium S2:
Epigenetics, inheritance and evo-devo

SAL B

Organizer: Carlos Guerrero-Bosagna
Chair: Carlos Guerrero-Bosagna

S2-01 Developmental programming of cardiac function in ectothermic vertebrates
Galli, Gina (University of Manchester, GBR)

S2-02 Transgenerational epigenetic inheritance and evolution: the role of the germ line epigenome in generating genomic evolutionary novelties
Guerrero-Bosagna, Carlos (Linköping University, SWE)

S2-03 Methylation QTL analysis in the chicken
Wright, Dominic (Linköping University, SWE)

S2-04 Transgenerational and plastic phenotypic effects in Arabidopsis in response to mild drought stress
Van Dooren, Tom (Institute of Ecology and Environmental Sciences, Paris, FRA)

09.00 – 10.40 Symposium S3:
Understanding morphological diversification of plants and animals: paths from molecules to phenotypes

SAL C

Organizers: Miltos Tsiantis and Angela Hay
Chairs: Miltos Tsiantis and Angela Hay

S3-01 Morphomechanical innovation drives explosive seed dispersal
Hay, Angela (Max Planck Institute for Plant Breeding Research, Köln, DEU)

S3-02 Towards understanding development and diversity of leaf shape
Tsiantis, Miltos (Max Planck Institute for Plant Breeding Research, Köln, DEU)

S3-03 Reproductive capacity evolves in response to ecology through common developmental mechanisms
Extavour, Cassandra G. (Harvard University, Boston, USA)

S3-04 Development, selection, and species diversification
Khila, Abderrahman (Ecole Normale Supérieure de Lyon, FRA)

09.00 – 10.40 Symposium S4:
Theoretical perspectives in evo-devo

K3/K4

Organizers: Christine Mayer and Thomas F. Hansen
Chair: Christine Mayer

S4-01 Resolving the relationship between evolvability and robustness using Boolean Genotype-Phenotype Maps
Mayer, Christine (University of Oslo, NOR); Hansen, Thomas F. (University of Oslo, NOR)

S4-02 Core theoretical issues of EvoDevo: biased variation, non-linear

transition, emergent novelty.
Müller, Gerd B. (University of Vienna; KLI, Klosterneuburg, AUT)

S4-03 Regulatory motifs of trait individualization
Pavlicev, Mihaela (Cincinnati Children's Hospital Medical Center, USA); Todtova, Kristina (Cincinnati Children's Hospital Medical Center, USA); Widder, Stefanie (Cincinnati Children's Hospital Medical Center, USA)

S4-04 Morphological variation at different spatial scales: A morphometric study of developmental control in the human cranium
Mitteroecker, Philipp (University of Vienna, AUT)

11.10 – 12.25 Contributed Session C1: Development and evolution of sensory cells and organs I

STORA SALEN

Chair: Sally Leys

C1-01 The origin of the synapse and principles of cell type functional evolution
Musser, Jacob M. (EMBL, Heidelberg, DEU)

C1-02 Sense and sensitivity in glass sponges: physiological evidence for sensory cells in the osculum
Leys, Sally (University of Alberta, CAN)

C1-03 Chiton eye photoreceptor cells employ both: a rhabdomeric opsin and a protostome specific ciliary opsin
Vöcking, Oliver (Sars Centre, Bergen, NOR); Kourtesis, Ioannis (Sars Centre, Bergen, NOR); Tumu, Sharat C. (Sars Centre, Bergen, NOR); Hausen, Harald (Sars Centre, Bergen, NOR)

C1-04 Molecular characterization and embryonic origin of the eyes in the common house spider Parasteatoda tepidariorum
Schomburg, Christoph (Georg-August-University, Göttingen, DEU); Turetzek, Natascha (Georg-August-University, Göttingen, DEU); Schacht, Magdalena I. (Georg-August-University, Göttingen, DEU); Schneider, Julia (Georg-August-University, Göttingen, DEU); Prpic, Nikola-Michael (Georg-August-University, Göttingen, DEU); Posnien, Nico (Georg-August-University, Göttingen, DEU)

C1-05 Deciphering genomic and developmental mechanisms that underlie vision adaptations in noctilionoid bats
Sadier, Alexa (University of Illinois USA); Davalos, Liliana (Stony Brook University, New York, USA); Dumont, Elizabeth (University of Massachusetts at Amherst, USA); Rossiter, Stephen (Queen Mary University of London, GBR); Sears, Karen (University of Illinois USA)

11.10 – 12.25 Contributed Session C2: Regulatory capacity in early embryos and axis formation:

self-regulation or self-organization in axis formation

SAL B

Chair: Mette Handberg-Thorsager

C2-01 β-catenin-dependant mechanotransduction dates back to the common ancestor of Cnidaria and Bilateria

Pukhlyakova, Ella (University of Vienna, AUT); Aman, Andy (University of Washington, USA); Technau, Ulrich (University of Vienna, AUT)

C2-02 In-depth cell lineage analysis of the spiralian development

Handberg-Thorsager, Mette (MPI-CBG, Dresden, DEU); Tomer, Raju (Stanford University, USA); Amat, Fernando (Howard Hughes Medical Institute, Ashburn, USA); Vopalensky, Pavel (MPI-CBG, Dresden, DEU); Lombardot, Benoit (MPI-CBG, Dresden, DEU); Tomancak, Pavel (MPI-CBG, Dresden, DEU); Keller, Philipp (Howard Hughes Medical Institute, Ashburn, USA); Arendt, Detlev (EMBL, Heidelberg)

C2-03 Instead of bicoid: germ cell less is required for axis formation in a beetle

Ansari, Salim (Georg-August-University Göttingen, DEU); Troelenberg, Nicole (University of Erlangen-Nuremberg, DEU); Bucher, Gregor (Georg-August-University Göttingen, DEU); Klingler, Martin (University of Erlangen-Nuremberg, DEU)

C2-04 Functional evolution of a morphogenetic gradient

Chun, Wai K. (University of Chicago, USA)

C2-05 Linking Noggin and Terminal patterning

Dearden, Peter K. (University of Otago, Dunedin, NZL); Duncan, Elizabeth J. (University of Leeds, GBR); Tidswell, Olivia (University of Otago, Dunedin, NZL); Beck, Caroline (University of Otago, Dunedin, NZL)

11.10 – 12.25 Contributed Session C3:

Understanding morphological diversification of plants and animals: paths from molecules to phenotypes

SAL C

Chair: Miltos Tsiantis

C3-01 The evolution of morphology, one base pair at a time

Preger-Ben Noon, Ella (HHMI Janelia Research Campus, Ashburn, USA); Stern, David (HHMI Janelia Research Campus, Ashburn, USA

C3-02 The role of miR-199a in Arctic charr morphogenesis

Kapralova, Kalina H. (University of Iceland, ISL); Franzdottir, Sigridur Rut (University of Iceland, ISL); Snorrason, Sigurður S. (University of Iceland, ISL); Maier, Valerie H. (University of Iceland, ISL; Palsson, Arnar (University of Iceland, ISL); Jonsson, Zophonias O. (University of Iceland, ISL)

C3-03 Gain and loss of floral ultra-violet absorbance is controlled by a single transcription factor

Hester, Sheehan (University of Cambridge, GBR); Moser, Michel (University of Bern, DEU); Klahre, Ulrich (University of Bern, DEU); Esfeld, Korinna

(University of Bern, DEU); Dell'Olivo, Alexandre (University of Bern, DEU); Mandel, Therese (University of Bern, DEU); Metzger, Sabine (University of Cologne, DEU); Vandenbussche, Michiel (Ecole Normale Supérieure de Lyon, FRA); Freitas, Loreta (Universidade Federal do Rio Grande do Sul, Porto Alegre, BRA); Kuhlemeier, Cris (University of Bern, DEU)

C3-04 Modelling tooth development and predicting its morphological variation. On the interplay between cell adhesion and biomechanics
Marin-Riera, Miquel (University of Helsinki, FIN); Salazar-Ciudad, Isaac (University of Helsinki, FIN)

C3-05 More than one way to build a backbone: Exploring developmental mechanisms underlying the diversity of vertebral morphology
Kishida, Marcia (University of Cambridge, GBR); Fleming, Angeleen (University of Cambridge, GBR); Keynes, Roger (University of Cambridge, GBR)

11.10 – 12.25 Contributed Session C4: Theoretical and process perspectives in Evo-devo

K3/K4

Chair: Ezzat El-Sherif

C4-01 Flexibility of temporal regulation as a basis for short- to long-germ evolution in insects
El-Sherif, Ezzat (FAU, DEU)

C4-02 On the origins of organismal complexity
Zimm, Roland (University of Helsinki, FIN); Salazar-Ciudad, Isaac (University of Helsinki, FIN, Universitat Autónoma de Barcelona, ESP)

C4-03 How can complex morphology evolve through changes in development
Hagolani, Pascal F. (Helsingfors University, FIN)

C4-04 Adaptation by natural improvisation
Soen, Yoav (Weizmann Institute of Science, Rehovot, ISR); Knafo, Maor (Weizmann Institute of Science, Rehovot, ISR); Elgart, Michael (Weizmann Institute of Science, Rehovot, ISR)

C4-05 What is a developmental mechanism and what is an evolutionary mechanism
Salazar-Ciudad, Isaac (University of Helsinki, FIN)

14.00 – 15.40 Symposium S5: Regulatory capacity in early embryos and axis formation: self-regulation or self-organization in axis formation

STORA SALEN

Organizer: Hiroki Oda
Chair: Hiroki Oda

S5-01 A spider model to study mechanisms behind the capacity for

self-regulation in axis formation
Oda, Hiroki (JT Biohistory Research Hall, Osaka, JPN); Iwasaki, Sawa (JT Biohistory Research Hall, Osaka, JPN); Akiyama-Oda, Yasuko (JT Biohistory Research Hall, Osaka, JPN)

S5-02 Self-regulatory mechanisms of dorsoventral axis formation in insects
Roth, Siegfried (University of Cologne, DEU)

S5-03 Body axes formation mechanisms in a bilaterally symmetric cnidarian
Genikhovich, Grigory (University of Vienna, AUT)

S5-04 Symmetry breaking in mouse development
Hiiragi, Takashi (EMBL, Heidelberg, DEU)

14.00 – 15.40

Symposium S6:
Development and evolution of sensory cells and organs II: Evolution of cranial sense organs in vertebrates

SAL B

Organizers: Gerhard Schlosser
Chair: Gerhard Schlosser

S6-01 An old brain in a new head: evolution of vertebrate sensory systems from ancestral sensory cells
Tosches, Maria (Max Planck Institute for Brain Research, Frankfurt am Main, DEU); Martinez-Vergara, Hernando (EMBL, Heidelberg, DEU), Bertucci, Paola Y. (EMBL, Heidelberg, DEU); Arendt, Detlev (EMBL, Heidelberg, DEU)

S6-02 Specification of the lateral plate ectoderm in the Ciona neural plate
Horie, Takeo (Princeton University, USA); Horie, Ryoko (Princeton University, USA); Hazbun, Alex (Princeton University, USA); Levine, Michael (Princeton University, USA

S6-03 When to stay together and when to split: molecular basis of sensory cell and sensory organ diversification in the vertebrate ear
Frizsch, Bernd (University of Iowa, USA)

S6-04 The development and evolution of vertebrate electroreceptors
Baker, Clare (University of Cambridge, USA)

14.00 – 15.40 Symposium S7:
Life cycle evolution

SAL C

Organizers: Mark Cock and Susana Coelho
Chairs: Mark Cock and Susana Coelho

S7-01 What uses are mating types? The developmental-switch model
Perrin, Nicolas (University of Lausanne, CHE)

S7-02 From minus to males:Coevolution of sexes and multicellularity in Volvocine Algae
Umen, James G. (Donald Danforth Plant Science Center, St. Louis, USA); Hamaji, Takashi (Donald Danforth Plant Science Center, St. Louis, USA); Miyagi, Ayano (Donald Danforth Plant Science Center, St. Louis, USA); Geng, Sa (Donald Danforth Plant Science Center, St. Louis, USA)

S7-03 Serial changes of eight types of stem cells in the life cycle of the moss Phsycomitrella patens
Hasebe, Mitsuyasu (National Institute for Basic Biology, Okazaki, Japan)

S7-04 The effect of ploidy and molecular constraints on the evolution of the land plant life cycle.
Szövényi, Péter (Duke University, Durham, USA)

14.00 – 15.40 Symposium S8:
Developmental complexity and diversity in animals and plants, parallels and differences

K3/K4

Organizer: Kirsten ten Tusscher
Chair: Kirsten ten Tusscher

S8-01 Evolution of diverse inflorescence architectures
Koes, Ronald (University of Amsterdam, NLD); Bliek, Mattijs (University of Amsterdam, NLD); Verbree, Bets (University of Amsterdam, NLD); Castel, Rob (University of Amsterdam, NLD); Kusters, Elske (University of Amsterdam, NLD); Della Serena (University of Amsterdam, NLD); Souer, Erik (University of Amsterdam, NLD)

S8-02 Turing pattern in fins and limbs
Onimaru, Koh (The Barcelona Institute of Science and Technology, ESP; Universitat Pompeu Fabra. Barcelona, ESP)

S8-03 Inflorescences as a model of branching structure development
Prusinkiewicz, Przemyslaw (University of Calgary, CAN); Owens, Andrew (University of Calgary, CAN); Cieslak, Mikolaj (University of Calgary, CAN)

S8-04 In silico evo-devo: reconstructing stages in the evolution of animal segmentation
Vroomans, Renske (Utrecht University, NLD); Hogeweg, Paulien (Utrecht University, NLD); ten Tusscher, Kirsten (Utrecht University, NLD)

16.10 – 17.10

Contributed Session C5:
Development and evolution of sensory cells and organs II

STORA SALEN

Chair: Cedric Patthey

C5-01 **Neurotransmission and signal transduction in the tunicate coronal organ and the evolution of mechanoreception based on secondary sensory cells**
Manni, Lucia (Università degli Studi di Padova, ITA); Rigon, Francesca (Università degli Studi di Padova, ITA); Gasparini, Fabio (Università degli Studi di Padova, ITA)

C5-02 **Understanding the origins of animal vision using marine larvae**
Valero-Gracia, Alberto (Stazione Zoologica Anton Dohrn, Naples, ITA); Kirwan, John D. (Lund University, SWE);Nilsson, Dan-Eric (Lund University, SWE); Arnone, M. Ina (Stazione Zoologica Anton Dohrn, Naples, ITA)

C5-03 **Visual photoreception in Atlantic cod - Evolutionary restrictions, neurogenesis and life history transformation**
Valen, Ragnhild (University of Bergen, NOR)

C5-04 **Photoreceptors of a polychaete with a very long pelagic phase**
Kumar, Suman (Sars Centre, Bergen, NOR)

16.10 – 17.10

Contributed Session C6:
Epigenetics, inheritance and Evo-devo

SAL B

Chair: Carlos Guerrero-Bosagna

C6-01 **Neuronal reprogramming of the germline**
Zuoco, Giuseppina (University of Warwick, GBR); Pires da Silva, Andre (University of Warwick, GBR)

C6-02 **Allele-specific whole genome sequencing during mouse embryonic development**
Marcho, Chelsea (University of Massachusetts – Amherst, USA); Mager, Jesse (University of Massachusetts – Amherst, USA)

C6-03 **Phenotypic variation in Drosophila melanogasteris caused by expression changes in a microRNA**
Kittelmann, Sebastian (Oxford Brookes University, GBR); Arif, Saad (Oxford Brookes University, GBR); Almudi, Isabel (CABD, Sevilla, ESP); Nunes, M. Daniela S. (Oxford Brookes University, GBR); McGregor, Alistair P. (Oxford Brookes University, GBR)

C6-04 **Analyses of gene expression and epigenetic differences in brains of Red Junglefowl selected for tameness**
Bélteky, Johan (University of Linköping, SWE)

16.10 – 17.10 Contributed Session C7:
Life cycle evolution

SAL C

Chair: Mark Cock

C7-01 **Genetic regulation of the haploid-diploid life cycle of the brown alga Ectocarpus**
Cock, J. Mark (Station Biologique de Roscoff, FRA); Arun, Arok (Station Biologique de Roscoff, FRA); Godfroy, Olivier (Station Biologique de Roscoff, FRA); Scornet, Delphine (Station Biologique de Roscoff, FRA); Bourdareau, Simon (Station Biologique de Roscoff, FRA); Peters, Akira F. (Bezhin Rosko, Santec, FRA); Coelho, Susana M. (Station Biologique de Roscoff, FRA)

C7-02 **Marchantia MpRKD regulates the gametophyte-sporophyte transition by keeping egg cells quiescent in the absence of fertilization**
Rövekamp, Moritz (University of Zurich, CHE); Bowman, John L. (Monash University, Clayton, Melbourne, AUS; UC Davis, Davis, USA)

C7-03 **Medusozoan genomes and the origin of a jellyfish body plan**
Khalturin, Konstantin (Okinawa Institute of Science and Technology, JPN); Khalturina, Maria (Okinawa Institute of Science and Technology, JPN); Fujie, Manabu (Okinawa Institute of Science and Technology, JPN); Koyanagi, Ryo (Okinawa Institute of Science and Technology, JPN); Goto, Hiroki (Okinawa Institute of Science and Technology, JPN); Satoh, Noriyuki (Okinawa Institute of Science and Technology, JPN)

C7-04 **Co-option of germ layers related TFs shows regionalized expression during two non-embryonic developments**
Tiozzo, Stefano (Sorbonne Université, Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA)

16.10 – 17.10 Contributed Session C8:
Palaeobiology and deep time

K3/K4

Chair: Javier Ortega-Hernández

C8-01 **Cambrian ecdysozoans: a microscopic perspective**
Harvey, Thomas H. P. (University of Leicester, GBR); Butterfield, Nicholas J. (University of Cambridge, GBR)

C8-02 **An embryological perspective on the arthropod early fossil record**
Chipman, Ariel D. (Hebrew University of Jerusalem, ISR)

C8-03 **Development and evolution of the synarcual in Placoderms and the Elephant shark**
Chevrinais, Marion (Université du Québec à Rimouski, CAN); Johanson, Zerina (Natural History Museum, GBR); Trinajstic, Kate (Curtin University, AUS); Long, John (Flinders University, Adelaide, AUS); Morel, Catherine (Université du Québec à Rimouski, CAN)

C8-04 **The new organizers hypothesis for chordate origins**

Sato, Noriyuki (Graduate University, Onna, JPN)

17.20 – 18.00
ROOMS C1&2

Keynote Lecture (K2)

Evo-devo of iterative body axis patterning; of mice and plants

Kirsten ten Tusscher
(University of Utrecht, NLD)
Chair: Charlie Scutt

18.00 – 20.00
FLOOR 6

Poster Session 1
(even numbers)

Thursday, July 28th

09.00 – 10.40 Symposium S9:

Phenotypic plasticity driving evolution? Evidence from skeletal elements

STORA SALEN

Organizers: Antonio Cordero and Nathalie Feiner
Chairs: Antonio Cordero and Nathalie Feiner

S9-01 **Developmental evolution, plasticity and integration of the avian beak**
Abzhanov, Arkhat (Imperial College, London, GBR)

S9-02 **Developmental evolution of - and through - phenotypic plasticity: case studies on horned beetles and beetle horns**
Moczek, Armin (Indiana University, Bloomington, USA)

S9-03 **Developmental modules in the diversification of the turtle shell**
Moustakas-Verho, Jacqueline (University of Helsinki, FIN)

S9-04 **Questioning the „early equals important rule" in ontogenetic processes: case studies from amniote ossification**
Werneburg, Ingmar (Museum für Naturkunde Berlin, DEU)

09.00 – 10.40 Symposium S10:

Old questions, young approaches

SAL B

Organizers: José Martín-Durán and Bruno Vellutini
Chair: Bruno C. Vellutini

S10-01 Microbiome research and the eco-immunity of biological individuals
Chiu, Lynn C. (University of Bordeaux, FRA)

S10-02 Tiny changes, big effects: the impact of microexons on neuronal differentiation, function and evolution
Irimia, Manuel (Centre for Genomic Regulation, Barcelona, ESP)

S10-03 Early animal evolution – Insights from exceptionally preserved Cambrian fossils
Ma, Xiaoya (Natural History Museum, London, GBR)

S10-04 The Evolution of pleiotropy and modularity
Melo, Diogo (University of São Paulo, BRA); Marroig, Gabriel (University of São Paulo, BRA)

09.00 – 10.40 Symposium S11:
Ancestral reconstruction of proteins, networks and genomes in plants and animals

SAL C

Organizers: Jerome Salse and Koen Geuten
Chair: Jerome Salse

S11-01 Ancestral complex and network evolution of MADS domain proteins and the origin of flowering plant lineages
Geuten, Koen (University of Leuven, BEL)

S11-02 Lineage-specific radiations and the evolution of the genetic tool-kit
Brockington, Sam (University of Cambridge, GBR)

S11-03 Reconstruction of the ancestral repertoire of proteins domains suggests modern genomes are deprived of building blocks
Bornberg-Bauer, Erich (Westfälische Wilhelms-Universität, DEU)

S11-04 Paleogenomics in plants and animals to unveil evolutionary forces
Salse, Jerome (INRA, FRA)

09.00 – 10.40 Symposium S12:
Process thinking for evo-devo

K3/K4

Organizer: Johannes Jaeger
Chair: Johannes Jaeger

S12-01 Process Thinking for Evo-Devo: an Introduction
Jaeger, Johannes (KLI, AUT)

S12-02 Explanatory idealization and developmental processes
DiFrisco, James (KLI, AUT)

S12-03 Inheritance of Process: A dynamical systems view of development and evolution
Monk, Nick (University of Sheffield, GBR)

S12-04 A damped oscillator drives posterior gap gene expression in Drosophila melanogasters

Verd, Berta (KLI, AUT)

11.10 – 12.25 Contributed Session C9:
Phenotypic plasticity driving evolution? Evidence from skeletal elements

STORA SALEN Chair: Philipp Mitteroecker

C9-01 **Allometry and sexual dimorphism in the human pelvis**
Fischer, Barbara (KLI, AUT); Mitteroecker, Philipp (University of Vienna, AUT)

C9-02 **Climate change will impact biodiversity through multiple forms of phenotypic plasticity**
Campbell, Calum (University of Glasgow, GBR); Parsons, Kevin (University of Glasgow, GBR)

C9-03 **Balance of natural selection and development in the origin of snakes**
Oliveira da Silva, Filipe (University of Helsinki, FIN); Di-Poï, Nicolas (University of Helsinki, FIN)

C9-04 **Geometric morphometrics of developmental modularity and phenotypic integration in pinniped skull and teeth**
Savriama, Yoland (University of Helsinki, FIN)

C9-05 **Diverse gene networks underlie development of convergent morphologies in turtles**
Cordero, Gerardo Antonio (Lund University, SWE); Liu, Haibo (Iowa State University, USA); Wimalanathan, Kokulapalan (Iowa State University, USA); Weber, Rachel (Iowa State University, USA); Quinteros, Kevin (Iowa State University, USA); Janzen, Fredric (Iowa State University, USA)

11.10 – 12.25 Contributed Session C10:
Old questions, young answers

SAL B Chair: Kevin Pang

C10-01 **Mapping the chemical connectome in the marine worm Platynereis dumerilii**
Williams, Elizabeth A. (Max Planck Institute for Developmental Biology, Tübingen, DEU); Jékely, Gáspár (Max Planck Institute for Developmental Biology, Tübingen, DEU)

C10-02 **A single 3D chromatin compartment in amphioxus reveals stepwise evolution of vertebrate Hox bimodal regulation**
Maeso, Ignacio (Universidad Pablo de Olavide, Seville, ESP); de la Calle-Mustienes, Elisa (Universidad Pablo de Olavide, Seville,ESP); Bertrand, Stéphanie (Université Pierre et Marie Curie, Paris, FRA; Observatoire Océanologique de Banyuls-sur-Mer, FRA); Diaz, Sergio G. (Universidad Pablo de Olavide, Seville, ESP); Aldea, Daniel (Université Pierre et Marie Curie, Paris, FRA; Observatoire Océanologique de Banyuls-sur-Mer, FRA);

Aury, Jean-Marc (Commissariat à l'Energie Atomique (CEA), Institut de Génomique (IG), Genoscope, Evry, FRA); Mangenot, Sophie (Commissariat à l'Energie Atomique (CEA), Institut de Génomique (IG), Genoscope, Evry, FRA); Holland, Peter W. H. (University of Oxford, GBR); Devos, Damien P. (Universidad Pablo de Olavide, Seville, ESP); Escrivá, Hector (Université Pierre et Marie Curie, Paris, FRA; Observatoire Océanologique de Banyuls-sur-Mer, FRA); Gómez-Skarmeta, José L. (Universidad Pablo de Olavide, Seville, ESP)

C10-03 **Transcriptomic signatures shaped by cell proportions shed light on differences in serial organ morphogenesis**
Sémon, Marie (Ecole Normale Supérieure de Lyon, FRA); Guéguen, Laurent (Université de Lyon, Villeurbanne, FRA); Petit, Coraline (Ecole Normale Supérieure de Lyon, FRA); Lambert, Anne (Ecole Normale Supérieure de Lyon, FRA); Renata Peterkova (Institute of Experimental Medicine,Prague, Czech Republic); Pantalacci, Sophie (Ecole Normale Supérieure de Lyon, FRA)

C10-04 **Understanding the origin of an evolutionary novelty: the male-specific turbanate eyes of the mayfly Cloeon dipterum**
Almudi, Isabel (CSIC-Univ. Pablo de Olavide. 41013, Seville, ESP; Martín-Blanco, Carlos (CSIC-Univ. Pablo de Olavide. 41013, Seville, ESP); Davie, Kristofer (University of Leuven, BEL); Aerts, Stein (University of Leuven, BEL); Alba-Tercedor, Javier (University of Granada, ESP); Casares, Fernando (CSIC-Univ. Pablo de Olavide. 41013, Seville, ESP)

C10-05 **Nervous system patterning in the Acoelomorpha**
Pang, Kevin (Sars Centre, Bergen, NOR); Hejnol, Andreas (Sars Centre, NOR)

11.10 – 12.25 Contributed Session C11:
Ancestral reconstruction of proteins, networks and genomes in plants and animals

SAL C

Chair: Jordi Paps

C11-01 **Reconstructing the genome of the first animal: the impact of novelty in the origins of metazoans**
Paps, Jordi (University of Essex, GBR); Holland, Peter W. H. (University of Oxford, GBR)

C11-02 **TopAnat enrichment of anatomical expression patterns shows that selection on expression in nervous tissues is a major determinant of duplicate gene retentions**
Robinson-Rechavi, Marc (University of Lausanne, CHE); Roux, Julien (University of Lausanne, CHE); Liu, Jialin (University of Lausanne, CHE)

C11-03 **Comparative genomics of an adaptive radiation: transposable elements in Hox gene clusters correlate with patterns of diversification**

Feiner, Nathalie (Lund University, SWE)

C11-04 Using the Physcomitrella pseudochromosomal genome assembly as a tool to probe the duplication history of this plant's MADS-box gene family.s
Ashton, Neil W. (University of Regina, Saskatchewan, CAN); Barker, Elizabeth I. (University of Regina, Saskatchewan, CAN)

C11-05 Neofunctionalization of a duplicate dachshund gene underlies the evolution of a novel leg segment in arachnids
Turetzek, Natascha (Georg-August-University Göttingen, DEU); Pechmann, Matthias (Universität zu Köln, DEU); Schomburg, Christoph (Georg-August-University Göttingen, DEU); Schneider, Julia (Georg-August-University Göttingen, DEU); Prpic, Nikola-Michael (Georg-August-University Göttingen, DEU)

11.10 – 12.25 Contributed Session C12:
Integrating the genotype-phenotype map with concepts of evolutionary-developmental biology

K3/K4 Chair: Michael Schubert

C12-01 Integrating developmental knowledge to quantitative genetic models: Mapping the genetic determinants of molar sizes in mice
Navarro, Nicolas (PSL Research University, Paris, FRA; Université de Bourgogne Franche-Comté, Dijon, FRA); Maga, A. Murat (University of Washington, Seattle, USA; Seattle Children's Research Institute, Seattle, USA)

C12-02 Endoplasmic reticulum chaperones control developmental buffering under thermal stress
Sato, Atsuko (Ochanomizu University, JPN); Shimeld, Seb (University of Oxford, GBR)

C12-03 Genetic basis of petal number variation
Monniaux, Marie (Max Planck Institute for Plant Breeding Research, Köln, DEU); Pieper, Bjorn (Max Planck Institute for Plant Breeding Research, Köln, DEU); Hay, Angela (Max Planck Institute for Plant Breeding Research, Köln, DEU)

C12-04 Lineage-specific duplication of amphioxus CYP26-type retinoic acid degrading enzymes resulted in sub-functionalization of patterning and homeostatic roles in the embryo
Schubert, Michael (Sorbonne Université, Paris 06, FRA; Observatoire Océanologique de Villefranche-sur-Mer, FRA)

C12-05 Evolutionary comparison of gene regulatory networks for organogenesis
Arnone, M. Ina (Stazione Zoologica Anton Dohrn, Naples, ITA); Andrikou,

Carmen (Stazione Zoologica Anton Dohrn, Naples, ITA); Annunziata, Rossella (Stazione Zoologica Anton Dohrn, Naples, ITA); Cuomo, Claudia (Stazione Zoologica Anton Dohrn, Naples, ITA); Lowe, Elijah (Stazione Zoologica Anton Dohrn, Naples, ITA); Perillo, Margherita (Stazione Zoologica Anton Dohrn, Naples, ITA)

14.00 – 15.40 Symposium S13:

Integrating the genotype-phenotype map with concepts of evolutionary-developmental biology

STORA SALEN

Organizers: Claudius Kratochwil and Joost Woltering
Chairs: Claudius Kratochwil and Joost Woltering

S13-01 Adaptive divergence and the dynamics of the genotype-phenotype map
Parsons, Kevin (University of Glasgow, GBR)

S13-02 The evo-devo and physics of skin appendages and skin colours in reptiles
Milinkovitch, Michel C. (University of Geneva, CHE)

S13-03 Molecular mechanism and evolutionary process of female-limited Batesian mimicry in Papilio butterfly.
Fujiwara, Haruhiko (University of Tokyo, JPN)

S13-04 Floral organ specification: evolutionarily conserved master regulators with variable target genes
Kaufmann, Kerstin (University of Potsdam, DEU)

14.00 – 15.40 Symposium S14:

Progress in animal phylogeny and its impact on the evolution of organ systems

Organizer: Andreas Hejnol

SAL B

Chair: Andreas Hejnol

S14-01 The role of Xenacoelomorpha in understanding the evolution of animal diversity
Cannon, Joie (Naturhistoriska Riksmuseet, Stockholm SWE); Vellutini, Bruno (Sars Centre, Bergen, NOR); Jondelius, Ulf (Naturhistoriska Riks-

museet, Stockholm SWE); Hejnol, Andreas (Sars Centre, Bergen, NOR)

S14-02 Ancient deuterostome origins of a cis-regulatory element involved in vertebrate forebrain patterning
Lowe, Christopher J. (Stanford University, USA); Minor, Paul (Stanford University, USA); Yao, Yao (University of Pennsylvania, USA); Pani, Ariel (University of Chicago, USA); Epstein, Douglas (University of Pennsylvania, USA)

S14-03 How small-scale meiofauna may inform on large-scale evolution, of the nervous system in Spiralia.
Worsaae, Katrine (University of Copenhagen, DEN)

S14-04 The developmental basis for the recurrent evolution of deuterostomy and protostomy
Martín-Durán, José M. (Sars Centre, Bergen, NOR)

14.00 – 15.40 Symposium S15:
The evo-devo of domestication

Organizers: Marcelo Sánchez-Villagra and Leif Andersson

SAL C Chairs: Marcelo Sánchez-Villagra and Leif Andersson

S15-01 The genetic basis for crop domestication
Purugganan, Michael (New York University, USA)

S15-02 Genetics of animal domestication
Andersson, Leif (Uppsala University, SWE)

S15-03 Does paedomorphism and neoteny explain the cranial morphology of domestic animals
Dobney, Keith (University of Liverpool, GBR)

S15-04 Skeletal growth and life history evolution in domestic dogs
Geiger, Madeleine (University of Zurich, CHE); Sánchez-Villagra, Marcelo R. (University of Zurich)

14.00 – 15.40 Symposium S16:
Branching across the tree of life

Organizers: Yoan Coudert and Hélène Adam

K3/K4 Chairs: Yoan Coudert and Thomas Harrop

S16-01 Branching in Seed Plants : facts, questions and perspectives

Edelin, Claude (French Institute of Pondacherry, IND)

S16-02 Branching in the brown alga Ectocarpus, from genetic variations to computer simulation: what do we gain?
Charrier, Bénédicte (Station Biologique Roscoff, FRA)

S16-03 From networks to function - computational models of organogenesis
Iber, Dagmar (ETH, Zurich, CHE)

S16-04 Modelling and analysis of growth and form in branching scleractininan corals
Kaandorp, Jaap A. (University of Amsterdam, NLD)

16.10 – 17.10 Contributed Session C13: Biomimetics – evolutionary inspired engineering

Organizer: Naomi Nakayama

STORA SALEN

Chair: Naomi Nakayama

C13-01 Evolutionary biomimetics: tracing the natural history of biological designs
Nakayama, Naomi (University of Edinburgh, GBR)

C13-02 Nature vs robotics: from plants and animals to soft robots
Mazzolai , Barbara (Istituto Italiano di Tecnologia, Pontedera, ITA)

C13-03 Evolutionary origin of „snapping" shrimps: Crossing the gap between pinching and snapping claws
Kaji , Tomonari (University of Alberta, CAN); Anker, Arthur (Museu Paraense Emílio Goeldi, Belém, BRA); Wirkner, Christian (Universität Rostock, DEU); Palmer, A. Richard (University of Alberta, CAN)

C13-04 Engineering trades-off with biology
Vincent, Julian (University of Oxford, GBR)

16.10 – 17.10 Contributed Session C14: Progress in animal phylogeny and its impact on the evolution of organ systems

SAL B

Chair: Katrine Worsaae

C14-01 Xenacoelomorpha and the origin of excretory organs
Andrikou, Carmen (Sars Centre, Bergen, NOR); Thiel, Daniel (Sars Centre, Bergen, NOR); Ruiz-Santiesteban, Antonio-Juan (Sars Centre, Bergen, NOR); Hejnol, Andreas (Sars Centre, Bergen, NOR)

C14-02 Embryogenesis of the sponge Amphimedon queenslandica and the evolution of metazoan developmental hallmarks
Larroux, Claire (University of Queensland, Brisbane, AUS); Richards, Gemma (University of Queensland, Brisbane, AUS); Nakanishi, Nagayasu (University of Florida, USA); Adamska, Maja (Autralian National University, Canberra, AUS); Degnan, Bernard (University of Queensland,

Brisbane, AUS)

C14-03 Molluscan MorphoEvoDevo: The morphogenetic and molecular basis of body plan evolution in the most diverse animal phylum
Wanninger, Andreas (University of Vienna, AUT)

C14-04 Conserved traits of spiralian development in the cell lineage and molecular patterning of the bryozoan Membranipora membranacea
Vellutini, Bruno C. (Sars Centre, Bergen, NOR); Martín-Durán, José M. (Sars Centre, Begen, NOR); Hejnol, Andreas (Sars Centre, NOR)

16.10 – 17.10 Contributed Session C15:
Contributions to Evo-devo

SAL C

Chair: Jannik Vollmer

C15-01 Growth control during development
Vollmer, Jannik (ETH Zurich, CHE)

C15-02 Dynamics of the circulation system during development of a colonial chordate are driven by the activity of multiple vertebrate-like hearts
Gasparini, Fabio (Università degli Studi di Padova, ITA); Cognolato, Moira (Università degli Studi di Padova, ITA); Salamon, Davide (Università degli Studi di Padova, ITA); Donaggio, Elisa (Università degli Studi di Padova, ITA); Viviani, Laura (Università degli Studi di Padova, ITA); Manni, Lucia (Università degli Studi di Padova, ITA)

C15-03 Patterns of oligomerization and carpel reduction in angiosperm gynoecia
Sokoloff, Dmitry D. (Moscow State University, RUS); Fomichev, Constantin I. (Moscow State University, RUS); Karpunina, Polina V. (Moscow State University, RUS); Nuraliev, Maxim S. (Moscow State University, RUS); Oskolski, Alexei A. (University of Johannesburg, ZAF; V.L. Komarov Botanical Institute of Russian Academy of Sciences, St Petersburg, RUS); Remizowa, Margarita V. (Moscow State University, RUS)

C15-04 Potential developmental constraints on vertebrate bodyplan evolution
Irie, Naoki (University of Tokyo, JPN); Hu, Haiyang (CAS-MPG Partner Institute for Computational Biology, Chinese Academy of Sciences, CHN); Guo, Song (CAS-MPG Partner Institute for Computational Biology, Chinese Academy of Sciences, CHN); Uesaka, Masahiro (University of Tokyo, JPN); Shimai, Kotaro; Lu, Tsai-Ming; Li, Fang, Fujimoto, Satoko; Ishikawa, Masato; Liu, Shiping; Sasagawa, Yohei; Zhang, Guojie; Kuratani, Shigeru; Yu, Jr-Kai; Kusakabe, Takehiro G. (EXPANDE Consortium); Khaitovich, Philipp (CAS-MPG Partner Institute for Computational Biology, Chinese Academy of Sciences, CHN)

16.10 – 17.10 Contributed Session C16:
Branching across the tree of life

K3/K4 Chairs: Yoan Coudert and Thomas Harrop

C16-01 Mechanisms underlying the parallel evolution of inflorescence phenotype during independent domestication of African and Asian rice
Harrop, Thomas (Institut de Recherche pour le Développement (IRD), Montpellier, FRA)

C16-02 Gastrovascular branching morphogenesis in the jellyfish Aurelia aurita
Cornelissen, Annemiek J. M. (CNRS & Université Paris-Diderot, FRA); Song, Solène (CNRS & Université Paris-Diderot, FRA); Gambini, Camille (CNRS & Université Paris-Diderot, FRA); Peaucelle, Alexi (CNRS & Université Paris-Diderot, FRA); Dantan, Phillipe (CNRS & Université Paris-Diderot, FRA); Balavoine, Guillaume (CNRS & Université Paris-Diderot, FRA)

C16-03 Hormonal control and evolution of branching forms in mosses
Coudert, Yoan (CNRS/Museum National d'Histoire Naturelle Paris, FRA); Palubicki, Wojtek (Adam Mickiewicz University in Poznań, POL); Bell, Neil (Royal Botanic Garden Edinburgh, Scotland, GBR); Leyser, Ottoline (University of Cambridge, GBR); Harrison, J. (University of Bristol, GBR)

C16-04 Modelling the development and diversity of leaves
Runions, Adam (Max Planck Institute for Plant Breeding Research, Köln, DEU); Prusinkiewicz, Przemyslaw (University of Calgary, CAN); Tsiantis, Miltos (Max Planck Institute for Plant Breeding Research, Köln, DEU)

17.20 – 18.00 Keynote Lecture (K3)
A trick of the light? Petal surface structures influence animal behaviour
STORA SALEN Beverley Glover
(University of Cambridge, GBR)
Chair: Graham Budd

18.00 – 20.00 Poster Session 2
FLOOR 6 (odd numbers)

09.00 – 10.40

Symposium S17:
Evolutionary developmental genomics

STORA SALEN

Organizers: David Ferrier and Sebastian Shimeld
Chairs: David Ferrier and Sebastian Shimeld

S17-01 Identifying the triggers of animal origins: what protists are telling us
Ruiz-Trillo, Iñaki (Pompeu Fabra University, Barcelona, ESP)

S17-02 Developmental genomics of sponges
Adamska, Maja (Australian National University, Canberra, AUS)

S17-03 Denser taxon sampling in genomics and transcriptomics allows to test hypothesis about the evolution of development and morphology
Hejnol, Andreas (Sars Centre, Bergen, NOR)

S17-04 The genome of the medusozoan Clytia hemisphaerica and life-cycle stage dependent gene expression
Copley, Richard (CNRS, Biologie du Développement de Villefranche sur mer, FRA)

09.00 – 10.40

Symposium S18:
Serial homology and segmentation

K3/K4

Organizer: Rui Diogo
Chair: Rui Diogo

S18-01 A gene regulatory network perspective on homology and serial homology
Wagner, Günter (Yale University, USA)

S18-02 Surprising developmental, evolutionary, pathological and comparative perspectives on serial homology of the head and limbs/fins: from dissimilarity to derived serial similarity
Diogo, Rui (Howard University, USA); Esteve-Altava, Borja (Royal Veterinary College, London, GBR); Molnar, Julia (Howard University, USA); Ziermann, Janine (Howard University, USA)

S18-03 The rise in complexity of the vertebral column

Galis, Frietson (Naturalis Biodiversity Center, NLD)

S18-04 A paleontological perspective on the serial homology of appendages and sexual organs
Johanson, Zerina (Natural History Museum London, GBR); Trinajstic, Kate (Curtin University, Perth, AUS)

09.00 – 10.40 Symposium S19:
Evolution of plant and animal epidermal patterns

SAL C

Organizer: Beverley Glover
Chair: Beverley Glover

S19-01 Land plants recruited the ancient membrane anchored calpain DEFECTIVE KERNEL1 (DEK1) to monitor and promote epidermis cell fate
Demko, Viktor (Norwegian University of Life Sciences, Ås, NOR); Johansen, Wenche (Hedmark University of Applied Sciences, Hamar, NOR); Ako, Eugene (Hedmark University of Applied Sciences, Hamar, NOR); Perroud, Pierre-François (Philipps-University Marburg, DEU); Owens, Ray (Harwell Science and Innovation Campus, Oxfordshire, GBR); De Moraes, Isabel (Harwell Science and Innovation Campus, Oxfordshire, GBR); Gevaert, Kris (VIB, Ghent, BEL); Olsen, Odd-Arne (Norwegian University of Life Sciences, Ås, NOR)

S19-02 The evolution of the MBW protein complex
Airoldi, Chiara (University of Cambridge, GBR); Brockington, Samuel (University of Cambridge, GBR); Glover, Beverley (University of Cambridge, GBR)

S19-03 Stomatal patterning in land plants
Rudall, Paula (Royal Botanic Gardens, Kew, GBR)

S19-04 How did the butterfly get its blue colour?
Nadeau, Nicola J. (The University of Sheffield, GBR); Curran, Emma (The University of Sheffield, GBR)

09.00 – 10.40 Symposium S20:
Micro-evo-devo – integrating evolution, development and population genetics

K3/K4

Organizers: Sebastian Kittelmann and Nico Posnien
Chairs: Sebastian Kittelmann and Nico Posnien

S20-01 A single nucleotide polymorphism in eyeless/Pax6 drives natural variation in eye size
Ramaekers, Ariane (KU Leuven, BEL); Weinberger, Simon (KU Leuven, BEL); Claeys, Annelies (KU Leuven, BEL); Jan, Jiekun (KU Leuven, BEL); Wolf, Reinhard (KU Leuven, BEL); Buchner, Erich (KU Leuven, BEL); Hassan, Bassem A. (KU Leuven, BEL)

S20-02 Evolution and development of Drosophila male genitalia

Santos Nunes, M. Daniela (Oxford Brookes University, GBR)

S20-03 Developmental crosstalk in root system adaptation to acidic soil
Hardtke, Christian (UNIL, Lausanne, CHE)

S20-04 The quest for understanding the genetic and developmental basis of morphological shape variation in the house mouse
Pallares, Luisa F. (MPI Evolutionary Biology, Plön, DEU); Tautz, Diethard (MPI Evolutionary Biology, Plön, DEU)

11.10 – 12.25 Contributed Session C17:
Evolutionary developmental genomics

STORA SALEN Chairs: Sebastian Shimeld and David Ferrier

C17-01 Nemertean and phoronid genomes reveal lophotrochozoan evolution and bilaterian head origin
Luo, Yi-Jyun (Graduate University, Onna, Okinawa, JPN); Kanda, Miyuki (Graduate University, Onna, Okinawa, JPN); Koyanagi, Ryo (Graduate University, Onna, Okinawa, JPN); Hisata, Kanako (Graduate University, Onna, Okinawa, JPN); Satoh, Noriyuki (Graduate University, Onna, Okinawa, JPN)

C17-02 Functional diversity of bZIP transcription factors in the sponge Amphimedon queenslandica: insights into the ancestral animal regulatory genome
Jindrich, Katia (The University of Queensland, Brisbane, AUS); Roper, Kathrein E. (The University of Queensland, Brisbane, AUS); Lemon, Sussan (The University of Queensland, Brisbane, AUS); Yuen, Benedict (The University of Queensland, Brisbane, AUS); Degnan, Sandie (The University of Queensland, Brisbane, AUS); Degnan, Bernard (The University of Queensland, Brisbane, AUS)

C17-03 The evolution of developmental gene expression programs in mammals
Cardoso-Moreira, Margarida (University of Heidelberg, DEU); Kaessmann, Henrik (University of Heidelberg, DEU)

C17-04 Pre-metazoan origin of animal microRNAs
Bråte, Jon (University of Oslo, NOR); Neumann, Ralf S. (University of Oslo, NOR); Fromm, Bastian (Oslo University Hospital, NOR); Haraldsen, Arthur A. B. (University of Oslo, NOR); Grini, Paul E. (University of Oslo, NOR); Shalchian-Tabrizi, Kamran (University of Oslo, NOR)

C17-05 Discovering the genomic basis underlying species' phenotypic differences
Hiller, Michael (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU)

11.10 – 12.25 Contributed Session C18:

Serial homology and segmentation

SAL B

Chair: Sandro Minelli

C18-01 **Serial homology in plants from a evo-devo perspective**
Minelli, Alessandro (University of Padova, ITA)

C18-02 **Amphioxus illuminates the origin of the vertebrates' head**
Aldea, Daniel (Observatoire Oceanologique de Banyuls-sur-Mer, FRA); Escrivá, Hector (Observatoire Oceanologique de Banyuls-sur-Mer, FRA); Bertrand, Stéphanie (Observatoire Oceanologique de Banyuls-sur-Mer, FRA)

C18-03 **New clues on origins of axial skeleton regionalization and appendicular skeleton: Ontogenetic evidence from fossil and extant jawless vertebrates**
Chevrinais, Marion (Université du Québec à Rimouski, CAN); Johanson, Zerina (Natural History Museum London, GBR); Trinajstic, Kate (Curtin University, Perth, AUS); Long, John (Flinders University, Adelaide, AUS); Morel, Catherine (Université du Québec à Rimouski, CAN); Renaud, Claude B. (Canadian Museum of Nature, Ottawa, CAN); Cloutier, Richard (Université du Québec à Rimouski, CAN)

C18-04 **HoxD patterning of the fin-fold compartment of basal gnathostomes: Implications for the fin to limb transition**
Tulenko, Frank J. (Kennesaw State University, USA); Massey, James L. (University of Colorado Boulder, USA); Davis, Marcus C. (Kennesaw State University, USA)

C18-05 **Developmental morphology of the head in sturgeons (Acipenseriformes: Acipenseridae)**
Warth, Peter (FSU Jena, DEU); Konstantinidis, Peter (Virginia Institute of Marine Science, USA); Hilton, Eric J. (Virginia Institute of Marine Science, USA); Naumann, Benjamin (FSU Jena, DEU); Olsson, Lennart (FSU Jena, DEU)

11.10 – 12.25

Contributed Session C19: Evolution of plant and animal epidermal patterns

SAL C

Chair: Beverley Glover

C19-01 **How to spot a Daisy**
Mellers, Greg (University of Cambridge, GBR); Glover, Beverley (University of Cambridge, GBR); Ellis, Allan (University of Stellenbosch, ZAF)

C19-02 **Root Hair Development in Arabis alpina**
Mapar, Mona (Max Planck Institute for Plant Breeding Research, Köln, DEU)

C19-03 **Sculpting the surface: understanding the development, function and evolution of nanopatterning in petals**
Moyroud, Edwige (University of Cambridge, GBR)

C19-04 Comparative genomics suggests evolutionary adaptations of epidermal differentiation in squamate reptiles
Eckhart, Leopold (Medical University of Vienna, AUT); Holthaus, Karin B. (Medical University of Vienna, AUT); Mlitz, Veronika (Medical University of Vienna, AUT); Strasser, Bettina (Medical University of Vienna, AUT); Tschachler, Erwin (Medical University of Vienna, AUT); Alibardi, Lorenzo (University of Bologna, Italy)

C19-05 Conspicuous coloration in Trachemys scripta: mechanism of ontogenetic color change and the first description of iridophores in a turtle
Brejcha, Jindřich (Charles University in Prague, CZE; National Museum, Prague, CZE); Kleisner, Karel (Charles University in Prague, CZE); Font, Enrique (University of Valencia, ESP))

11.10 – 12.25 Contributed Session C20:
Evolution of gene regulatory networks and the origin of novelties I

K3/K4 Chair: Pete Olson

C20-01 Wing homologs in a crustaceans
Tomoyasu, Yoshinori (Miami University, Oxford, USA); Clark-Hachtel, Courtney (Miami University, Oxford, USA); Patel, Nipam (University of California Berkeley, USA); Bellés, Xavier (Institut de Biologia Evolutiva, Barcelona, ESP); Buschbeckm, Elke (University of Cincinnati, USA)

C20-02 Evolution of gene regulatory networks and the origin of novelties
Clark, Erik (University of Cambridge, GBR); Akam, Michael (University of Cambridge, GBR)

C20-03 Evolution of gene regulatory networks and the origin of novelties Investigating origins of butterfly eyespots via gene regulatory network co-option
Connahs, Heidi (National University of Singapore, SGP); Das Gupta, Mainak (National University of Singapore, SGP); Monteiro, Antónia (National University of Singapore, SGP)

C20-04 A phylogenetic framework for the carpel development regulation: mixing and matching old with new
Becker, Annette (Justus-Liebig-University Giessen, DEU); Pfannebecker, Kai C. (Justus-Liebig-University Giessen, DEU)

C20-05 From planarians to parasitism: Wnt/Hedgehog signalling controls AP patterning during larval and strobilar development in tapeworms
Jarero, Francesca (Natural History Museum, London, GBR); Koziol, Uriel (Universidad de la República, Montevideo, URY); Olson, Pete (Natural History Museum, London, GBR)

13.50 – 15.30 Symposium S21:

The evolution of gene regulatory networks and the origins of novelties

STORA SALEN

Organizers: Heidi Connahs and Antónia Monteiro
Chair: Heidi Connahs and Antónia Monteiro

S21-01 **Evolution of transcription factor function in development**
Hinman, Veronica (Carnegie Mellon University, Pittsburgh, USA); Cary, Greg (Carnegie Mellon University, Pittsburgh, USA); Jarvela, Alys (Carnegie Mellon University, Pittsburgh, USA); Francolini, Rene (Carnegie Mellon University, Pittsburgh, USA)

S21-02 **Role of novel genes in the evolution of behavioral and physiological novelty**
Johnson, Brian R. (University of California, Davis, USA)

S21-03 **Tracing the mosaic ancestry of a novel tissue organizer's regulatory circuitry**
Glassford, B. (University of Pittsburgh, USA); Smith, Sarah J. (University of Pittsburgh, USA); Rebeiz, Mark (University of Pittsburgh, USA)

S21-04 **Gene regulatory complexity in chordate spinal patterning**
Shimeld, Sebastian (University of Oxford, GBR)

13.50 – 15.30 Symposium S22:

The vertebrate limb as an evolving dynamical system

SAL B

Organizers: Gerd Müller and Stuart A. Newman
Chair: Gerd Müller

S22-01 **Dynamics and phylogenomics of the two-galectin tetrapod limb patterning network**
Newman, Stuart (New York Medical College, Valhalla, USA)

S22-02 **Development and evolution of the jerboa limb skeleton**
Cooper, Kimberley (Harvard Medical School, Boston, USA)

S22-03 **Changing while staying the same: Self-organized patterning allows a deeply-conserved gene circuit to produce varying skeletal arrangements during limb evolution**
Sharpe, James (Centre for Genomic Regulation, Barcelona, ESP)

S22-04 **Avian digit identity in light of digit formation models**
Capek, Daniel (Institute of Science and Technology, Gugging, AUT); Müller, Gerd (University of Vienna, AUT)

13.50 – 15.30 Symposium S23:

The role of developmental evolution in reproductive medicine

SAL C

Organizers: Mihaela Pavlicev and Günter Wagner

Chairs: Mihaela Pavlicev and Günter Wagner

S23-01 Marsupials as biomedical models for reproduction and development
Renfree, Marilyn B. (University of Melborne, AUS)

S23-02 How do mammals beat the heat? The evolution of the inflammatory response in pregnancy and the origin of decidual stromal cells
Chavan, Arun R. (Yale University, USA); Griffith, Oliver (Yale University, USA); Maziarz, Jamie (Yale University, USA); Tzika, Athanasia (University of Geneva, CHE); Milinkovitch, Michel (University of Geneva, CHE); Wagner, Günter (Yale University, USA)

S23-03 Placenta transcriptomics and the evolution of obstetrical syndromes
Armstrong, Don L. (University of Illinois, Urbana-Champaign, USA); McGowen, Michael R. (Queen Mary, University of London, GBR); Weckle, Amy (University of Illinois, Urbana-Champaign, USA); Caravas, Jason (Wayne State University School of Medicine, Detroit, USA); Agnew, Dalen (Michigan State University, East Lansing, USA); Benirschke, Kurt (UC San Diego, USA); Savage-Rumbaugh, Sue (Bonobo Hope Sanctuary, Iowa, USA); Nevo, Eviatar (University of Haifa, ISR); Kim, Chong J. (WSU School of Medicine, Detroit, USA); Wagner, Günter (Yale University, USA); Romero, Roberto (WSU School of Medicine, Detroit, USA); Wildman, Derek E. (University of Illinois, Urbana-Champaign, USA)

S23-04 Modularity and evolution in the placenta
Elliot, Michael G. (University of Cambridge, GBR)

13.50 – 15.30 Symposium S24:
Symmetry in plants and animals

K3/K4

Organizers: Sophie Nadot, Catherine Damerval and Vincent Debat
Chairs: Sophie Nadot and Vincent Debat

S24-01 Symmetry and asymmetry of segmentation
Fusco, Giuseppe (University of Padova, ITA)

S24-02 From chiral shells to chiral cells
Davison, Angus (University of Nottingham, GBR)

S24-03 Evolution of floral symmetry in Lamiales
Zhong, Jinshun (University of Vermont, Burlington, USA); Kellogg, Elizabeth A. (Donald Danforth Plant Science Center, Creve Coeur, USA)

S24-04 Characterization of CYCLOIDEA-like genes in Proteaceae, a basal eudicot family with multiple shifts in floral symmetry
Damerval, Catherine (CNRS, Gif/Yvette, FRA); Citerne, Hélène (Université Paris-Sud, FRA); Reyes, Elisabeth (Université Paris-Sud, FRA); le Guilloux, Martine (Université Paris-Sud, FRA); Delannoy, Etienne (CEA, Saint-Paul-lez-Durance, FRA); Simonnet, Franck (Université Paris-Sud, FRA); Sauquet, Hervé (Université Paris-Sud, FRA); Weston, Peter H. (Royal Botanic

Garden, Sydney, AUS); Nadot, Sophie (Université Paris-Sud, FRA)

16.00 – 17-00 Contributed Session C21:
Evolution of gene regulatory networks and the origin of novelties II

STORA SALEN Chair: M. Ina Arnone

C21-01 **Evolution of early acting events in development: Regulation and evolution of complex gene networks**
Cridge, Andrew G. (University of Otago, Dunedin, NZL); Permina, Elizabeth (University of Otago, Dunedin, NZL); Dearden, Peter K. (University of Otago, Dunedin, NZL)

C21-02 **Convergent cis-regulatory modification leads to the evolution of mimetic wing patterns in Heliconius butterflies**
Hanly, Joe (University of Cambridge, GBR); Supple, Megan (Smithsonian Tropical Research Institute, PAN); Jiggins, Chris (University of Cambridge, GBR)

C21-03 **Uncovering the development of a novel abdominal structure in Black Scavenger Flies**
Rajaratnam, Gowri (National University of Singapore, SGP); Su, Kathy (National University of Singapore, SGP)

C21-04 **Global analysis of dorsoventral patterning in the wasp Nasonia reveals extensive incorporation of novelty in a regulatory network**
Pers, Daniel (University of Illinois at Chicago, USA)

16.00 – 17.00 Contributed Session C22:
The vertebrate limb as an evolving dynamical system

SAL B Chair: Stuart A. Newman

C22-01 **Regeneration and preaxial polarity in limb development in tetrapod evolution**
Fröbisch, Nadia B. (Museum für Naturkunde, Berlin, DEU); Bickelmann, Constanze (Museum für Naturkunde, Berlin, DEU); Olori, Jennifer (SUNY Oswego, USA); Witzmann, Florian (Museum für Naturkunde, Berlin, DEU)

C22-02 **Preaxial polarity in limb development - a comparison of larval and direct developing salamanders (Caudata) to other tetrapods**
Triepel, Sandra (Museum für Naturkunde, Berlin, DEU); Müller, Hendrik (Friedrich-Schiller-Universität Jena, DEU); Mitgutsch, Christian (Museum für Naturkunde, Berlin, DEU); Fröbisch, Nadia B. (Museum für Naturkunde, Berlin, DEU)

C22-03 **Migrating muscle precursors contribute to the formation of appendicular muscles of cartilaginous fishes**
Tanaka, Mikiko (Tokyo Institute of Technology, JPN); Okamoto, Eri (Tokyo Institute of Technology, JPN); Kusakabe, Rie (RIKEN, Kobe, JPN); Kuraku,

Shigehiro (RIKEN, Kobe, JPN); Hyodo, Susumu (University of Tokyo, JPN); Onimaru, Koh (Tokyo Institute of Technology, JPN); Kuratani, Shigeru (RIKEN, Kobe, JPN)

C22-04 Longshanks mice as a tool to study the cell and molecular determinants of limb length variation within populations
Marchini, Marta (University of Calgary, CAN); Rolian, Campbell (University of Calgary, CAN)

16.00 – 17.00 Contributed Session C23:
Developmental evolution and reproductive medicine

SAL C

Chairs: Peter Holland

C23-01 Light-induced oocyte maturation in the hydrozoan Clytia hemisphaerica
Quiroga Artigas, Gonzalo (Sorbonne Université, Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA)

C23-02 Molecular evolution of the totipotent mammalian embryo
Holland, Peter (University of Oxford, GBR); Dunwell, Thomas (University of Oxford, GBR); Maeso, Ignacio (University of Oxford, GBR; CABD, Seville, ESP); Wyatt, Chris (CRG, Barcelona, ESP); Marletaz, Ferdinand (University of Oxford, GBR; OIST, JPN); Irimia, Manuel (CRG, Barcelona, ESP)

C23-03 Cavefish evolution as a natural model for metabolic diseases
Rohner, Nicolas (Stowers Institute for Medical Research, Kansas City, USA); Aspiras, Ariel (Harvard Medical School, USA); Tabin, Cliff (Harvard Medical School, USA)

C23-04 Can human cranial developmental malformations be a model for evolutionary change?
Rasskin-Gutman, Diego (University of Valencia, ESP); Esteve-Altava, Borja (The Royal Veterinary College, London, GBR); Sanchís García, Juan Manuel (University of Valencia, ESP)

16.00 – 17.00 Contributed Session C24:
Micro-evo-devo – integrating evolution, development and population genetics

K3/K4

Chairs: Luke Hayden and Peter Dearden

C24-01 Winding paths in development: the link between developmental and morphological variation in mouse molar teeth
Hayden, Luke (LBMC, ENS de Lyon, FRA); Rubod, Alain (LBMC, ENS de Lyon, FRA); Sémon, Marie (LBMC, ENS de Lyon, FRA); Pantalacci, Sophie (LBMC, ENS de Lyon, FRA)

C24-02 Evolutionary novelty in a butterfly wing pattern through enhancer shuffling
Wallbank, Richard (University of Cambridge, GBR)

C24-03 Origin and evolution of phenotypic plasticity in eyespot size across nymphalid butterflies
Bhardwaj, Shivam (National University of Singapore, SGP); Monteiro, Antónia (National University of Singapore; Yale-NUS College, SGP)

C24-04 The genetic and developmental bases of genital evolution between Drosophila species
Mendes, Claudia C. (Oxford Brookes University, GBR); Hagen, Joanna F. (Oxford Brookes University, GBR); Tanaka, Kentaro M. (Tokyo Metropolitan University, JPN); Gaspar, Pedro M. (Oxford Brookes University, GBR); Herbet, Mathew R. (Oxford Brookes University, GBR); Nunes, M. Daniela S. (Oxford Brookes University, GBR); McGregor, Alistair P. (Oxford Brookes University, GBR)

17.05 – 17.15 Student Poster Prizes
STORA SALEN

17.15 – 17.55 Keynote Lecture (K4)
Dear ants, what have you done for Evo-devo?
STORA SALEN
Ehab Ebouheif
(McGIll University, CAN)
Chair: Frietson Galis

17.55 – 18.00 Conference Closing
STORA SALEN

18.10 – 19.00 EED Business Meeting
STORA SALEN

19.30 Conference Dinner (Castle, see map) - music from 19.15

Posters

Posters

P-001 Investigating the potential regulation of gap gene homologues by pair-rule genes in the red flour beetle Tribolium castaneum
Sharma, Rahul (University of Leeds, GBR); Peel, Andrew D. (University of Leeds, GBR)

P-002 Ediacaran developmental biology
Dunn, Frankie (University of Bristol, GBR)

P-003 Finite element analysis of abdominal appendage development in the sepsid Themira biloba
Peterson, Tim (University of Vienna); Müller, Gerd B. (University of Vienna, AUT); Bowsher, Julia (North Dakota State University, USA)

P-004 Analysis of Wnt genes and their embryonic expression patterns in the priapulid worm Priapulus caudatus
Hogvall, Mattias (Uppsala University, SWE); Budd, Graham E. (Uppsala University, SWE); Janssen, Ralf (Uppsala University, SWE)

P-005 A potential decapod shrimp model for getting insights into crustacean aquaculture and evolution
Chan, Ting-Fung (Chinese University of Hong Kong, CHN); Chu, Ka-Hou (Chinese University of Hong Kong, CHN); Hui, Ho-Lam; (Chinese University of Hong Kong, CHN)

P-006 Chemically perturbed axis formation: Can experimental phenotype data help in understanding the interconnectivity of laterality establishing processes ?
Petrasko, Anne (University of Vienna, AUT)

P-007 Prenatal androgen exposure: Effects on human facial shape and its perception
Schaefer, Katrin (University of Vienna, AUT); Windhager, Sonja (University of Vienna, AUT); Müller, Gerd B. (University of Vienna, AUT); Mitteroecker, Philipp (University of Vienna, AUT)

P-008 Insights into changes in regulation of gastrulation during evolution
Machačová, Simona (Institute of Molecular Genetics of the ASCR, v.v.i., Prague, CZE)

P-009 History and philosophy of biology and the Extended Evolutionary Synthesis: theoretical and historiographical perspectives from Latin America
Fàbregas-Tejeda, Alejandro (Universidad Nacional Autónoma de México,

MEX); Casanueva, Mario (Universidad Autónoma Metropolitana- Cuajimalpa, MEX); Vergara-Silva, Francisco (Universidad Nacional Autónoma de México, MEX)

P-010 Causality in complex archaeo-societies and the extended evolutionary synthesis: an example from the Archaic and Preclassic periods in the Tehuacán Valley (Mesoamerica)
Vergara-Silva, Francisco (Universidad Nacional Autónoma de México, MEX)

P-011 Tol2 mediated transgenesis in the midas cichlid species complex (Amphilophus spp.)
Sefton, Maggie (University of Konstanz, DEU); Liang, Yipeng (University of Konstanz, DEU); Kratochwil, Claudius (University of Konstanz, DEU); Meyer, Axel (University of Konstanz, DEU)

P-012 Evaluation of horizontally transferred genes in ten genomes of stick insects
Jaron, Kamil S. (University of Lausanne, CHE); Bast, Jens (University of Lausanne, CHE); Schwander, Tanja (University of Lausanne, CHE); Robinson-Rechavi, Marc (University of Lausanne, CHE; Swiss Institute of Bioinformatics, Lausanne, CHE)

P-013 Postembryonic development of the ctenophores inferred from gene expression data
Røsæg, Line L. (University of Oslo, NOR); Evenstad, Andreas (University of Oslo, NOR); Andresen, Ina J. (University of Oslo, NOR); Bråte, Jon (University of Oslo, NOR); Shalchian-Tabrizi, Kamran (University of Oslo, NOR)

P-014 Evolution of non-coding RNAs in ctenophores)
Evenstad, Andreas (University of Oslo, NOR); Røsæg, Line L. (University of Oslo, NOR); Andresen, Ina J. (University of Oslo, NOR); Shalchian-Tabrizi, Kamran (University of Oslo, NOR); Bråte, Jon (University of Oslo, NOR)

P-015 Investigation of the cytoskeletal dynamics during spiral cleavage
Hsieh, Yu-Wen (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU); Handberg-Thorsager, Mette (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU); Tomancak, Pavel (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU)

P-016 A histological study of limb regeneration of the salamander Ambystoma mexicanum
Bothe, Vivien (Museum für Naturkunde, Berlin, DEU); Mahlow, Kristin (Museum für Naturkunde, Berlin, DEU); Fröbisch, Nadia B. (Museum für Naturkunde, Berlin, DEU)

P-017 Cobalamin receptors in vertebrates: transitions to novel functions?
Ruivo, Raquel (University of Porto, PRT); Oliveira, Diogo (University of Porto, PRT); Castro, L. Filipe C. (University of Porto, PRT)

P-018 A pipeline for the systematic identification of non-redundant full-ORF

cDNAs for polymorphic and evolutionary divergent genomes: application to the ascidian Ciona intestinalis

Rothbächer, Ute (University of Innsbruck, AUT; CNRS/Université Aix-Marseille, FRA); Gilchrist, Michael J. (The Francis Crick Institute, Mill Hill Laboratory, London, GRB); Lemaire, Patrick (CNRS/Université Montpellier, FRA)

P-019 Life-cycle traits of marsh frog Pelophylax ridibundus can be transformed without change in locus RC08604

Scobeyeva, Victoria A. (Moscow State University, RUS); Dmitrieva, Elena V. (Moscow State University, RUS); Burskaya, Valentina O. (Moscow State University, RUS); Lyapkov, Sergey M. (Moscow State University, RUS)

P-020 Long-term developmental arrest in the embryogenesis of the common toad (Bufo bufo) as a non-specific adaptation to adverse environmental conditions

Dmitrieva, Elena V. (Instituto Gulbenkian de Ciência, Lisboa, PRT); Hazbun, Alexis (Moscow State University, RUS)

P-021 Draft genomes of two marine cladocerans

Wai Tak, Leung R. (Chinese University of Hong Kong, CHN)

P-022 De novo myogenesis and neurogenesis during ascidian colony propagation

Prünster, Maria M. (University of Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA); Ricci, Lorenzo (University of Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA); Lotito, Sonia (University of Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA)

P-023 The origin of the vertebrate stomach: insights from the catshark gut development

Gonçalves, Odete (CIIMAR, POR; ICBAS, POR); Castro, Philipe (CIIMAR, Porto, PRT); Ferreira, Patrícia G. (CIIMAR, POR; ICBAS, POR); Mazan, Sylvie (SBR, Roscoff, FRA); Freitas, Renata (IBMC, Porto, POR); Wilson, Jonathan (CIIMAR, POR; Wilfrid Laurier University, Waterloo, CAN)

P-024 The evolution of the piRNA pathway - insights from the starlet sea anemone

Praher, Daniela (University of Vienna, AUT); Genikhovich, Grigory (University of Vienna, AUT); Zimmermann, Robert (University of Vienna, AUT); Moran, Yehu (Hebrew University of Jerusalem, ISR); Technau, Ulrich (University of Vienna, AUT)

P-025 Fog is rising: A signaling pathway used for morphogenesis across insects

Conrads, Kai H. (University of Cologne, DEU); Lynch, Jeremy A. (University of Illinois at Chicago, USA); Roth, Siegfried (University of Cologne, DEU)

P-026 Evolution of a Gene Regulatory Network for gut development downstream of Xlox and Cdx in two echinoderms
Cuomo, Claudia (Stazione Zoologica Anton Dohrn, Napoli, ITA); Lowe, Elijah K. (Stazione Zoologica Anton Dohrn, Napoli, ITA); Gómez-Skarmeta, José L. (Centro Andaluz de Biología del Desarrollo, Sevilla, ESP); Arnone, M. Ina (Stazione Zoologica Anton Dohrn, Napoli, ITA)

P-027 The iBeetle large-scale RNAi screen reveals new genes for dorsoventral pattern formation in Tribolium castaneum
Din Muhammad, Muhammad S. (University of Cologne, DEU); Roth, Siegfried (University of Cologne, DEU)

P-028 Dissecting the functional role of Wnt signalling in the development of Platynereis dumerilii
Zidek, Radim (Institute of Molecular Genetics of ASCR, v. v. i., Prague, CZE); Kozmik, Zbynek (Institute of Molecular Genetics of ASCR, v. v. i., Prague, CZE)

P-029 Molluscan Wnt gene expression and the evolution of morphological novelties
Rodríguez Monje, Sonia V. (University of Vienna, AUT)

P-030 The roles of the Wnt antagonists Axin and Lrp4 during embryogenesis of the red flour beetle Tribolium castaneums
Schröder, Reinhard (University of Rostock, DEU); Prühs, Romy (University of Rostock, DEU); Beermann, Anke (University of Tübingen, DEU)

P-031 Amphioxus SCP1: a case of retrogene replacement and co-option of regulatory elements adjacent to the ParaHox cluster
Garstang, Myles G. (University of St Andrews, GBR); Ferrier, David E.K. (University of St Andrews, GBR)

P-032 Evolution of microRNA target interactions in animals)
Nong, Wenyan (Chinese University of Hong Kong, CHN); Cheung, Fiona K. (Chinese University of Hong Kong, CHN); Leung, Ricky W. T. (Chinese University of Hong Kong, CHN); Huang, Dandan (Chinese University of Hong Kong, CHN); Holland, Peter W. H. (University of Oxford, GBR); Hui, Jerome H. L. (Chinese University of Hong Kong, CHN)

P-033 Whole genome duplications in two Asian horseshoe crabs
Hui, Jerome (Chinese University of Hong Kong, CHN); Chan, Ting F. (Chinese University of Hong Kong, CHN); Cheung, Siu G. (City University of Hong Kong, CHN); Kwan, Hoi S. (Chinese University of Hong Kong, CHN); Ngai, Sai M. (Chinese University of Hong Kong, CHN); Panagiotou, Gianni (University of Hong Kong, CHN); Qiu, Jian W. (Hong Kong Baptist University, CHN); Holland, Peter W. H. (University of Oxford, GBR)

P-034 A pycnogonid draft genome reveals different genomic situation to the euchelicerates

Cheung, Fiona K. M. (Chinese University of Hong Kong, CHN); Hui, Jerome H. L. (Chinese University of Hong Kong, CHN)

P-035 The polycistronic smORF milli-pattes is essential for Rhodnius prolixus embryogenesis
Tobias Santos, Vitória (Universidade Federal do Rio de Janeiro, Macaé, BRA); Nunes da Fonseca, Rodrigo (Universidade Federal do Rio de Janeiro, Macaé)

P-036 Genetics underlying the evolution of a key morphological innovation: the propelling fan of the water walking bug Rhagovelia sp.
Santos, M. Emilia (Institute of Functional Genomics of Lyon, FRA); Khila, Abderrahman (Institute of Functional Genomics of Lyon, FRA)

P-037 Investigating the evolution of the functional specificity of Wnt ligands
Holzem, Michaela (Oxford Brookes University, GBR); Gaspar, Pedro M. (Oxford Brookes University, GBR); McGregor, Alistair P. (Oxford Brookes University, GBR)

P-038 sp5 and nlk are expressed during tail development and regeneration in the European amphioxus.
Dailey, Simon (University of St Andrews, GBR); Somorjai, Ildiko (University of St Andrews, GBR)

P-039 Marine annelid larvae and evolution of Associative Learning
Chartier, Thomas (EMBL, Heidelberg, DEU); Arendt, Detlev (EMBL, Heidelberg, DEU)

P-040 Evolutionary innovation in vertebrate late development
Liu, Jialin (University of Lausanne, CHE); Robinson-Rechavi, Marc (University of Lausanne, CHE)

P-041 Statistical rule of variation in floral organ numbers
Kitazawa, Miho (Osaka University, JPN); Fujimoto, Koichi (Osaka University, JPN)

P-042 Elucidating the dynamics of the dorsoventral gene regulatory network in Tribolium castaneum
Frey, Nadine (University of Cologne, DEU); Stappert, Dominik (University of Cologne, DEU); Benton, Matthew (University of Cologne, DEU); Roth, Siegfried (University of Cologne, DEU)

P-043 Light perception in Amphioxus: insights into evolution of photoreception in vertebrates
Pergner, Jiri (Institute of Molecular Genetics of AS CR, Prague, CZE); Pantzartzi, Chrysoula N. (Biological centre in Vestec - BIOCEV, Vestec, CZE); Kozmik, Zbynek (Institute of Molecular Genetics of AS CR, Prague, CZE)

P-044 BMP signaling regulates left-right asymmetry in amphioxus

Soukup, Vladimir (Institute of Molecular Genetics of the AS CR, Prague, CZE); Kozmik, Zbynek (Institute of Molecular Genetics of AS CR, Prague, CZE)

P-045 Interpreting gene regulatory information of invertebrate chordate amphioxus: an insight from transgenic studies in amphioxus and fish
Kozmik, Zbynek (Institute of Molecular Genetics of AS CR, Prague, CZE); Kozmikova, Iryna (Institute of Molecular Genetics of AS CR, Prague, CZE)

P-046 Dual-rowed dentition of the Mexican axolotl develops from a common single dental primordium
Yamazaki, Yosuke (Charles University in Prague, CZE); Soukup, Vladimir (Institute of Molecular Genetics of the AS CR, Prague, CZE); Cerny, Robert (Charles University in Prague, CZE)

P-047 Convergent evolution of embryonic pigmentation in the Gerromorpha
Bonneton, François (Ecole Normale Supérieure de Lyon, FRA); Vargas-Lowman, Aidamalia (Ecole Normale Supérieure de Lyon, FRA); Armisén, David (Ecole Normale Supérieure de Lyon, FRA); Santos, M. Emilia (Ecole Normale Supérieure de Lyon, FRA); Abderrahman, Khila (Ecole Normale Supérieure de Lyon, FRA)

P-048 Computational representation and manual curation of homology relations between anatomical structures
Robinson-Rechavi, Marc (University of Lausanne, CHE); Niknejad, Anne (Swiss Institute of Bioinformatics, Laussanne, CHE); Bastian, Frederic B. (Swiss Institute of Bioinformatics, Laussanne, CHE)

P-049 Fluctuating asymmetry as an outcome of phenotypic plasticity: morphological responses of floral organs in Iris pumila to environmental heterogeneity
Radović, Sanja (University of Belgrade, SER); Manitašević Jovanović, Sanja (University of Belgrade, SER); Vuleta, Ana (University of Belgrade, SER); Tucić, Branka (University of Belgrade, SER); Klingenberg, Christian P. (University of Manchester, GBR)

P-050 Identification of differentially expressed genes of developing mouse and vole tooth
Das Roy, Rishi (University of Helsinki, FIN); Hallikas, Outi; University of Helsinki, FIN); Renvoisé, Elodie (University of Helsinki, FIN); Jernvall, Jukka (University of Helsinki, FIN)

P-051 Evolution and development of the limbs in the gecko Hemidactylus: a new squamate non-model organism
van der Vos, Wessel (Museum für Naturkunde, Berlin, DEU); Bickelmann, Constanze (Museum für Naturkunde, Berlin, DEU)

P-052 External gills of bichir develop by accelerated formation of all germ layers of the hyoid metamere
Stundl, Jan (Charles University in Prague, CZE); Soukup, Vladimir (Aca-

demy of Sciences of the Czech Republic, Prague, CZE); Minarik, Martin (Charles University in Prague, CZE); Metscher, Brian D. (University of Vienna, AUT); Jandzik, David (University of Colorado, Boulder, USA; Comenius University in Bratislava, SVK); Cerny, Robert (Charles University in Prague, CZE)

P-053 Miniaturization and ontogeny: a paleobiological approach
Pérez Ben, Celeste (University of Buenos Aires, ARG; State Museum of Natural History Stuttgart, DEU)

P-054 Developmental strategies of skeletogenesis in bichirs and sturgeons: comparative analysis of two disparate cranial architecturess
Pospisilova, Anna (Charles University in Prague, CZE); Stundl, Jan (Charles University in Prague, CZE); Minarik, Martin (Charles University in Prague, CZE); Gela, David (University of South Bohemia in České Budějovice, CZE); Cerny, Robert (Charles University in Prague, CZE)

P-055 Evolution and development of nectar spurs
Cullen, Ellen V. (University of Cambridge, GBR)

P-056 Unique variation in the active retinal peripheral zone among squamate reptiles
Eymann, Julia (University of Helsinki, FIN); Di-Poï, Nicolas (University of Helsinki, FIN)

P-057 Cells without borders: how syncytia and cells form the adult glass sponge body plan at metamorphosis
Leys, Sally (University of Alberta, CAN); Zaman, Afyqah Kamarul (University of Alberta, CAN); Boury-Esnault, Nicole (Aix Marseille Université, FRA)

P-058 Central complex development and evolution: cellular and genetic mechanisms
Farnworth, Max S. (Georg-August-University Göttingen, DEU); Koniszewski, Nikolaus B. (Georg-August-University Göttingen, DEU); Büscher, Marita (Georg-August-University Göttingen, DEU); Bucher, Gregor (Georg-August-University Göttingen, DEU)

P-059 Role of the Nodal signaling pathway in amphioxus neural induction
Florian, Luis A. L. (Observatoire Oceanologique de Banyuls-sur-mer, FRA)

P-060 Pelvic, Pectoral, Median: The developmental basis of fin evolution
Winkler, Viola (University of Vienna, AUT); Müller, Gerd B. (University of Vienna, AUT); Metscher, Brian D. (University of Vienna, AUT)

P-061 Exploring the biology of a three-gendered nematode
Tandonnet, Sophie (University of Warwick, GBR); Pires da Silva, Andre (University of Warwick, GBR)

P-062 The tubular collar cord of hemichordates and the chordate neural

tube: homology or homoplasy?
Kaul-Strehlow, Sabrina (University of Vienna, AUT)

P-063 Multiple origins of multicuspid teeth in squamate reptiles
Lafuma, Fabien (University of Helsinki, FIN); Salomies, Lotta (University of Helsinki, FIN); Van Hout, Maaike (University college Odisee, Ghent, BEL); Clavel, Julien F. (Ecole Normale Supérieure de Lyon, FRA); Di-Poï, Nicolas (University of Helsinki, FIN)

P-064 A comprehensive pipeline for identifiying lincRNAs on the basal-branching chordate Amphioxus
Herrera, Carlos (Universitat de Barcelona, ESP)

P-065 A comparative differential expression analysis approach to the study of Hox3/zen gene evolution in insects
Gurska, Daniela (University of Cologne, DEU); Panfilio, Kristen A. (University of Cologne, DEU)

P-066 Evolution of olfactory channels in Drosophila
Arguello, J. Roman (University of Lausanne, CHE); Abuin, Liliane (University of Lausanne, CHE); Benton, Richard (University of Lausanne, CHE)

P-067 Genetic paths underlying the convergent evolution of pigmented spots on fly wings
Hinaux, Hélène (Ludwig Maximilians Universität München, DEU); Arnoult, Laurent (Institut de Biologie du Développement de Marseille, FRA); Hein, Irina (Ludwig Maximilians Universität München, DEU); Prud'homme, Benjamin (Institut de Biologie du Développement de Marseille, FRA); Gompel, Nicolas (Ludwig Maximilians Universität München, DEU)

P-068 The sequencing and manual curation of the first water strider genome (Gerris buenoi)
Armisén, David (Institut de Génomique Fonctionnelle de Lyon, FRA); The water strider genome consortium

P-069 Genome-wide screening of early patterning genes in spider Parasteatoda tepidariorum
Iwasaki-Yokozawa, Sawa (JT Biohistory Research Hall, Takatsuki, JPN); Akiyama-Oda, Yasuko (Osaka Medical College, JPN); Oda, Hiroki (JT Biohistory Research Hall, Takatsuki, JPN)

P-070 Comparative tissue-specific transcriptomics of priapulids allows the characterization of blood and nephridia cell types and provides insights into their evolution
Aguilera, Felipe (Sars Centre, Bergen, NOR)

P-071 The role of FoxQ2 in insect brain development
He, Bicheng (Georg-August-Universitat, Göttingen, DEU); Büscher, Mari-

ta (Georg-August-Universitat, Göttingen, DEU); Bucher, Gregor (Georg-August-Universitat, Göttingen, DEU)

P-072 Whole Transcriptome Profiling during embryogenesis of the echiuran worm Urechis unicinctus
Cho, Sung-Jin (ChungBuk National University, KOR); Han, Yong-Hee (National University, KOR)

P-073 Unusual rodent homeobox genes in preimplantation development
Royall, Amy (University of Oxford, GBR)

P-074 The extra-ocular muscles of the lamprey and their evolutionary implication
Suzuki, Daichi G. (University of Tsukuba, JPN; Karolinska Institutet, SWE)

P-075 Genetic interactions regulating leg length in water striders
Amélie Decaras (Institute of Functional Genomics of Lyon, FRA); Toubiana, William (Institute of Functional Genomics of Lyon, FRA); Khila, Abderrahman (Institute of Functional Genomics of Lyon, FRA)

P-076 Ontogeny of the basicranium in lizards
Werneburg, Ingmar (Eberhard Karls Universität Tübingen, DEU); Yaryhin, Oleksandr (National Academy of Science of Ukraine, Kiev, UKR)

P-077 Evolutionary & developmental analysis of the Alx homeobox gene family in chordates
Wang, Huijia (University of Manchester, GBR)

P-078 High variation in the onset of ossification and conserved regions of bone contact in the bony skull development of marsupial mammals
Werneburg, Ingmar (Eberhard Karls Universität Tübingen, DEU); Spiekman, Stephan (Paläontologisches Institut und Museum der Universität Zürich, CHE)

P-079 A history of polydactyly in development and evolution
Lange, Axel (University of Vienna, AUT); Müller, Gerd B. (University of Vienna, AUT)

P-080 Epigenetic mechanisms of phenotypic plasticity in response to changing environments in cockroaches
Villalba, Mariana (University of Manchester, GBR)

P-081 Outside-in: studying the invagination process during embryogenesis of the milkweed bug Oncopeltus fasciatus
Novikova, Asya (Hebrew University of Jerusalem, ISR)

P-082 Characterization of gene regulatory network for adult skeletogenesis in a starfish Patiria pectinifera: Implications for innovation of larval skeletons in echinoderm
Yamazaki, Atsuko (University of Tsukuba, JPN); Morino, Yoshiaki (University of Tsukuba, JPN); Nitobe, Mao (University of Tsukuba, JPN); Hiroshi Wada (University of Tsukuba, JPN)

P-083 Effect of ANO5 on osteoblast differentiation
Hu, Ying (Capital Medical University School of Medicine, Beijing, CHN)

P-084 Comparative transcriptomics of eye and head development in three closely related Drosophila species
Elisa, Buchberger (Georg-August-University Göttingen, DEU); Torres-Oliva, Montserrat (Georg-August-University Göttingen, DEU); Posnien, Nico (Georg-August-University Göttingen, DEU)

P-085 The role of SFRP2 in multi-differentiation potentials of stem cells from apical papilla
Xia, Dengsheng (Capital Medical University School of Medicine, Beijing, CHN)

P-086 IGFBP5 enhanced osteogenic differentiation potentials of mesenchymal stem cells via JNK and MEK/Erk signaling pathways
Shan, Zhaochen (Capital Medical University School of Medicine, Beijing, CHN)

P-087 Analysis of senescence-related differentiation potential and gene expression profiles in human dental pulp stem cells
Fan, Zhipeng (Capital Medical University School of Medicine, Beijing, CHN)

P-088 Embryonic expression patterns of Sox9-related genes in the hagfish: implication for the evolution of the vertebrate axial skeleton
Ota, Kinya G. (Institute of Cellular and Organismic Biology, Academia Sinica, TWN); Fujimoto, Satoko (Laboratory for Evolutionary Morphology, RIKEN, Kobe, JPN); Oisi, Yasuhiro (Laboratory for Evolutionary Morphology, RIKEN, Kobe, JPN); Shigeru Kuratani (Laboratory for Evolutionary Morphology, RIKEN, Kobe, Japan)

P-089 Ranunculacean flower terata: morpho-anatomical characterization and clues about floral developmental genetics and evolution
Espinosa, Felipe (National Museum of Natural History, Paris, FRA); Derolin, Thierry (National Museum of Natural History, Paris, FRA); Damerval, Catherine (UMR de Génétique Végétale, CNRS, Gif/Yvette, FRA); Nadot, Sophie (Université Paris-Sud, FRA); Jabbour, Florian (National Museum of Natural History, Paris, FRA)

P-090 Flower development schedule and BC gene expression patterns in two morphs of Nigella damascena (Ranunculaceae) differing in floral architecture
Jabbour, Florian (National Museum of Natural History, Paris, FRA); Gonçalves, Beatriz (John Innes Center, Norwich, GBR); le Guilloux, Martine (UMR de Génétique Végétale, CNRS, Gif/Yvette, FRA); Manicacci, Domenica (UMR de Génétique Végétale, CNRS, Gif/Yvette, FRA); Nadot, Sophie (Université Paris-Sud); Damerval, Catherine (UMR de Génétique Végétale, CNRS, Gif/Yvette, FRA)

P-091 Characterization of cellular mechanisms involved in regeneration and

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Peron, Sophie (Sorbonne Université, Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA)

P-092 Germ line dynamics in bivalve molluscs: a comparative analysis
Pecci, Andrea (University of Bologna, ITA); Milani, Liliana (University of Bologna, ITA); Ghiselli, Fabrizio (University of Bologna, ITA); Passamonti, Marco (University of Bologna, ITA); Franceschini, Valeria (University of Bologna, ITA); Maurizii Maria G. (University of Bologna, ITA)

P-093 Sex chromosome evolution in organisms with haploid-diploid life cycles
Coelho, Susana (CNRS; Roscoff, FRA)

P-094 From sticklebacks to humans: Evolving skeletal traits by cis-regulatory changes in bone morphogenetic proteins
Indjeian, Vahan (Imperial College, London, GBR)

P-095 Evolution of the panarthropod ventral nerve cord: a palaeobiological perspective
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P-096 Origins and regulation of an eutherian novelty: The BGW cluster
Navas-Pérez, Enrique (University of Barcelona, ESP); Garcia, Cristina V. (Centro Andaluz de Biología del Desarrollo, Sevilla, ESP); Burguera-Hernández, Demian (University of Barcelona, ESP): Mirra, Serena (Centro de Investigación Biomédica en Red sobre Enfermedades Neurodegenerativas, Madrid, ESP); (Centre for Genomic Regulation, Barcelona, ESP); Soriano, Eduardo (Centro de Investigación Biomédica en Red sobre Enfermedades Neurodegenerativas, Madrid, ESP); Carvajal, Jaime (Centro Andaluz de Biología del Desarrollo, Sevilla, ESP); Garcia-Fernàndez, Jordi (University of Barcelona, ESP)

P-097 Tbx5 genes role in retina development in zebrafish
Pi-Roig, Aina (University of Barcelona, ESP); Minguillón, Carolina (University of Barcelona, ESP); Garcia-Fernàndez, Jordi (University of Barcelona, ESP)

P-098 Globins and hematopoiesis in the annelid Platynereis
Song, Solène (Matière et Systèmes Complexes, Paris, FRA; Institut Jacques Monod, Paris, FRA); Kerner, Pierre (Institut Jacques Monod, Paris, FRA); Cornelissen, Annemiek J. M. (Matière et Systèmes Complexes, Paris, FRA); Balavoine, Guillaume (Institut Jacques Monod, Paris, FRA)

P-099 Neuropeptides control larval specific behavior in nemerteans and brachiopods
Thiel, Daniel (Sars Centre, Bergen, NOR); Bauknecht, Philipp (Max Planck

Institute for Developmental Biology, Tübingen, DEU); Jékely, Gáspár (Max Planck Institute for Developmental Biology, Tübingen, DEU); Hejnol, Andreas (Sars International Centre for Marine Molecular Biology, Bergen, NOR)

P-100 The bulbus organ of Parasteatoda tepidariorum - precise maneuvers with a numb structure? Revisited
Quade, Felix S. C. (Georg-August-Universität Göttingen, DEU); Töpperwien, Mareike (Georg-August-Universität Göttingen, DEU); Ruhwedel, Torben (Max-Planck-Institut für Experimentelle Medizin, Göttingen, DEU); Möbius, Wiebke (Max-Planck-Institut für Experimentelle Medizin, Göttingen

P-101 The cost of evolving the life cycle: development of Trachylina
Kraus, Yulia (Lomonosov Moscow State University, RUS); Osadchenko, Boris (Lomonosov Moscow State University, RUS); Mayorova, Tatiana (Koltzov Institute of Developmental Biology, Russian Academy of Sciences, Moscow, RUS); Kremnyov, Stanislav (Lomonosov Moscow State University, RUS)

P-102 Polyp-to-medusa transition as a model for studying the life cycle evolution
Sukhoputova, Alena (Lomonosow Moscow State University); Kraus, Yulia (Lomonosow Moscow State University, RUS)

P-103 TCF/β-catenin mediated transcriptional repression in ascidians
Rothbächer, Ute (University of Innsbruck, AUT); Kari, Willi (University of Innsbruck, AUT)

P-104 Extraembryonic membranes in insects: how an evolutionary novelty can provide a model for epithelial remodeling
Panfilio, Kristen (University of Cologne, DEU); Hilbrant, Maarten (University of Cologne, DEU); Seibert, Jan (University of Cologne, DEU); Horn, Thorsten (University of Cologne, DEU); Koelzer, Stefan (University of Cologne, DEU)

P-105 Neuropeptide atlas of the marine annelid Platynereis dumerilii
Jasek, Sanja (Max Planck Institute for Developmental Biology, Tübingen, DEU); Conzelmann, Markus (CureVac GmbH, Tübingen, DEU); Williams, Elizabeth (Max Planck Institute for Developmental Biology, Tübingen, DEU); Jékely, Gáspár (Max Planck Institute for Developmental Biology, Tübingen, DEU)

P-106 Geometric morphometrics of fly wings
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Wimmer (Georg-August-University Göttingen, DEU); Posnien, Nico (Georg-August-University Göttingen, DEU)

P-107 Taste, Teeth, and Trinity: RNA-Seq reveals shared and unique gene expression profiles between tooth and taste bud progenitors in the shark, Scyliorhinus canicula
Martin, Kyle (University of Sheffield, GBR); Fraser, Gareth (University of Sheffield, GBR); Johanson, Zerina (Natural History Museum, London, GBR)

P-108 Transcriptomic profiling of cnidarian muscle cells provides insights into the evolution of muscles
Jahnel, Stefan (University of Vienna, AUT); Zimmermann, Robert (University of Vienna, AUT); Kraus, Johanna (Sars Centre, Bergen, NOR); Technau, Ulrich (University of Vienna, AUT)

P-109 Genomic changes of symbiont for the multi-algae retaining protists
Ogura, Atsushi (Nagahama Institute of Bio-science and Technology, JPN); Akizuki, Yuki (Nagahama Institute of Bio-science and Technology, JPN); Minei, Ryuhei (Nagahama Institute of Bio-science and Technology, JPN); Hosanna, Roy (Nagahama Institute of Bio-science and Technology, JPN)

P-110 Quantifying gene expression dynamics of developmentally important genes
Hallikas, Outi (University of Helsinki, FIN); Das Roy, Rishi (University of Helsinki, FIN); Renvoisé, Elodie (University of Helsinki, FIN); Jernvall, Jukka (University of Helsinki, FIN)

P-111 DISTAG/EsTBCCd1 orchestrates apical-basal axis formation and organ initiation in Ectocarpus
Coelho, Susana (Sorbonne Université, Paris, FRA; Station Biologique de Roscoff, FRA)

P-112 A genomic perspective on the evolution of development in Xenoturbella and implications for its position on the bilaterian tree
Schiffer, Philipp H. (University College London, GBR); Robertson, Helen (University College London, GBR); Müller, Steven (University College London, GBR); Telford, Max (University College London, GBR)

P-113 Phototactic navigation in marine larvae with ciliary eyes
Döring, Clemens (Sars Centre, Bergen, NOR); Hausen, Harald (Sars Centre, Bergen, NOR)

P-114 Arthropod sesquiterpenoid hormonal system and microRNAs
Qu, Zhe (Chinese University of Hong Kong, CHN); Hui, Jerome H. L. (Chinese University of Hong Kong, CHN)

P-115 Regulatory evolution leading to morphological innovations: the case of the mesmerizing turtle carapace
Pascual-Anaya, Juan (RIKEN, Kobe, JPN); Kuratani, Shigeru (RIKEN, Kobe, JPN)

P-116 Xenoturbella bocki - A revised perspective
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P-117 Molecular characterisation of skeletal regeneration in the brittle star
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P-118 Comparative transcriptomics reveals extensive developmental system drift in serial appendages morphogenesis
Pantalacci, Sophie (Université de Lyon, FRA); Petit, Coraline (Université de Lyon, FRA); Rey, Carine (Université de Lyon, FRA); Peltier, Manon (Université de Lyon, FRA); Sémon, Marie (Université de Lyon, FRA)

P-119 Evolution-Development congruence in pattern formation dynamics: bifurcations in gene expression and regulation of networks structures
Kohsokabe, Takahiro (University of Tokyo, JPN); Kaneko, Kunihiko (University of Tokyo, JPN)

P-120 MicroCT Imaging for EvoDevo: 3D embryos, digital beasties, and virtual museums
Metscher, Brian D. (University of Vienna, AUT); Müller, Gerd B. (University of Vienna, AUT)

P-121 Evolution and development of the nervous system in Sepia officinalis
Imarazene, Boudjema (MNHN, Paris, FRA); Dos Santos, Sandra E. (Universidade Federal do Rio de Janeiro, BRA); Botelho, Louise (Universidade Federal do Rio de Janeiro, BRA); Herculano-Houzel, Suzana (Universidade Federal do Rio de Janeiro, BRA); Bonnaud- Ponticelli, Laure (MNHN, Paris FRA)

P-122 Germ-disc formation in the common house-spider Parasteatoda tepidariorum
Pechmann, Matthias (University of Cologne, DEU)

P-123 Skeletal development in ophiuroids provides insights into evolution of gene regulatory networks
Oliveri, Paola (University College London, GBR); Dylus, David (University College London, GBR); Czarkwiani, Anna (University College London, GBR); Liu, Prudence (University College London, GBR)

P-124 Regulation of gene expression divergence in three closely related Drosophila species
Torres-Oliva, Montserrat (University of Göttingen, DEU); Posnien, Nico (University of Göttingen, DEU); Elisa, Buchberger (University of Göttingen, DEU); Jüds, Melissa (University of Göttingen, DEU)

P-125 Biting into the Genome to Phenome map: developmental genetic modularity of cichlid fish dentitions
Hulsey, C. Darrin (University of Konstanz, DEU); Fraser, Gareth (University

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P-126 Seasonal plasticity of thermal reaction norms for development within and between generations in insects
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P-127 Origin and evolution of caste differentiation genes in ants
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P-128 Endoderm out of the mouth: pre-oral gut in non-teleost fishes reveals an ancient mode of foregut development
Cerny, Robert (Charles University in Prague, CZE); Metscher, Brian D. (University of Vienna, AUT); Arias Rodriguez, Lenin (Universidad Juárez Autónoma de Tabasco, Villahermosa, Mexico); Gela, David (University of South Bohemia in České Budějovice, CZE); Minarik, Martin (Charles University in Prague, CZE)

P-129 A role for the dorsal surface selector gene apterous in generating morphological diversification of wing patterns in butterflies
Prakash, Anupama (National University of Singapore, SGP); Monteiro, Antónia (National University of Singapore)

P-130 Retinoic acid patterns the oral skeleton of vertebrates along the dorso-ventral axis
Jandzik, David (University of Colorado Boulder, USA; Comenius University in Bratislava, SVK); Square, Tyler A. (University of Colorado Boulder, USA); Cattell, Maria V. (University of Colorado Boulder, USA); Romasek, Marek (University of Colorado Boulder, USA); Medeiros, Daniel M. (University of Colorado Boulder, USA)

P-131 Genome-wide identification of Hedgehog signaling targets in axial patterning of the early embryo of the spider Parasteatoda tepidariorum
Akiyama-Oda, Yasuko (Osaka Medical College, JPN; JT Biohistory Research Hall, Takatsuki, JPN); Iwasaki-Yokozawa, Sawa (JT Biohistory Research Hall, Takatsuki, JNP); Oda, Hiroki (JT Biohistory Research Hall, Takatsuki, JPN)

P-132 Evolving Eusociality: Using Drosophila to understand how queen pheromone inhibits reproduction in worker honeybees
Lovegrove, Mackenzie R. (University of Otago, NZL); Duncan, Elizabeth J. (University of Leeds, GBR); Dearden, Peter K. (University of Otago, NZL)

P-133 Commissureless regulation of Slit-Robo signalling in insects
Seeger, Mark (Ohio State University, USA); Glasbrenner, David (Ohio State University, USA)

P-134 Assembly of a novel gene network in a conserved developmental field yields an evolutionary novelty

Hu, Yonggang (Georg-August-University Göttingen, DEU); Bucher, Gregor (Georg-August-University Göttingen, USA)

P-135 Shaping the embryo from outside: The role of Dorsocross in extraembryonic morphogenesis
Horn, Thorsten (University of Cologne, DEU)

P-136 Toll genes have an ancestral role in axis elongation
Benton, Matthew A. (University of Cologne, DEU)

P-137 Super-sizing teeth - from mice to elephants
Christensen, Mona (University of Helsinki, FIN); Di-Poï, Nicolas (University of Helsinki, FIN); Asher, Robert (University of Cambridge, GBR); Jernvall, Jukka (University of Helsinki, FIN)

P-138 How ancient is the vertebrate kidney: did the simple Xenacoelomorph worms lose or never have kidney-like structures?
Robertson, Helen (University College London, GBR)

P-139 Endoderm on the face: fate-mapping the pre-oral gut in sturgeon
Minarik, Martin (Charles University in Prague, CZE); Metscher, Brian D. (Universität Wien, AUT); Gela, David (University of South Bohemia in České Budějovice, CZE); Cerny, Robert (Charles University in Prague, CZE)

P-140 An evolutionary novelty in insect eggs
van der Zee, Maurijn (Leiden University, NLD); Jacobs, Chris G. C. (Max Planck Institute for Chemical Ecology, Jena, DEU); van der Hulst, Remy (Leiden University, NLD); Sotiris, Moudouris (Leiden University, NLD); Roth, Siegfried (University of Cologne, DEU)

P-141 Using sponges as a model to study the evolution of the Wnt/beta-catenin signaling pathwayi
Schippers, Klaske J. (University of Geneva, CHE); Nichols, Scott A. (University of Denver, USA)

P-142 Gut-like ectodermal tissue in a sea anemone challenges germ layer homology
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P-143 The evolution of collagen and SPARC secretion during tooth development in vertebrates
Debiais-Thibaud, Melanie (University of Montpellier, FRA); Enault, Sébastien (University of Montpellier, FRA); Muñoz, David (University of Concepción, CHL); Ventéo, Stéphanie (University of Montpellier, FRA); Sire, Jean-Yves (Université Pierre et Marie Curie, Paris, FRA); Marcellini, Sylvain (University of Concepción, CHL)

P-144 Analysing dynamics of spiral cleavage and the cell lineage of the flatworm Maritigrella crozieri by home-built SPIM microscopy

Girstmair, Johannes (University College, London, GBR)

P-145 Amphioxus witnessed the dorso-ventral inversion
Morov, Arseniy R. (Hiroshima University, JPN; Kazan Federal University, RUS); Kaji, Takao (Tohoku University, Sendai, JPN); Yasui, Kinya (Hiroshima University, JPN)

P-146 Identification of a novel gene required for maintaining differentiation states in telotrophic Tribolium castaneum oogenesis
Teuscher, Matthias (FAU Erlangen-Nürnberg, Erlangen, DEU); Ströhlein, Nadi (FAU Erlangen-Nürnberg, Erlangen, DEU); Schoppmeier, Michael (FAU Erlangen-Nürnberg, Erlangen, DEU)

P-147 Spiralian specific TALE homeobox genes and evolution of spiralian development
Morino, Yoshiaki (The Hebrew University of Jerusalem, ISR); Stahi, Reut (The Hebrew University of Jerusalem, ISR); Chipman, Ariel D. (The Hebrew University of Jerusalem, ISR)

P-148 No new head without a new heart: FoxN3is involved in the development of the interatrial septum in the African clawed frog, Xenopus laevis (Anura, Pipidae)
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Abstracts of Talks

Tuesday, July 26th

14.00 – 18.00 Registration

18.00 – 18.20 Opening

STORA SALEN Welcome addresses by Graham Budd (chair, local organisers) and Gerd B. Müller (President of the EED)

18.20 – 19.00 Keynote Lecture (K1)

Fossils, embryos and the origin of the vertebrate jawed head

STORA SALEN

Per Erik Ahlberg
(Evolutionary Biology Centre, Uppsala University, SWE)

Chair: Gerd B. Müller

The transformation of the vertebrate head during the evolution of gnathostomes involved a great deal more than just the origin of jaws: the forebrain lengthened, the hypophysis became widely separated from the olfactory bulbs, the trabeculae appeared, the patterning of the dermal skeleton came to reflect the underlying visceral arch architecture, and the shoulder girdle separated from the head. By examining the cranial anatomy of jawless and jawed stem gnathostomes against a comparative framework of cyclostome and gnathostome development, it has been possible to propose developmental hypotheses for certain fossil taxa, and specifically to determine that the projecting prenasal „upper lip" of primitive placoderms such as antiarchs, Brindabellaspis and Romundina likely represents a retained agnathan character. However, numerous problems of interpretation remain: most importantly, the well-supported position of osteostracans as the most crownward jawless stem gnathostomes conflicts with the nasohypophysial anatomy, where galeaspids are much more similar to jawed vertebrates. Here I present a new analysis that attempts to resolve these problems. Key points are the recognition that separate left and right nasal placodes (implying also a separate hypophysial placode) probably characterized not only galeaspids but also heterostracans and arandaspids, and that the osteostracan pharynx is strongly displaced anteriorly compared to all other vertebrates. The superficially lamprey-like nasohypophysial region of osteostracans is a necessary corollary of this pharyngeal anatomy and may thus be autapomorphic. By contrast, anaspids appear genuinely lamprey-like in combining a dorsal nasohypophysial opening with posteriorly positioned gills. The anteriorly rotated pharyngeal arches of early placoderms such as Brindabellaspis and Romundina are not associated with anterior displacement or dorsal rotation of midline structures, unlike in osteostracans, and probably represent an independently evolved morphology.

19.00 – 21.00 Welcome Reception at the Venue

Wednesday, July 27th

09.00 – 10.40 Symposium S1:

Development and evolution of sensory cells and organs I: Evolution of sensory cell types

STORA SALEN

Organizers: Detlev Arendt and Jacob Musser
Chair: Jacob Musser

S1-01 **From nerve net to centralized nervous system: the evolution of sensory cell types**

Arendt, Detlev (European Molecular Biology Laboratory, Heidelberg, DEU)

How animals progressed from a simple nerve net, as observed in some marine animals, to the most complex centralized nervous system, as found in human, remains one of the most exciting and unsolved question of animal evolution. In recent years, the molecular characterization of neurodevelopment and -differentiation in a variety of marine invertebrates has yielded new insight into nervous system evolution and the diversification of neural cell types. In our laboratory, we are working on marine animal model systems including the annelid Platynereis dumerilii, sea anemone and sponges to unravel ancestral features that existed in the metazoan ancestor, the cnidarian-bilaterian ancestor or the urbliaterian. This way first insight into the step-wise nervous system centralization in the divergent evolutionary lineages is beginning to emerge. I will present and discuss recent insight into several key steps of neural cell type origins and diversification in animal evolution with an emphasis on sensory cell types such as the emergence of mechanosensory, chemosensory and photosensory cells from ancient choanocyte-like precursors. These processes involved changes in the composition of cellular modules, such as the sensory apparatus, transduction, ion channels and presynapse. I will present and discuss recent efforts to use cellular expression maps and single cell transcriptomics in marine species, in order to reveal the hierarchy of sensory cell type diversification in animal evolution.

S1-02 **Evolution of the sensory nervous system: From protoneurons to**

elementary receptors to complex sensory arrays

Hartenstein, Volker (UCLA, USA)

Sensory system evolution entails two consecutive stages, the appearance of elementary sensory neurons/sensory units, and the formation of complex, multi-unit sensory organs. Sensory neurons are quite likely the first type of neurons that evolved. Debated among the evolutionary forerunners of sensory neurons are ciliated epidermal cells that acquired sensory function, but also secretory endocrine cells, which are omnipresent among metazoa, including taxa lacking a nervous system. Our research in Drosophila demonstrates that endocrine cells of the intestinal epithelium share with sensory neurons a significant fraction of molecular markers, and are specified in the same manner by a pHLH/proneural gene-Notch dependent signaling event that selects endocrine precursors from a pool of proliferating cells. Complex sensory organs, such as image forming eyes, arose at later stages in evolution, possibly multiple times in different clades. Developmental mechanisms controlling the formation of complex sensory organs have to account for (1) the regular spacing and repetitive composition of the individual modules, as well as (2) for the strictly ordered, homotopic connectivity between sensory neurons and their targets in the CNS. I will summarize our research into these processes in the Drosophila visual system and draw comparisons to vertebrates. The vertebrate retina and tectum, and fly eye and optic lobe, develop from a partitioned, unidirectionally proliferating neurectodermal domain specified by a conserved set of transcriptional regulators. In this domain, slowly dividing neuroepithelial stem cells are juxtaposed to rapidly amplifying progenitors to generate large numbers and different types of neurons in a temporally and spatially highly ordered way. This peculiar „conveyor belt neurogenesis“, which may play an essential role in generating the topographically ordered circuitry of the visual system, might have been present in rudimentary form at the ancestral bilaterian stage, and became more elaborate in bilaterian taxa that evolved complex image-forming visual systems.

S1-03 ### Is the evolution of sensory structures phylogenetic tree-like?

Oakley, Todd (University of California, Santa Barbara, USA)

In this paper we present data from our recent research into pig and dog domestication that explores phenotypic variation in time and space. We show how distinct dental phenotypes can be found in wild and domestic populations and challenge the traditional assumption that size reduction is a reliable signature for domestication. Finally, we show that the long-held belief that many of the unique phenotypic features distinguishing domestic animals from their wild ancestors is the result of heterochrony to be false - at least for pigs.

S1-04 ### Antibody-based sorting for cell type profiling in Evo-Devo:

example from placode derived cell types and technical advances in various species

Patthey, Cedric (Umeå University, SWE)

The evolution of cell types is key to understanding the evolution of vertebrate traits such as the cranial sensory placodes that form the cranial nerve ganglia. While our understanding of cranial placode development and evolution has made a lot of progress during recent years, placode-derived cell types have been less studied because knowledge of their transcriptional characteristics have been lacking. To address this issue and define cell type-specific markers, we have established transcriptional profiles for FACS purified placode-derived neurons from 5 specific placodes. In order to address the question of placode-derived cell type evolution, we are now examining expression of newly discovered markers in the invertebrate chordate Amphioxus. Finally, I will present our efforts to extend the method to various vertebrate and invertebrate non-model species.

09.00 – 10.40

Symposium S2: Epigenetics, inheritance and evo-devo

SAL B

Organizer: Carlos Guerrero-Bosagna

Chair: Carlos Guerrero-Bosagna

S2-01 Developmental programming of cardiac function in ectothermic vertebrates

Galli, Gina (University of Manchester, GBR)

Unlike mammals which normally develop under relatively stable conditions, embryonic development in ectothermic vertebrates often occurs in fluctuating environments. For example, freshwater turtles typically develop without parental care in subterranean nests where oxygen levels vary dramatically due to changes in gas conductance and the metabolic activity of microorganisms. Typical turtle nest oxygen concentrations range from 11-20% oxygen, and are likely to be even lower. Such a severe hypoxic insult during development is known to trigger epigenetic modifications in mammals which permanently alter organismal morphology, physiology and behaviour. In particular, developmental hypoxia triggers pathological cardiac remodelling which persists into adulthood, renders the heart more susceptible to hypoxic stress and predisposes the individual to heart disease. In contrast to mammals, we have recently shown cardiac hypoxia tolerance in juvenile turtles is increased by previous exposure to developmental hypoxia. Developmental programming of cardiac hypoxia tolerance may provide a phenotypic advantage for turtles, as they regularly encounter hypoxic, and even anoxic (zero environments) environments throughout their lifetime. As such, we believe the programmed turtle heart provides a novel system to understand, and possibly even treat, oxygen-related diseases of the human heart.

Here, I will discuss the progress we have made recently in identifying the cellular pathways that are programmed by developmental hypoxia, and speculate on the epigenetic mechanisms underlying the programmed phenotype.

S2-02 Transgenerational epigenetic inheritance and evolution: the role of the germ line epigenome in generating genomic evolutionary novelties

Guerrero-Bosagna, Carlos (Linköping University, SWE)

Epigenetic mechanisms have a fundamental role in phenotype formation. However, the role of epigenetic mechanisms in generating genetic diversification, a fundamental process in evolution, has only recently started to be investigated. Research reporting transgenerational epigenetic inheritance has shown how environmental factors can alter epigenetic marks in the germ line and induce long-lasting phenotypic changes in lineages of organisms. Moreover, environmentally-induced germ line epigenetic changes are also correlated with subsequent genetic changes such as copy number variations. The mechanism involves exposure of the germ line to drastic environmental conditions during critical developmental periods. The main purpose of the present study was to investigate the role of germ line epigenetic changes in generating heritable genomic variation, using the chicken diversification model. The diversification of the domesticated breeds of chicken is a unique model for this purpose because it is a recent process, the ancestral and the derived breeds are available, and the genome is well described. The present study focuses on the recent process of diversification of the domesticated chicken, taking advantage of the phenotypic and genotypic variability that has emerged. We identified correlations between germ line DNA methylation in the domestic chicken ancestor, Red Jungle Fowl (RJF), and genomic changes in many derived domesticated breeds. Such correlations indicate that DNA methylation in the germ line is an important factor in generating genetic variability at the levels of both single nucleotide polymorphisms (SNPs) and copy number variations (CNVs).

S2-03 Methylation QTL analysis in the chicken

Wright, Dominic (Linköping University, SWE)

Chickens were domesticated from the Red Junglefowl about 8000 years ago. During this period, they have undergone immense changes in morphology, physiology and behaviour. Such vast phenotypic changes in a short evolutionary time may be related to a plethora of genetic mechanisms other than simply selection among different mutations in protein coding sequences. For example, regulatory mutations affecting gene expression appear to be of high evolutionary significance, and also epigenetic mechanisms might be involved in cases like this. By using an advanced intercross (AIL) between wild and domestic chi-

ckens, and a combination of methylation, gene expression analysis and behavioural phenotyping, we have examined the role of methylation in the domestication process. By combining X30 MeDiP sequencing of the hypothalamus in over 100 AIL birds with genome-wide expression through microarrays in the same tissue and a dense genotype map, we have performed a combined of expression quantitative trait locus (eQTL) mapping, methylation QTL (methQTL) and behavioural QTL mapping. Over 600 eQTL, 40 behavioural QTL and 2000 methQTL were identified. By combining these different QTL and correlating methylation expression with gene expression, we have identified a number of potential differentially methylated candidates that underlie the domestication syndrome in the chicken.

S2-04 Transgenerational and plastic phenotypic effects in Arabidopsis in response to mild drought stress

Van Dooren, Tom (Institute of Ecology and Environmental Sciences, Paris, FRA)

We evaluated the role of abiotic stress in inducing phenotypic effects in the model plant Arabidopsis thaliana. A multi-generational experiment designed to identify stress-induced trans-generational phenotypic effects was carried out on the Phenoscope automated phenotyping platform and included five distinct accessions (Col-0, Shah, Bur-0, Tsu and Cvi-0). Each accession was grown for four generations under well-watered conditions (60% soil water content) and mild drought stress (30% soil water content) during early vegetative development. We investigated plastic responses and trans-generational effects of stress in the great-grandparental and grandparental generations followed by a control generation („memory"). We analysed projected rosette area PRA in most detail. For Col-0 we observed a trend for plants to be larger at the start of the experiment when ancestors had experienced stress. In the other accessions, there was no effect on mean PRA. For final PRA (21 days after the start of the experiment) and relative growth rates we found plasticity but no memory effects on average PRA. We found significant plasticity and memory effects on trait variances, but with accession-specific patterns. Other phenotypic traits investigated were rosette compactness, circle radius and convex hull area, leaf temperature and the red, blue and green parameters of the rosette RGB picture. For these traits we found significant memory effects on trait means and variances at day one and 21, but only for some traits and usually in an accession-specific pattern. Our results do demonstrate in a controlled experiment that trans-generational phenotypic effects which persist after a control generation can occur in response to relatively mild stress, next to immediate plastic responses. Parallel analysis of DNA methylation changes induced by mild drought showed that these were transient and do not seem to work as a mecha-

nisms for transgenerational transmission of stress memories.

09.00 – 10.40

Symposium S3: Understanding morphological diversification of plants and animals: paths from molecules to phenotypes

SAL C

Organizers: Miltos Tsiantis and Angela Hay
Chairs: Miltos Tsiantis and Angela Hay

S3-01 **Morphomechanical innovation drives explosive seed dispersal**
Hay, Angela (Max Planck Institute for Plant Breeding Research, Köln, DEU)

How mechanical and biological processes are coordinated across cells, tissues, and organs to produce complex traits is a key question in biology. In this work, we combine experimental and theoretical approaches to study explosive seed dispersal - a key life history trait underpinning invasive behavior in the common weed Cardamine hirsuta. We exploit the experimental tractability of C. hirsuta - a close relative of the model organism Arabidopsis thaliana - to understand the mechanism of explosive seed dispersal and provide insights into the origin of this striking trait.

S3-02 **Towards understanding development and diversity of leaf shape**
Tsiantis, Miltos (Max Planck Institute for Plant Breeding Research, Köln, DEU)

A key challenge in biology is to understand how diversity in organismal form is generated. Genetic analyses in model systems have identified key regulators that sculpt the body plans of metazoa and seed plants. However, less is known about how the action of such regulators produces particular organ shapes, or how the balance of conservation versus divergence of such form regulating pathways generated the tremendous morphological diversity of multicellular eukaryotes. One impediment to answering these questions is the relative paucity of experimental platforms where genetic tools can be utilized to unambiguously study morphogenesis and its evolution in a genome-wide, unbiased fashion. To circumvent this problem we developed theÂ Arabidopsis thalianaÂ relativeÂ Cardamine hirsutaÂ into a versatile system for studying morphological evolution. We aim to understand the molecular mechanisms through which leaf morphology evolved in these species, resulting in simple, undivided leaves in A. thaliana and dissected leaves with distinct leaflets inÂ C. hirsuta.Â This presentation will discuss our progress towards understanding the genetic pathways that specify dissected versus entire leaf shapes and that regulate the number, position and timing of leaflet production.

S3-03 **Reproductive capacity evolves in response to ecology through common developmental mechanisms**
Extavour, Cassandra G. (Harvard University, Boston, USA)

Evolution by natural selection relies on heritable variation in traits affect fitness. One such trait is lifetime reproductive capacity, or the total number of offspring that an individual gives rise to in its lifetime. In female insects, reproductive capacity is determined largely by the number of ovarioles, which are the egg-producing subunits of the ovary. Ovariole number is a quantitative trait that is highly variable and largely heritable, but also displays some phenotypic plasticity under different environmental conditions, including nutritional input. The greatest variation in ovariole number within a single genus has been reported to lie among the Hawaiian Drosophilid species, where ovariole number can range from one to over 100 ovarioles per ovary. However, the genetic basis of this extreme morphological divergence remains unknown. To address this problem, first we used the power of D. melanogaster genetics to elucidate the developmental and genetic mechanisms that regulate ovariole number. Then we examined several species of wild-caught Hawaiian Drosophilids, to see if the same or different mechanisms might be the proximal mechanism for evolutionary change in natural populations. Finally, we used comparative phylogenetic methods to examine the interaction between these heritable mechanisms and the ecologies of these flies. We show that (1) the principle mechanism regulating D. melanogaster ovariole number in the lab also regulates ovariole number in natural populations; (2) there is a trade-off between ovariole number and egg size; (3) convergent reductions in ovariole number evolve concurrent with habitat shifts to specific food sources; and (4) ovariole number variation among species with different food sources is best explained by adaptation to specific ecological niches. These results show that molecular mechanisms that regulate morphogenesis and also mediate physiological interactions with the environment, can help provide mechanistic explanations for the linked contributions of genetics and ecology to evolutionary change.

S3-04 Development, selection, and species diversification

Khila, Abderrahman (Ecole Normale Supérieure de Lyon, FRA)

Understanding how the acquisition of new ecological opportunities can shape the evolutionary trajectory of groups of organisms is a major challenge for modern biology. Water striders (Heteroptera, Gerromorpha) have conquered water surfaces and diversified to occupy various niches including ponds, streams and even oceans. In this talk, we will explain how this group of animals conquered water surface niches and how this transition shaped the evolutionary history of the group. We will try to link specific selective pressures to changes in the phenotype and the underlying genotype. This work represents an example of how the interplay between ultimate ecological forces and developmental genetic processes can drive adaptive evolution.

09.00 – 10.40

Symposium S4: Theoretical perspectives in evo-devo

K3/K4

Organizers: Christine Mayer and Thomas F. Hansen
Chairs: Christine Mayer and Thomas F. Hansen

S4-01 Resolving the relationship between evolvability and robustness using Boolean Genotype-Phenotype Maps

Mayer, Christine (University of Oslo, NOR); Hansen, Thomas F. (University of Oslo, NOR)

Evolvability and robustness are crucial concepts to understand evolutionary processes. By exploring their relationship, we are able to improve our understanding of evolutionary change and the origination of evolutionary innovations and novelties. Although, the relationship between evolvability and robustness is a still unanswered question subject to debate that can be studied by using the concept of the genotype-phenotype map. We explore the relationship between evolvability and robustness by introducing a combination of a multilinear model and the idea of Boolean networks. The different Boolean logic operators are thereby expressed as multilinear functions. We are using this approach to calculate different genotype-phenotype maps using different logical Boolean operations and varying grade of pleiotropy to demonstrate that the relationship between evolvability and robustness depends on the definition of the underlying genotype-phenotype map. We were able to show that evolvability and robustness can be positively correlated, as well as negatively. Hence, the direction of the correlation is dependent on the complexity and definition of the underlying genotype-phenotype map based on the used logical Boolean operations and the grade of pleiotropy.

S4-02 Core theoretical issues of EvoDevo: biased variation, non-linear transition, emergent novelty.

Müller, Gerd B. (University of Vienna; KLI, Klosterneuburg, AUT)

EvoDevo has generated a multitude of theoretical concepts that pertain to variation and innovation in the evolution of complex organisms. Three of these concepts – biases in the generation of phenotypic variation, non-linear features of character transition, and emergent developmental novelty – are central for an adequate conceptualization of the evolving genotype-to-phenotype relation. This presentation will examine each concept in the light of recent empirical advances in vertebrate limb development. It is concluded that the necessary integration of EvoDevo theory with evolutionary theory entails a distinction between continuous and discontinuous variation and a revised understanding of the

role of natural selection in organismal evolution.

S4-03 Regulatory motifs of trait individualization

Pavlicev, Mihaela (Cincinnati Children's Hospital Medical Center, USA); Todtova, Kristina (Cincinnati Children's Hospital Medical Center, USA); Widder, Stefanie (Cincinnati Children's Hospital Medical Center, USA)

Individualizaton of body parts is a concept central to both evolutionary population genetics as well as evolutionary molecular genetics. In the first, the notion captures the ability to respond to selection independently of other traits, and entails the capacity to produce independent heritable variation. In the second, individualization of traits and specifically cell types is the basis for the evolution of increasingly complex phenotypes, and is driven by the evolution of gene regulation. In spite of the apparent continuity of this question for organismal evolution, these approaches are rarely connected. Here we use systems-biological models of small gene regulatory motifs to study the effect of regulatory topology on population variation. In particular, we use the knowledge of motif transition that occurs during developmental differentiation of cell types, and compare how a specific motif transition between feed forward and feedback loop, may affect the pattern of trait variation in a population during evolutionary change. A population genetic simulation of regulated feedback loop dynamics under small perturbations shows a weak decoupling of variation in gene expression between the upstream gene and the responding downstream gene. We furthermore observe that the ranges of dynamics that can be generated by feedback and feed-forward networks overlap. Such phenotypic overlap enables genetic accessibility of network-specific expression dynamics. To test the results, we assessed the enrichment of the motifs, as well as the tissue-specificity of the genes on the dynamical core of the gene-regulatory networks from different tissues of mouse and human origin.

S4-04 Morphological variation at different spatial scales: A morphometric study of developmental control in the human cranium

Mitteroecker, Philipp (University of Vienna, AUT)

The human cranium is composed of multiple bones, which vary in both size and shape, and comprises different functional units. Because of the numerous spatial constraints and functional relationships, the cranial bones can neither develop nor evolve independently. Does developmental control - enforced by stabilizing selection - act at a local level, i.e., on the separate bones, or instead at a larger spatial scale, such as the overall form of the entire cranium? In the first case, individual bones may be more constrained than overall cranial form, whereas in the latter case individual bones may vary considerably among individuals and populations while keeping overall cranial form constrained. I present a morphometric approach to study variation in size and shape of composite structures at different spatial scales. In an application to 30 CT scans

of human crania, digitized with 65 midsagittal landmarks each, I show a considerable excess of size variation at larger spatial scales over smaller scales, indicating strong size integration in the cranium. For shape, by contrast, I found overall cranial shape less variable than the shape of the separate bones, presumably resulting from canalization and stabilizing selection at larger spatial scales to maintain functional integrity. I discuss the manifold implications of these findings for EvoDevo studies.

11.10 – 12.25

Contributed Session C1: Development and evolution of sensory cells and organs I

STORA SALEN

Chair: Sally Ley

C1-01 **The origin of the synapse and principles of cell type functional evolution**

Musser, Jacob M. (EMBL, Heidelberg, DEU)

Synapses are the core functional machinery of neurons, and their evolution in early animals preceded the emergence of complex animal nervous systems. However, the evolutionary origin of synapses remains obscure. For instance, although several early animal lineages, including sponges and placozoans, lack synapses, their genomes contain many orthologs of synaptic genes. This suggests that components of the synapse evolved prior to the evolution of a functional synapse. Here, we illustrate how evolution of new protein-protein interactions has likely played an important role in synaptic evolution. To investigate this, we are utilizing comparative proteomics to explore the evolution of synaptic protein complexes and their physical interactions during animal evolution. We present preliminary data from this project, and discuss several conceptual advances that illustrate how evolution at the protein level can result in new cell type functional machinery.

C1-02 **Sense and sensitivity in glass sponges: physiological evidence for sensory cells in the osculum**

Leys, Sally (University of Alberta, CAN)

Sponges, one of the earliest evolving animal lineages, lack nerves yet have at least two well-documented sensory cells which effect overt behaviour. Ciliary photoreceptors allow larvae to navigate towards light or dark for the respective adult habitat. Primary cilia in the sponge osculum (excurrent vent) are thought to detect clogging of the filter system and trigger contractions (sneezes) to expel unwanted debris. In other animals primary cilia also detect subtle changes in the environment such as pH, temperature, chemicals and fluid motion. Here I provide evidence that sponges detect changes in ambient flow conditions and adjust both their filtration rate and oxygen consumption accordingly. We have studied metabolism of reef-forming glass sponges at 170-200 m depths on the continental shelf of the pacific coast of Canada. Flow and oxygen

sensors placed in and adjacent to the oscula of Farrea occa show that at low ambient currents 1.2 uMol of oxygen is consumed per liter filtered whereas at ambient currents greater than 8 cm/s oxygen consumption is reduced by one third, while the volume of water filtered is doubled. Recordings over 24 hours illustrate that behavioural adaptations of the sponge rather than a purely passive mechanisms are involved in the control of pumping rate, especially under low ambient flows. Primary cilia in the osculum of glass sponges are implicated as flow sensors for this subtle behaviour, a hypothesis supported by the differential expression of genes in the sponge osculum. If filter feeding as seen in modern sponges was a feeding mechanism used by the earliest evolving animals, then reducing the cost of filtration would have been an effective driver of the evolution of sensory and signaling systems.

C1-03 Chiton eye photoreceptor cells employ both: a rhabdomeric opsin and a protostome specific ciliary opsin

Vöcking, Oliver (Sars Centre, Bergen, NOR); Kourtesis, Ioannis (Sars Centre, Bergen, NOR); Tumu, Sharat C. (Sars Centre, Bergen, NOR); Hausen, Harald (Sars Centre, Bergen, NOR)

Ciliary and rhabdomeric opsins are the best studied visual pigments. Both opsin types arose early in animal evolution and both co-occur in many organisms being expressed in different locations and serving different functions. The most prominent distinction is their role in vision, i.e. the employment of rhabdomeric opsins in the microvillar photoreceptors predominant in protostome eyes and of ciliary opsins in the rods and cones of the vertebrate retina, cells differing fundamentally in structure, molecular physiology and also in specification. We report cellular co-expression of a ciliary kind of opsin and r-opsin within the photoreceptor cells of larval eyes of the chiton Leptochiton asellus. The photoreceptors bear both, microvilli and also cilia and express several transporters known to be involved in both, microvillar and ciliary opsin trafficking. Due to this particular finding we reanalyzed with a broad approach evolution of ciliary kinds of opsins accompanied by gene structure analysis providing strong evidence that protostomes do not have only one, but two clearly distinct kinds of ciliary opsins. One type known from non-visual deep-brain photoreceptors encompasses the orthologs to deuterostome ciliary opsins. Another type including the characterized Leptochiton pigment seemingly shows a broader distribution in protostome eyes and has been lost in deuterostomes. The findings have impact on the current view on photoreceptor evolution.

C1-04 Molecular characterization and embryonic origin of the eyes in the common house spider Parasteatoda tepidariorum

Schomburg, Christoph (Georg-August-University, Göttingen, DEU); Turetzek, Natascha (Georg-August-University, Göttingen, DEU); Schacht, Magdalena I. (Georg-August-University, Göttingen, DEU); Schneider,

Julia (Georg-August-University, Göttingen, DEU); Prpic, Nikola-Michael (Georg-August-University, Göttingen, DEU); Posnien, Nico (Georg-August-University, Göttingen, DEU)

Most of our current knowledge about the developmental and molecular mechanisms involved in eye formation in arthropods comes from research in the model system Drosophila melanogaster. Here, a core set of retinal determination genes, namely, sine-oculis (so), eyes absent (eya), dachshund (dac), and the two pax6 orthologues eyeless (ey) and twin of eyeless (toy) govern early retinal development. By contrast, not much is known about the development of the up-to-eight eyes present in spiders. Therefore, we analyzed the embryonic expression of core retinal determination genes in the common house spider Parasteatoda tepidariorum. We show that the anlagen of the median and lateral eyes in P. tepidariorum originate from different regions of the non-neurogenic ectoderm in the embryonic head. The median eyes are specified as two individual anlagen in an anterior median position in the developing head and subsequently move to their final position following extensive morphogenetic movements of the non-neurogenic ectoderm. The lateral eyes develop from a more lateral position. Intriguingly, they are specified as a unique field of cells that splits into the three individual lateral eyes during late embryonic development. Using gene expression analyses, we identified a unique combination of determination gene expression in the anlagen of the lateral and median eyes, respectively. The development of the individual lateral eyes via the subdivision of one single eye primordium might be the vestige of a larger composite eye anlage, and thus supports the notion that the composite eye is the plesiomorphic state of the lateral eyes in arthropods. The molecular distinction of the two visual systems is similar to the one described for compound eyes and ocelli in Drosophila, suggesting that a unique core determination network for median and lateral eyes, respectively, might have been in place already in the last common ancestor of spiders and insects.

C1-05 Deciphering genomic and developmental mechanisms that underlie vision adaptations in noctilionoid bats

Sadier, Alexa (University of Illinois USA); Davalos, Liliana (Stony Brook University, New York, USA); Dumont, Elizabeth (University of Massachusetts at Amherst, USA); Rossiter, Stephen (Queen Mary University of London, GBR); Sears, Karen (University of Illinois USA)

Key innovations, novel traits that promote diversification, often involve sensory adaptations. Among these adaptations, the ability to see new wavelengths has been linked to advantages in foraging and hunting in multiple groups, including primates and fishes. This begs the question, „why don't all species evolve the ability to see all wavelengths?" To investigate this question, we studied vision evolution in noctilionoid bats.

Noctilionoids exhibit high diet variability (e.g., blood, fruit, pollen, nectar, insects), and diet can place selective pressures on vision evolution. At the gross scale, uMRI scans of adults from 20 diverse species demonstrated an association of eye phenotype and diet, as frugivores and nectarivores have significantly larger eyes than insectivores, relative to skull size. Photoreceptor composition is also linked to diet, as indicated by immunohistochemistry for S (blue/UV) and L (red/green) cones in adults of 15 species. Insectivores have only L cones, while S cones have likely re-evolved in frugivores and nectarivores, such that they now possess L and S cones. Consistent with this, RNAseq found that S opsin transcripts are absent from most insectivores, but present in some frugivores and nectarivores. S and L cones, and rods (low-light vision), arise from a single set of photoreceptor progenitors through a series of molecular switches. Immunohistochemistry and in situ hybridization on developing bats from 6 species suggests that the switches that turn progenitors into S cones differ in frugivores and nectarivores, and are not turned on in insectivores (resulting in more rods). Together with existing behavioral data, our results suggest that S cones and UV vision evolved independently through separate mechanisms in multiple noctilionoid lineages with plant-based diets. Insectivores, in contrast, shifted photoreceptors to a rod-identity likely in response to selective pressures for hunting. A trade-off between UV (S cones) and low-light vision (rods) therefore seemingly exists in noctilionoids.

11.10 – 12.25 Contributed Session C2:

Regulatory capacity in early embryos and axis formation: self-regulation or self-organization in axis formation

SAL B

Chair: Mette Handberg-Thorsager

C2-01 ### β-catenin-dependant mechanotransduction dates back to the common ancestor of Cnidaria and Bilateria

Pukhlyakova, Ella (University of Vienna, AUT); Aman, Andy (University of Washington, USA); Technau, Ulrich (University of Vienna, AUT)

The ability of cells to sense and respond to both external and internal mechanical cues is very important and is involved in coordination of cell movements, cell differentiation and morphogenesis. It has been shown in zebrafish and Drosophila that the expression of mesoderm-specific genes, brachyury and twist, during gastrulation is mechxnosensitive. Increased tension leads to the translocation of beta-catenin from the adherens junctions to the nucleus and activation of gene expression. However, it is unclear whether the mechanotransduction mechanism during gastrulation is present only in Bilateria, or whether it has a more ancient origin. Nematostella vectensis belongs to Cnidaria, a sister group of Bilateria, is a good model organism to study the evolutionary origin of mechanotransduction. During gastrulation of Nematostella cells of

the pre-endodermal plate, the future endoderm, apically constrict and invaginate. This leads to stretching of the neighboring cells at the blastoporal margin, where brachyury is expressed. We found that upon the inhibition of invagination by selective myosin light chain kinase (MLCK) inhibitor treatment the brachyury expression is strongly reduced. However, MLCK-inhibitor-induced suppression of brachyury expression can be rescued by applying an external mechanical stress to the embryos, which may mimic cell tensions at the blastopore during gastrulation. This mechanotransduction mechanism is beta-catenin dependent, since there was no rescue in beta-catenin knockdown embryos upon MO injection. Our data on the mechanosensitive brachyury expression in Nematostella vectensis show that mechanotransduction and mechanosensitive gene expression is conserved between Bilateria and Cnidaria and thus predated their divergence some 600 million years ago.

C2-02 In-depth cell lineage analysis of the spiralian development

Handberg-Thorsager, Mette (MPI-CBG, Dresden, DEU); Tomer, Raju (Stanford University, USA); Amat, Fernando (Howard Hughes Medical Institute, Ashburn, USA); Vopalensky, Pavel (MPI-CBG, Dresden, DEU); Lombardot, Benoit (MPI-CBG, Dresden, DEU); Tomancak, Pavel (MPI-CBG, Dresden, DEU); Keller, Philipp (Howard Hughes Medical Institute, Ashburn, USA); Arendt, Detlev (EMBL, Heidelberg). Metazoans specify germ layers during early development in a process called gastrulation. Gastrulation involves massive cell movements during which the specified germ layers are divided into molecularly distinct domains, which give rise to diverse differentiated cell types. Gastrulation movements have been described on both the cellular and molecular levels in the vertebrates and insects in considerable detail. Similarly in-depth analysis in other animals is hampered by technical difficulties, both at the level of imaging techniques and available molecular tools. This lack of information is particularly noticeable for larger branches of the metazoan phylogenetic tree e.g. the spiralians, which constitute 1/3rd of the metazoan phyla (Zhang, Z (2013), Laumer et al., 2015). Using the newly developed SiMView microscopy for high-speed in vivo and in toto imaging (Tomer et al., 2012), we have followed the development of the whole embryo of the spiralian annelid worm Platynereis dumerilii at cellular resolution. Through a combination of semi-automated cell segmentation and tracking (TGMM, Amat et al., 2014) and manual correction by using CATMAID (Saalfeld et al., 2009, Schneider-Mizell et al., 2016), we have obtained the entire cell lineages of a one-day old Platynereis embryo. I will present an analysis of the cellular movements and behavior during gastrulation and the mapping of genes important for gastrulation and axis formation onto the cell lineages. This work presents the first whole-embryo analysis at cellular resolution of the gastrulation process in a spiralian. It offers a resource for analyzing molecular underpinning of cell behavior in wildtype and functionally perturbed spiralian embryos.

C2-03 Instead of bicoid: germ cell less is required for axis formation in a beetle

Ansari, Salim (Georg-August-University Göttingen, DEU); Troelenberg, Nicole (University of Erlangen-Nuremberg, DEU); Bucher, Gregor (Georg-August-University Göttingen, DEU); Klingler, Martin (University of Erlangen-Nuremberg, DEU)

Axis formation is an essential early processes during bilaterian development. One of the crucial component during the axis determination in Drosophila is the maternally localized anterior morphogen bicoid. However, bicoid, is limited to Cyclorrapha flies. It has been shown that anterior determinants can be very diverse in nature. In case of Tribolium castaneum, repression of Wnt signalling is required for proper anterior development. This is done by the maternal anteriorly localized Tc-axin. However, no factor has been reported till now, the knock-down of which would lead to a duplication of posterior structures like seen in bicoid mutants. In the search of novel anterior patterning genes we mined the iBeetle Base, which stores the phenotypes recovered by the ongoing genome wide RNAi screen iBeetle. We found two unexpected candidates namely Tc-gcl and Tc-hbn. We found that knockdown of Tc-gcl and Tc-hbn gene produce mirror image double abdomen phenotype similar to Dm-bicoid and Dm-hunchback double mutants in Drosophila. Surprisingly, Dm-gcl is known for pole cell formation, but not for anterior patterning in Drosophila. No phenotypic or functional information is available for Dm-hbn. Our results indicate that Tc-gcl mRNA is maternally localized to the anterior pole of the oocyte. Tc-hbn mRNA was completely absent in gcl RNAi embryos which suggests that Tc-gcl directly or indirectly activates the Tc-hbn which later defines the anterior region. This hypothesis is further supported by anterior expansion of posterior marker gene (cad, vasa and eve) in gcl and hbn RNAi embryos. By using RNAi and In situ hybridization, we are trying to unravel the genetic interactions of Tc-gcl and Tc-hbn with previously known patterning genes. Together with previous work our results suggests that the first signals that establish the AP axis are highly diverse among insects.

C2-04 Functional evolution of a morphogenetic gradient

Chun, Wai K. (University of Chicago, USA)

While it is well established that gradients of diffusible morphogens produce stable forms and patterns during embryogenesis, the possibility that changes in the spatio-temporal pattern of morphogen gradients can drive morphological evolution rests largely on theoretical studies, due to the challenge of quantifying morphogen activity in species other than a few genetic model organisms. In early fly embryos, gradients of Bone Morphogenetic Protein (BMP) signaling specify the extraembryonic tissues; however, the number of extraembryonic tissues differs between

species. As in most insects, the scuttle fly Megaselia abdita develops two extraembryonic tissues, the serosa and amnion, while Drosophila melanogaster and related higher flies develop just one, the amnioserosa. Here we show that spatiotemporal differences in BMP signaling between these species account for the reduction of the number of extraembryonic cell types in the Drosophila lineage. Specifically, a Megaselia-specific broadening of the BMP gradient after the onset of gastrulation specifies amnion. In Drosophila, a positive feedback circuit is necessary for the intensification and spatial refinement of the BMP gradient prior to the onset of gastrulation. We show that in Megaselia there are differences in the genetic network controlling this positive feedback circuit, such that the feedback circuit acts over a wider spatial domain, resulting in the observed differences in BMP signaling. We suggest that the ancestral use of the positive feedback circuit was to promote the sequential specification of two extraembryonic membranes. Thus, we demonstrate that spatio-temporal changes in morphogen gradients can drive organismal evolution.

C2-05 Linking Noggin and Terminal patterning

Dearden, Peter K. (University of Otago, Dunedin, NZL); Duncan, Elizabeth (University of Leeds, GBR); Tidswell, Olivia (University of Otago, Dunedin, NZL); Beck, Caroline (University of Otago, Dunedin, NZL)

In vertebrates, Noggin proteins act to dorsalise embryos by blocking TGFb signalling. These proteins were thought not to exist in arthropods until we discovered Noggin-like molecules in a number of arthropod genomes These Noggin-like proteins provide an evolutionary link between Noggin and trunk, a component of terminal patterning in Drosophila. Trunk acts in terminal patterning to activate MAP kinase signalling, a very different molecular function to Noggin, despite their evolutionary relationship. Using a number of assay systems in vertebrates and insects, we have examined the function of Noggin-like molecules from arthropod and lophotrochozoan genomes and demonstrate an unexpected range of activities for these ancient patterning molecules.

11.10 – 12.25

Contributed Session C3: Understanding morphological diversification of plants and animals: paths from molecules to phenotypes

SAL C

Chair: Miltos Tsiantis

C3-01 The evolution of morphology, one base pair at a time

Preger-Ben Noon, Ella (HHMI Janelia Research Campus, Ashburn, USA); Stern, David (HHMI Janelia Research Campus, Ashburn, USA

Morphology evolves mainly through the accumulation of mutations in developmental enhancers, but we have a poor understanding of pre-

cisely how these mutations alter enhancer function. Here we decode the nucleotide changes in an embryonic enhancer for the shavenbaby gene that caused morphological evolution between closely related species of Drosophila. The shavenbaby gene encodes a transcription factor that directs the morphogenesis of cuticular hair-like projections, called trichomes. The dorsal and lateral surface of first-instar larvae of D. melanogaster is decorated with broad swathes of trichomes. Seven enhancers in the cis-regulatory region upstream of the shavenbaby promoter control the complex embryonic expression of shavenbaby in D. melanogaster. In D. sechellia, a sister species to D. melanogaster, multiple nucleotide changes in five of these enhancers led to the loss of shavenbaby expression in dorsal and lateral epidermis, resulting in a naked phenotype. Here we combined genetic, genomic, and biochemical approaches to identify the transcription factors that bind differentially to nucleotide sites that have evolved between D. melanogaster and D. sechellia in one of these enhancers. We found that the D. melanogaster enhancer encodes multiple binding sites for the transcriptional activator Arrowhead. Four Arrowhead sites were lost in the D. sechellia enhancer, causing partial reduction in embryonic enhancer activity and reduced robustness to genetic perturbations. In addition, the D. sechellia enhancer acquired a non-canonical binding site for the transcriptional repressor Abrupt, causing complete elimination of embryonic enhancer expression. These results provide an understanding, at unprecedented resolution, of how one enhancer has evolved altered function and reveal that reduction in enhancer function can result from both gain- and loss-of-function mutations. Gain of tissue-specific repression may provide an evolutionary mechanism to overcome robustness encoded by multiple activator sites and may allow maintenance of the pleiotropic roles of enhancers.

C3-02 The role of miR-199a in Arctic charr morphogenesis

Kapralova, Kalina H. (University of Iceland, ISL); Franzdottir, Sigridur Rut (University of Iceland, ISL); Snorrason, Sigurður S. (University of Iceland, ISL); Maier, Valerie H. (University of Iceland, ISL; Palsson, Arnar (University of Iceland, ISL); Jonsson, Zophonias O. (University of Iceland, ISL)

The Arctic charr morphs of Lake Thingvallavatn constitute an extreme example of local phenotypic diversity. Four morphs have been described in the lake: two limnetic; planktivorous (PL) and piscivorous (PI) charr, with pointed snout and evenly protruding jaws, and two benthic; small (SB) and large benthivorous (LB) charr, with blunt snout and short lower jaw. These morphs also differ extensively in life history characteristics (size and age at maturity) and embryology. Micro-RNAs (miRNAs) play an important role in animal development. These small non-coding RNAs are involved in post-transcriptional regulation of gene expression. Sequences of many miRNAs are highly conserved, yet they often exhibit temporal and spatial heterogeneity in expression among species and

have been proposed as an important reservoir for adaptive evolution and divergence. Small RNA-sequencing analysis of four developmental time points in two contrasting Arctic charr morphologies (the small benthic charr from Thingvallavatn and a charr from the Holar aquaculture program with a limnetic like morphology) showed that 53 known and 19 novel miRNAs have significantly different levels of expression. From these, miR-199a was selected for further studies. Whole month insitu hybridization of miR-199a showed that it is expressed in the upper, lower jaw and the gill arches of developing embryos of all four Thingvallavatn morphs. To gain a better understanding of the developmental processeses this miRNA is involved in, which genes it interacts with and regulate, several genes including the transcription factor Ets2 were identified as targets for miR-199a. We have started functional analysis, where miR-199a is inhibited or overexpressed in 1-cell zebrafish embryos. Craniofacial phenotypes of the injected and not injected embryos will be compared using geometric morphometrics. Our preliminary data indicates that inhibiting of miR-199a during zebrafish development leads to the shortening of the lower jaw and widening of the head mimicking the benthic morph phenotype.

C3-03 Gain and loss of floral ultra-violet absorbance is controlled by a single transcription factor

Hester, Sheehan (University of Cambridge, GBR); Moser, Michel (University of Bern, DEU); Klahre, Ulrich (University of Bern, DEU); Esfeld, Korinna (University of Bern, DEU); Dell'Olivo, Alexandre (University of Bern, DEU); Mandel, Therese (University of Bern, DEU); Metzger, Sabine (University of Cologne, DEU); Vandenbussche, Michiel (Ecole Normale Supérieure de Lyon, FRA); Freitas, Loreta (Universidade Federal do Rio Grande do Sul, Porto Alegre, BRA); Kuhlemeier, Cris (University of Bern, DEU)

Closely related plant species can display dramatically different floral traits and thus can attract different pollinators. We want to understand the concerted molecular and genetic changes that underlie the evolution of these differences, in particular in the Petunia genus. One important trait for pollinator attraction is colour and, in Petunia, flowers differ in visible colour but also ultra-violet (UV) colour. The majority of species, such as P. inflata, have UV-reflective, purple flowers and these species display the ancestral pollination syndrome of bee pollination. A clade of closely-related, derived species show different phenotypes in UV light and display different pollination syndromes. This includes P. axillaris that has white flowers that are UV-absorbing and attracts nocturnal moths, and its descendent, P. exserta, that has UV-reflecting, red flowers and shows a hummingbird pollination syndrome. The pigments that determine Petunia flowers' appearance in UV light are the UV-absorbing flavonols. The transition from the UV-reflective, bee-pollinated ancestors to UV-absorbent P. axillaris has involved a 10-fold increase in floral flavo-

nol levels, and the transition from P. axillaris to UV-reflective P. exserta has involved a comparable decrease in flavonol levels. Using inbred lines and wild accessions, we have shown that both of these transitions are due to alterations in the R2R3-MYB transcription factor, MYB-FL. In the first transition, a one kilobase insertion in the promoter of MYB-FL was likely the cause of upregulation of MYB-FL and its target, flavonol synthase (FLS), the structural gene responsible for flavonol production. In the second transition, the loss of flavonols was caused by a frame-shift mutation in MYB-FL in P. exserta. Modifications to MYB-FL also cause reciprocal alterations to anthocyanin levels, the compounds that determine visible floral colour and which are biochemically related to flavonols. This implies constraint on the diversity of visible and UV colour combinations in flowers.

C3-04 Modelling tooth development and predicting its morphological variation. On the interplay between cell adhesion and biomechanics

Marin-Riera, Miquel (University of Helsinki, FIN); Salazar-Ciudad, Isaac (University of Helsinki, FIN)

The mammalian tooth is a complex structure that shows great morphological variation across the phylogenetic tree. Morphological variation in teeth is mostly originated during development. Morphogenetic processes such as this are supposed to involve mechanical forces mediated by the adhesive properties of cells. Thus, in order to account for tooth morphology and its variation, we need to understand how moving cells and growing tissues exert mechanical forces on its surroundings during morphogenesis. Mathematical models of development integrate experimental knowledge and make quantitative predictions on the phenotype given a genetic or environmental perturbation. For that purpose we have built a new model of tooth development that implements realistic cell mechanics at all the cell layers in early tooth development. We have simulated tooth morphogenesis in a variety of scenarios assuming different rates of growth in the different tissues and different adhesive properties between them. The model predicts that the adhesive properties of cells within and between tissue types contribute significantly to the shaping of the tooth germ. More specifically, there are two main opposing forces that drive the direction of growth of the cervical loops, two epithelial folds that will create the flanks of the tooth crown. Adhesive interactions between epithelium and mesenchyme drive the cervical loops to grow ventrally, whereas adhesive interactions between epithelium and suprabasal cells, epithelial cells that compose the bulk of the tooth germ, drive the growth of the cervical loops in the buco-lingual direction. Our results provide new insights on how cell and tissue mechanics during tooth development can generate phenotypic variation and thus lead to evolutionary change.

C3-05 More than one way to build a backbone: Exploring developmental

mechanisms underlying the diversity of vertebral morphology

Kishida, Marcia (University of Cambridge, GBR); Fleming, Angeleen (University of Cambridge, GBR); Keynes, Roger (University of Cambridge, GBR)

A segmented vertebral column is one of the major innovations of the subphylum Vertebrata. However, most of our understanding of the developmental mechanisms of vertebra formation comes from studies in mice and chicks “amniotes“ l eaving the vast diversity of vertebrates understudied. Observations from histology in fish groups shows there is great diversity in how vertebrae form. Fossil evidence suggests that the components of the vertebra, the neural arches and the vertebral bodies, arose separately and that vertebrates have evolved multiple ways of building vertebral bodies. Zebrafish can be used as an experimental model to test hypothesised differences between amniote and teleost vertebral body formation. In amniotes, somite-derived sclerotome cells are solely responsible for building the vertebral arches and bodies. In zebrafish, evidence suggests that the notochord could be involved in the initial mineralising and patterning of the vertebral bodies. If so, these notochord cells represent a distinct cell population that evolved the ability to mineralise tissues. Using Cre recombinase to permanently mark cells, I aim to track somite-derived sclerotome cells at the time of vertebra formation. I am also using cell toxicity assays to eliminate specific cell populations “sclerotome or notochord“ and assess the effect on vertebral development. These experiments will allow me to elucidate the relative contributions of somite and notochord cells to the formation and segmental patterning of the vertebral bodies.

11.10 – 12.25

Contributed Session C4: Theoretical and process perspectives in Evo-devo

K3/K4

Chair: Ezzat El-Sherif

C4-01

Flexibility of temporal regulation as a basis for short- to long-germ evolution in insects

El-Sherif, Ezzat (FAU, DEU)

The anteroposterior (AP) axis of most insects is segmented in two different phases, each with a drastically different morphology. First, anterior segments arise in a „blastoderm‘, a structure with a fixed AP length. Then, more posterior segments form in a „germband‘, whose AP axis grows by convergent extension. Insects differ in the number of segments that form in the blastoderm vs germband. In short-germ insect, most segments form in a germband; while in long-germ insects, most segments form in a blastoderm. Short-germ embryogenesis is thought to be the ancestral mode of insect development, but it is not clear how

it evolved into a long-germ mode. Here I show that in the short-germ beetle, Tribolium castaneum, segmentation in both blastderm and germband are based on the same core mechanism: sequential activation of gene expression, temporally regulated by a gradient. I also show that this „temporal regulation"mechanism is so flexible that it can act interchangeably in both blastoderm and germband. This suggests a simple mechanism for short- to long-germ evolution in insects.

C4-02 On the origins of organismal complexity

Zimm, Roland (University of Helsinki, FIN); Salazar-Ciudad, Isaac (University of Helsinki, FIN, Universitat Autónoma de Barcelona, ESP)

Morphological complexity is generally considered a hallmark of most phyla of multicellular life. Thus, understanding the genetic and developmental commonalities of complex morphologies is crucial to ultimately understand macroevolutionary dynamics. We use an unprecedentedly realistic computational model of animal development, which includes gene regulatory networks (GRNs), biomechanics and all known cell behaviours in tissues of epithelial and mesenchymal cells, to draw and analyse the morphospace of possible morphologies. We explore this space by composing and mutating a large number of random GRNs with cell behaviours, since evolutionary history can be understood as a set of paths within this morphospace. Our approach allows to identify both common and complex morphologies that arise from the effects of gene interactions on the coordination of cell behaviours in tissues during development. We find that morphologies with high complexity exhibit commonalities in the distribution of their morphological variation (variational properties): with increasing complexity, gene mutations are more likely to lead to either very simple or complex, but dissimilar, morphologies. In other words, complexity and the probability of suffering morphological changes under genetic mutations are intrinsically correlated. Often, the evolutionarily easiest way to increase complexity is highly non-gradual, involving sudden morphological changes. The generality of these findings has deep implications for the origins of complex life as well as for the path of evolution. We also identify commonalities of developments that underly complex morphologies. For instance, our simulations show that synchronization of morphogenesis and inductive signalling (morphodynamic developments), a high degree of modularity and certain topological features as well as functional elements in the gene regulatory networks are correlated with morphological complexity. Our results, thus, make predictions on the structure of GRNs and development that may have been prerequisite for the evolution of complex organisms.

C4-03 How can complex morphology evolve through changes in development

Hagolani, Pascal F. (Helsingfors University, FIN)

The topology of gene networks, and the interplay between cell-cell signalling and cell movements are known to affect the genotype-phenotype map. We aim to understand how this effect on the genotype-phenotype map orchestrates evolutionary dynamics.Most of the models that aim to understand the genotype-phenotype map focus on genes or gene networks and do not include physical space nor realistic biophysical interactions between cells. Other models that do include realistic biophysical interactions are constrained to specific organs.Developmental models should ideally implement gene networks regulating cell behaviours (mitosis, adhesion, etc.) and realistic biophysical interactions in 3D space. These features are included in the EmbryoMaker modelling software. The Embryomaker is embedded in an evolution model. Every generation, mutation acts on each genotype and natural selection on the morphology resulting from each individual development. Similarity to a specific optimal morphology determines the fitness. Several groups of simulations were conducted with optima of increasing complexity. Our results show different rates of evolution for different types of developmental dynamics. In the case of a high interaction of morphogenetic mechanisms and inductive signalling, optima very different from the initial phenotypes are easier to get close to, however, the exact optimum is hardly ever reached. Lower interaction developmental types are not able to reach very disparate optima, but they are able to fine tune the phenotype to reach an almost exact match to those optima they are able to approach. Evolving from one developmental type to another determines the variational properties of the system and by doing so, its evolutionary dynamics.

C4-04 Adaptation by natural improvisation

Soen, Yoav (Weizmann Institute of Science, Rehovot, ISR); Knafo, Maor (Weizmann Institute of Science, Rehovot, ISR); Elgart, Michael (Weizmann Institute of Science, Rehovot, ISR)

During the lifetime of a developing organism, every individual encounters many combinations of diverse changes in its somatic genome, epigenome and microbiome. This gives rise to unimaginable number of novel combinations of internal perturbations which are unique to each individual. How any individual can tolerate this high load of new, individual-specific perturbations is not clear. We have recently proposed a conceptual solution to this problem based on a new principle of dynamic adaptation (termed „Adaptive Improvisation'). It explains how (biased) random variation of any kind (and scale) can safely and rapidly self-organize to confer a wide range of individual-specific adaptations beyond the existing outcomes of natural selection. This principle portrays gene regulation as an inseparable synergy between Darwinian selection and Lamarckian adaptation by improvisation. The division of workload between the two is regulated by stress, which is viewed as a

physical force that modifies the state of the organism until re-acquisition of a new homeostasis-like state. We evaluate this theory by exposing flies to conditions of stress that cannot be addressed solely by pre-evolved responses. Our work-in-progress findings provide initial support for the ability to acquire new adaptations by improvisation. In this talk, I will describe this adaptation theory and present the supportive evidence.

C4-05 What is a developmental mechanism and what is an evolutionary mechanism

Salazar-Ciudad, Isaac (University of Helsinki, FIN)

In this work I will critically review the different existing uses of the concept of developmental mechanisms. I will argue that many of them are living fossils that are inconsistent with what we currently know about embryonic development and that mostly reflect a largely non-operative eye-view approach. I will also review how these different views have implications not only on how development is understood to work (and on whether it can be said to "work") but also on the evolution of the phenotype and development. In addition, I will briefly review the different existing views about what is an evolutionary mechanism. This refers mostly to natural selection, drift, developmental constraints and related concepts. I will argue that there is often a strong interdependence between what a developmental mechanisms is understood to be an what are considered to be evolutionary mechanisms (and which are most relevant). The way these concepts are used is central to evo-devo but the identified inconsistencies represent a constraint for further advancement in the field. Several possibilities on how, and whether, developmental mechanisms should be defined and studied will be proposed. I will discuss how these relate to evolutionary mechanisms and how they allow to build more predictive and consistent theories on how development itself evolves and on how it drives morphological evolution. I will detail how these predictions are simply not possible from the modern synthesis but are starting to be possible in evo-devo. I will put examples of that based on my work on generalized models of pattern formation and morphogenesis by gene networks and cell inductive and mechanical interactions.

14.00 – 15.40 Symposium S5:
Regulatory capacity in early embryos and axis formation: self-regulation or self-organization in axis formation

STORA SALEN

Organizer: Hiroki Oda
Chair: Hiroki Oda

S5-01 A spider model to study mechanisms behind the capacity for self-regulation in axis formation

Oda, Hiroki (JT Biohistory Research Hall, Osaka, JPN); Iwasaki, Sawa (JT Biohistory Research Hall, Osaka, JPN); Akiyama-Oda, Yasuko (JT Biohisto-

ry Research Hall, Osaka, JPN)

Åke Holm (1909-1989), who worked at Uppsala University, demonstrated that embryos of a spider Agelena labyrinthica are induced to have double axes by grafting small pieces of specific tissues to certain positions. This fact is influential to the discussion of ancestral mechanisms of axis formation in arthropods and even in bilaterians. Now, based on molecular evidence from studies of another spider Parasteatoda tepidariorum, we can speculate that the tissue pieces Holm grafted must have expressed signaling molecules acting as a dorsal inducer. We are, however, far from understanding how the ventral cell fates are automatically inserted between the intact and ectopic dorsal inducers and how the dorsal-ventral and anterior-posterior axes are coordinately organized in such altered situations. What is more, we recently found that removal of a specific large portion from a P. tepidariorum germ-disc stage embryo can cause double axes. The P. tepidariorum embryo has a capacity to self-regulate in axis formation as well. In this symposium, although we are not currently able to answer the questions mentioned above, we will present the usability of the spider P. tepidariorum as a model to study mechanisms and principles behind the capacity for self-regulation in axis formation. The merits of this spider include its sequenced genome, tractability of the embryonic cellular patterning field, and applicability of a range of techniques (eg., cell labeling and tracking, multi-color FISH, RNAi, RNA-seq). Ongoing genome-wide analyses show that a Hedgehog (Hh) signaling-mediated mechanism operates in the whole germ disc to initiate waves of gene expression from both terminal regions of the embryo. The employment of Hh signaling for axis formation in a spider embryo and a vertebrate tissue tempts us to pursue an evolutionary link between them.

S5-02 Self-regulatory mechanisms of dorsoventral axis formation in insects
Roth, Siegfried (University of Cologne, DEU)

Toll-dependent patterning of the dorsoventral axis in Drosophila represents one of the best-understood gene regulatory networks. However, its evolutionary origin has remained elusive. Outside the insects Toll is not known for a patterning function, but rather for a role in pathogen defense. I will present our recent findings on the evolution of dorsoventral patterning in insects. In particular, I will describe our work on a hemimetabolous insect, the milkweed bug Oncopeltus fasciatus, whose lineage split from Drosophila's more than 350 million years ago. In Oncopeltus, Toll is only required to polarize a dynamic BMP signaling network. Modeling of this network reveals that shallow Toll signaling gradients are sufficient to initiate axis formation. Dynamic BMP signaling combined with long-range, shallow Toll signaling gradients can explain the twinning of embryos upon egg fragmentation, which has been observed in many insect lineages.

S5-03 Body axes formation mechanisms in a bilaterally symmetric cnidarian
Genikhovich, Grigory (University of Vienna, AUT)

Regulative capacity of animal embryos is known in multiple animal taxa ranging from Cnidaria to Chordata. This capacity is tightly bound to the ability of certain parts of the embryo to induce and regulate axis formation and to the scalability of the axis forming signaling gradients. In our work we are addressing the molecular mechanisms required for establishing and maintaining body axes in the bilaterally symmetric cnidarian - the sea anemone Nematostella vectensis, a member of the bilaterian evolutionary sister group. We showed that the signaling center regulating the formation of the two body axes is located in the blastopore lip. By combining transplantation experiments and molecular analysis, we discovered that the initial signal capable of inducing the main, oral-aboral body axis is conferred by two Wnt ligands, Wnt1 and Wnt3. We showed also that the initial Wnt signal is required for the circumbastoporal expression of BMPs and BMP antagonists, which then shifts to one side of the secondary, â€œdirectiveâ€ axis. This creates a Cartesian system of molecular coordinates allowing axial patterning of the embryo. Our data indicate that once the directive body axis is established, it becomes independent from the Wnt input. Mathematical modeling demonstrated that the core of the BMP signaling system consists of the evolutionary conserved module containing BMP4 and BMP5-8 homologues as well as BMP antagonist Chordin and metalloprotease Tolloid, however, additional components are used to fine-tune this system patterning the secondary body axis of the sea anemone. Our results allow us to approach the question of whether animal bilaterality evolved once or more than once.

S5-04 Symmetry breaking in mouse development
Hiiragi, Takashi (EMBL, Heidelberg, DEU)

A fundamental question in biology is the mechanism by which the embryonic polarity is established during development. Unlike many organisms, mammalian eggs lack polarity and symmetry among cells has to be broken during early embryogenesis. This symmetry breaking results in formation of the blastocyst, consisting of two major cell types, the inner cell mass and trophectoderm, which are distinct in their position and gene expression. Recent studies unexpectedly revealed that morphogenesis and gene expression is highly dynamic and stochastic during this process. What signal breaks the initial symmetry and how stochastic gene expression leads to the reproducibly patterned blastocyst remain open questions about the beginning of mammalian life. We have developed an experimental system to monitor early mouse embryogenesis by live-imaging at unprecedented spatio-temporal resolution. This provides us with a basis for investigating the cellular and molecular mechanism of symmetry breaking and self-organisation in early mammalian develop-

ment.

14.00 – 15.40

Symposium S6:
Development and evolution of sensory cells and organs II: Evolution of cranial sense organs in vertebrates

SAL B

Organizers: Gerhard Schlosser
Chair: Gerhard Schlosser

S6-01 **An old brain in a new head: evolution of vertebrate sensory systems from ancestral sensory cells**

Tosches, Maria (Max Planck Institute for Brain Research, Frankfurt am Main, DEU); Martinez-Vergara, Hernando (EMBL, Heidelberg, DEU), Bertucci, Paola Y. (EMBL, Heidelberg, DEU); Arendt, Detlev (EMBL, Heidelberg, DEU)

In vertebrates, neural crest and placodes contribute to organs that, as a whole, are clear vertebrate novelties, such as the nose, the ears and the adenohypophysis. However, the sensory modalities that these organs subserve are not novel. For example, ciliated chemosensory cells similar to vertebrate olfactory sensory neurons have been described in several invertebrate species, and some adenohypophyseal hormones are conserved in Bilateria. In 1917 Goodrich proposed that the adenohypophysis was originally a sensory organ opened to the external environment. Recent data from cyclostomes indicate that a nasohypophyseal plate was present in ancestral vertebrates, suggesting a kinship between chemosensation and the release of pituitary hormones. We studied the development and the molecular identity of chemosensory-neurosecretory neurons in the annelid Platynereis dumerilii. First of all, we identified a neurogenic region at the edge of the annelid anterior neuroectoderm characterized by expression of the vertebrate pre-placodal markers six1/2, six4/5 and eya. Within this annelid pre-placodal field, we found a population of annelid chemosensory cells expressing several adenohypophyseal markers, including specific transcription factors and neuropeptides. Moreover, in juvenile larvae these neurons are sensitive to an annelid pheromone, suggesting a functional role of these cells in the annelid neuroendocrine system. In line with recent data from ascidians and insects, we propose that a six1/2+ eya+ domain delimited the urbilaterian nervous system anteriorly, and gave rise to several types of sensory cells. In the vertebrate lineage, some of these cell types were lost and new cell types diversified and evolved. In particular, the adenohypophysis arose from chemosensory-neurosecretory cells, which lost their sensory role and were incorporated into novel circuits. The implications of this expansion and diversification of placodal-derived sensory neurons for the evolution of the vertebrate neural circuits will be discussed.

S6-02 Specification of the lateral plate ectoderm in the Ciona neural plate

Horie, Takeo (Princeton University, USA); Horie, Ryoko (Princeton University, USA); Hazbun, Alex (Princeton University, USA); Levine, Michael (Princeton University, USA)

Previous studies provide evidence for "proto-crest" and "proto-placodes" in the Ciona tapdole. To better understand the regulatory mechanisms underlying the specification of these vertebrate innovations we have conducted a combination of gene disruption and lineage tracing assays at the lateral border of the Ciona neural plate. These studies suggest that DMRT is a key determinant of the cranial proto-placode in anterior regions of the neural plate, whereas Msx delineates the proto-crest territory in the lateral plate ectoderm in the trunk. We present evidence that sensory hair cells and aATEN neurons arise from the proto-placode, whereas rATEN neurons and BTNs arise from proto-crest.

S6-03 When to stay together and when to split: molecular basis of sensory cell and sensory organ diversification in the vertebrate ear

Frizsch, Bernd (University of Iowa, USA)

The origin of the vertebrate ear is coupled to the origin of the otic placode and may represent a developmental grouping of ancestral molecular processes aggregating dispersed sensory cells. Position of the otic placode is integrated into rhombomeric hindbrain patterning domains and trunk and head mesoderm. Neurosensory cells split sensory cells with axon comparable to the olfactory receptor and most invertebrate sensory cells into a neuron conducting sensory information and a sensory cell for information acquisition. This over 650 million year old process is metastable even in mammals and neurons can be converted into intraganglionic hair cells. The ability to converge sensory signals and increase the dynamic range resolution may have provided strong selective pressure on this process.

S6-04 The development and evolution of vertebrate electroreceptors

Baker, Clare V. H. (University of Cambridge, GBR)

Electroreceptors detecting the weak, low-frequency electric fields surrounding animals in water (resulting from ion leakage across mucous membranes) are found in all major vertebrate groups (primarily used for hunting). In non-teleost jawed vertebrates, lateral line placodes give rise to electrosensory ampullary organs, neuromasts containing mechanosensory hair cells, and the neurons providing afferent innervation for both organ types. The electrosensory division of the lateral line system was lost in the bony fish lineages leading to teleosts and to frogs (amniotes lost the entire lateral line system). Lateral line electroreceptors and hair cells likely evolved via the diversification of ancestral mechanoreceptors: if so, we might expect conservation of developmental

mechanisms between electroreceptors and hair cells. We used a comparative RNA-Seq approach in a non-teleost fish, the paddlefish Polyodon spathula, to identify genes expressed in developing ampullary organs. These include many transcription factor and signalling pathway genes important for hair cell development, consistent with conserved developmental mechanisms. We have also identified genes expressed in ampullary organs but not neuromasts, including a transcription factor that may control electroreceptor differentiation. Within teleosts, low-frequency „ampullary" electroreceptors evolved independently at least twice, likely via the diversification of neuromast hair cells; a subset of electroreceptive teleost lineages also evolved electric organs and „tuberous" electroreceptors detecting high-frequency electric organ discharges. Using a cross-species approach, we have identified transcription factor genes expressed in ampullary organs in the catfish Ictalurus punctatus, based on RNA-seq data from the knifefish Apteronotus albifrons (from a sister group to catfishes, with both ampullary and tuberous organs). Our data suggest, at the least, conserved developmental mechanisms, and potentially support the evolution of ampullary organs in the common ancestor of knifefishes and catfishes.

14.00 – 15.40

Symposium S7: Life cycle evolution

SAL C

Organizers: Mark Cock and Susana Coelho
Chairs: Mark Cock and Susana Coelho

S7-01 **What uses are mating types? The developmental-switch model**
Perrin, Nicolas (University of Lausanne, CHE)

Why mating types exist at all is subject to much debate. Among hypotheses, mating types evolved to control organelle transmission during sexual reproduction, or to prevent inbreeding or same-clone mating. In this talk I will raise arguments against the above hypotheses, and argue instead for a role in triggering developmental switches. Genomes must fulfill a diversity of programs along the sexual cycle. As a haploid gametophyte, an individual may grow vegetatively (through haploid mitoses), or initiate gametogenesis and mating. As a diploid sporophyte, it may grow vegetatively (through diploid mitoses) or initiate meiosis and sporulation. Only diploid sporophytes (and not haploid gametophytes) should switch on the meiotic program. Similarly, only haploid gametophytes (not sporophytes) should switch on gametogenesis and mating, and should only do so when compatible gametophytes are ready to do the same in the neighborhood. As I will argue, mating types have evolved primarily to switch on the right program at the right moment.

S7-02 **From minus to males: coevolution of sexes and multicellularity in Volvocine Algae**

Umen, James G. (Donald Danforth Plant Science Center, St. Louis, USA); Hamaji, Takashi (Donald Danforth Plant Science Center, St. Louis, USA); Miyagi, Ayano (Donald Danforth Plant Science Center, St. Louis, USA); Geng, Sa (Donald Danforth Plant Science Center, St. Louis, USA)

Distinct male and female sexes have evolved repeatedly in eukaryotes, but the origins of dimorphic sexes and their relationship to mating types in unicellular species are poorly understood. Volvocine algae are a closely related monophyletic group that includes isogamous species such as Chlamydomonas reinhardtii, and oogamous multicellular species such as Volvox carteri (Volvox) with sperm-producing males and egg-producing females. Sexual differentiation and mating in volvocine algae are controlled by a multigenic mating locus (MT) with structurally divergent haplotypes. We found that a single conserved transcription factor gene—MID, with orthologs present in only the minus or male haplotype of each species—evolved from an ancestral role as a mating-type specifier to become a determinant of sperm and egg formation in the Volvox lineage. Transgenic female Volvox with ectopically expressed male MID have a pseudo-male phenotype forming functional sperm packets instead of eggs, while transgenic male Volvox with RNAi-knockdowns of MID have a pseudo-female phenotype forming functional eggs instead of sperm packets, or differentiating as self-fertile hermaphrodites. The uncoupling of sex chromosome identity from sexual differentiation in pseudo-males and pseudo-females of Volvox reveals antagonistic interactions between the MID pathway and other genes in the male and female MT haplotypes that impact sexual development and reproductive fitness. Cross-species complementation with MID orthologs revealed a surprising result that the spermatogenesis-promoting function of MID is present even in the simplest colonial genus, Gonium, whose species are all isogamous. Ongoing work is aimed at functional dissection of MID protein evolution, in the elucidation of MID gene regulatory networks from Chlamydomonas and Volvox, and in the identification of male-specific and female-specific fitness genes residing in Volvox MT.

S7-03 Serial changes of eight types of stem cells in the life cycle of the moss Phsycomitrella patens

Hasebe, Mitsuyasu (National Institute for Basic Biology, Okazaki, Japan)

Stem cells self-renew and produce cells that differentiate to become the source of the plant body. The moss Physcomitrella patens forms eight types of stem cells during its life cycle and serves as a useful model in which to explore the evolution of such cells. The common ancestor of land plants is inferred to have been haplontic and to have formed stem cells only in the gametophyte generation. A single stem cell would have been maintained in the ancestral gametophyte meristem, as occurs in extant basal land plants. During land plant evolution, stem cells diverged in the gametophyte generation to form different types of body parts,

including the protonema and rhizoid filaments, leafy-shoot and thalloid gametophores, and gametangia formed in moss. A simplex meristem with a single stem cell was acquired in the sporophyte generation early in land plant evolution. Subsequently, sporophyte stem cells became multiple in the meristem and were elaborated further in seed plant lineages, although the evolutionary origin of niche cells, which maintain stem cells is unknown. Comparisons of gene regulatory networks are expected to give insights into the general mechanisms of stem cell formation and maintenance in land plants and provide information about their evolution. Physcomitrella patens develops at least seven types of simplex meristem in the gametophyte and at least one type in the sporophyte generation and is a good material for regulatory network comparisons. In this talk, I summarize recently revealed molecular mechanisms of stem cell initiation and maintenance in the moss and its evolutionary implications in land plant life cycle.

S7-04 The effect of ploidy and molecular constraints on the evolution of the land plant life cycle.

Szövényi, Péter (Duke University, Durham, USA)

The alternation of haploid and diploid life history phases separated by syngamy and meiosis is arguably the most fundamental feature of sexual life cycles. Drastic differences in structure and function between the life history phases of a single organism are underlain by modifications in gene expression. Therefore, investigating phase-specific gene expression in diverse life cycles is critical to understand the mechanisms and driving forces of life cycle evolution both at the macro- and micro-evolutionary scales. The most prominent biphasic organisms are multicellular land plants, where a haploid gametophyte phase alters with a diploid sporophyte phase. Relative morphological complexity of haploid and diploid phases shows a clear evolutionary trend on the land plant phylogeny. It is widely agreed that embryophyte land plants have originated from a haplontic ancestor with a subsequent elaboration of the diploid and a parallel reduction of the haploid phase. Therefore, the origin of plant alternation of phases and that of land plants are tightly coupled, and for this reason, elucidating the genomic mechanisms associated with the origin of biphasic life cycles of land plants are of fundamental importance. Our group investigates the origin and evolution of basic eukaryotic life cycle types via analyzing the macroevolution and microevolutionary consequences of phase-specific gene expression in land plants. At the macroevolutionary scale, we study the interplay of phase-specific gene expression and genome evolution. Furthermore, we seek to elucidate the molecular mechanisms underlying the evolution of the multicellular diploid phase by testing candidate gene networks using reverse genetics. At the microevolutionary scale, we focus on the effect of ploidy on molecular evolution and on the constraints that ploidy may

impose on the developmental program. In my presentation I will highlight our major achievements and outline our ongoing and future work.

14.00 – 15.40

Symposium S8:
Developmental complexity and diversity in animals and plants, parallels and differences

K3/K4

Organizer: Kirsten ten Tusscher
Chair:Kirsten ten Tusscher

S8-01 **Evolution of diverse inflorescence architectures**

Koes, Ronald (University of Amsterdam, NLD); Bliek, Mattijs (University of Amsterdam, NLD); Verbree, Bets (University of Amsterdam, NLD); Castel, Rob (University of Amsterdam, NLD); Kusters, Elske (University of Amsterdam, NLD); Della Serena (University of Amsterdam, NLD); Souer, Erik (University of Amsterdam, NLD)

Higher plants are particularly useful for evo-devo- studies as they evolved a wide variation in architectures in relatively short time and because many plant species are, are amenable to genetic analyses. Angiosperms diverged, for example, widely with regard to flowering time and inflorescence architecture. In racemose inflorescences, like that of Arabidopsis, the apical meristem is indeterminate and flowers derive from lateral meristems, resulting in single (monopodial) axis bearing many lateral flowers. In cymose inflorescences, however, the apical meristem terminates development by forming a flower and growth continues via a lateral (sympodial) meristem resulting in a zigzag-shaped 'truss' consisting of serial sympodial units (sidebranches) that each terminate with a flower. We analyzed genes that control the identity of apical and lateral meristems in petunia, a cyme. Their orthologs in Arabidopsis, a raceme, encode functionally similar proteins, but display substantially different expression patterns and genetic regulation and in some cases even different functions in inflorescence development. Transgenic experiments underlined that the changes in expression patterns of these genes, rather than the encoded proteins, were a major factor in the divergence of inflorescence architectures, which could for some genes be traced to alterations in cis-regulatory sequences. The picture that emerges is that architectural diversity is associated with an extensive rewiring of the regulatory network that determines when (flowering time) and where (architecture) flowers are formed, which is at least in part due to changes in cis-regulatory gene elements that control transcription.

S8-02 **Turing pattern in fins and limbs**

Onimaru, Koh (The Barcelona Institute of Science and Technology, ESP; Universitat Pompeu Fabra. Barcelona, ESP)

A Turing-type reaction-diffusion mechanism is increasingly believed to

underlie digit patterning in mouse limb buds. A key feature of Turing systems is that they can flexibly create a variety of patterns with slight modifications of its parameters. We therefore considered whether this mechanism might contribute to the morphological diversity of vertebrate fins and limbs. In this talk, we will show evidence that a molecular Turing mechanism may underlie the pectoral fin development of a catshark, Scyliorhinus canicula. We explore a detailed time-course of the developing Sox9 expression pattern during pectoral fin development, to reveal the patterning differences between catshark fin and mouse digits. We then build a Turing mechanism-based computational model of this process, and show the high consistency between the simulations and experimental perturbations. Our study suggests that the morphological diversity of the distal fin and limb elements was achieved through the modulation of a deeply-conserved Turing system.

S8-03 Inflorescences as a model of branching structure development

Prusinkiewicz, Przemyslaw (University of Calgary, CAN); Owens, Andrew (University of Calgary, CAN); Cieslak, Mikolaj (University of Calgary, CAN)

Showy inflorescences - clusters of flowers - are a common feature of many plants, greatly contributing to their beauty. The clustering of flowers has a selective value: by being more visible, inflorescences can attract pollinators from a larger distance than individual flowers; furthermore, by supporting walking between adjacent flowers, inflorescences facilitate their pollination by insects. In many inflorescences, the canopy of individual flowers (florets) is supported by an intricate branching structure. Diverse branching architectures have traditionally been the focus of attention in the description and classification of inflorescences. Nevertheless, it is the distribution of florets in space, and not the underlying branching structure, that has a primary selective value. Extrapolating molecular-level data on the patterning of plant organs and vasculature, we have devised a computational model of inflorescences that accords primary importance to the distribution of florets in space, and considers branching structures as an emergent consequence of this distribution. The model reorganizes the traditional morphospace of inflorescences by showing that changes in inflorescence architecture considered fundamental may simply result from changes in the timing of development. This observation sheds new light on several questions regarding the evolution of inflorescences, such as the origin of flower heads. Furthermore, the model reveals unexpected analogies with the development of branching structures in many other contexts, from trees to lungs.

S8-04 In silico evo-devo: reconstructing stages in the evolution of animal segmentation

Vroomans, Renske (Utrecht University, NLD); Hogeweg, Paulien (Utrecht University, NLD); ten Tusscher, Kirsten (Utrecht University, NLD)

During the Cambrian explosion, a bewildering array of animal body plans emerged from a bilaterian ancestor. A subset of bilaterian phyla - vertebrates, arthropods and annelids - displays overt segmentation. Current data on segmentation in these clades seem to support multiple independent origins for segmentation rather than a shared ancestry. Still, the fact remains that in the majority of segmented animals, segments are laid down sequentially from anterior to posterior during extension of the main axis. In the current study we ask which selection pressures and ordering of evolutionary events can explain this predominance of sequential segmentation. To answer this question we design an \emph{in-silico} simulation model of evo-devo in which the tissue growth pattern and segmentation mechanism can freely evolve. We then determine the likelihood of evolving oscillatory sequential segmentation combined with posterior growth under various conditions, such as the presence or absence of persistent posterior morphogen or selection for determinate growth. We find that posterior growth with sequential segmentation is the predominant outcome of our simulations only if a persistent posterior signal is present and selection for determinate growth occurs secondarily. Otherwise, another mechanism dominates, in which divisions occur in large bursts through the entire tissue and all segments are created simultaneously. Our study supports the reported ancestry of a posterior signalling centre prior to the evolution of body axis extension and segmentation. In addition, it puts forward the hypothesis that early segmented animals displayed indeterminate growth. More generally, we demonstrate that it is possible to infer a likely order of evolutionary innovations by varying conditions as well as the onset of selection pressures.

16.10 – 17.10

Contributed Session C5:
Development and evolution of sensory cells and organs II

STORA SALEN

Chair: Clare Baker

C5-01

Neurotransmission and signal transduction in the tunicate coronal organ and the evolution of mechanoreception based on secondary sensory cells

Manni, Lucia (Università degli Studi di Padova, ITA); Rigon, Francesca (Università degli Studi di Padova, ITA); Gasparini, Fabio (Università degli Studi di Padova, ITA)

Tunicates, the sister group of vertebrates, represent an elective taxon for evo-devo studies aimed to clarify the origin of vertebrate sensory cells. Among tunicate sensory organs, the coronal organ is a mechanoreceptor located at the base of the oral siphon/mouth found in all species analyzed so far, thus representing a plesiomorphic feature of the subphylum. As peculiarity, the coronal organ is the only one constituted

of secondary sensory cells (SSCs). The coronal SSCs are provided with an apical bundle bearing cilia and microvilli (or stereovilli) and lack an axonal prolongation. They are related to the feeding behavior, representing a filtering barrier in the mouth. In the perspective of an evolutionary comparison between tunicates and vertebrates sensory organs, we considered aspects of coronal SSCs relative to their neurotransmitters and ion channels during the development of the tunicate ascidian Ciona intestinalis. In particular, we studied the expression of a set of genes related to neurotransmission already surveyed in C. intestinalis larvae, such as Ci-Syn (synapsin), Ci-VACHT (Acetylcholine transporter), Ach (actylcholin-esterase), Ci-GAD (Glutamic acid decarboxilase enzyme), Ci-GABA (É£-aminobutirric acid), Ci-TPH (Tryptophan hydroxilase enzyme), Ci-TH (Tyrosine hydroxilase enzyme). To enter in detail in the function of the coronal SSCs, we analyzed also the expression of two genes for ion channels: Ci-TRPA and Ci-TRPN, whose homologues in vertebrates are involved in the SSC (i.e., hair cell) signal transduction. Our data support the hypothesis that tunicate and vertebrate SSCs evolved from a SSC present in the common ancestor of the two sister groups.

C5-02 Understanding the origins of animal vision using marine larvae

Valero-Gracia, Alberto (Stazione Zoologica Anton Dohrn, Naples, ITA); Kirwan, John D. (Lund University, SWE); Nilsson, Dan-Eric (Lund University, SWE); Arnone, M. Ina (Stazione Zoologica Anton Dohrn, Naples, ITA)

Non-directional photoreceptors are the evolutionary precursors of all animal eyes; they enable the monitoring of ambient light intensity and regulate feeding, movement and reproduction. While the first animals were most likely benthic, they evolved larval stages very early on, thus conquering a new ecological niche: the pelagic. In this realm, the evolutionary pressure to prey but not be preyed upon became stronger. This implied strong selection for better sensory systems, including photoreception. How were the photoreceptor systems of the earliest primary larvae arranged? Did this system mediate vertical migration, the largest movement of biomass on Earth? To try to answer these questions, we chose the echinopluteus larva of the sea urchin Strongylocentrotus purpuratus as a model. A comprehensive array of techniques was applied, covering levels of organization from genes to behaviour. Opsin-positive cells were characterized in terms of molecular fingerprint and morphology. A custom-built behavioural set-up is used to investigate the vertical migration of these larvae under different light conditions. Based on our findings, a novel mechanistic model for understanding simple photodetection is proposed.

C5-03 Visual photoreception in Atlantic cod - Evolutionary restrictions, neurogenesis and life history transformation

Valen, Ragnhild (University of Bergen, NOR)

Teleost fishes show a great variety in visual adaption, largely shaped by evolutionary expansion and loss of the opsin complement. The repertoire ranges from monochromatic scotopic vision mediated by pure rod retinas, -typical for many deep-sea species, to multi-chromatic color vision in some pelagic species. We have investigated the opsin repertoire of Atlantic cod (G. morhua) and found that the entire families of SWS1 (UV sensitive) and LWS (red sensitive) opsin genes, have been lost from the cod genome. On the other hand, the blue-sensitive SWS2, and the green-sensitive RH2 have duplicated into numerous opsin paralogs. Our analysis shows that these cone opsins are used differentially throughout development, and are the only visual opsins expressed during the larval stage. Development of a duplex retina with the addition of rod photoreceptors coincides with cod metamorphosis. The indirect developmental strategy thus allows for separate studies of cones and rods development, which in nature correlates with visual changes linked to habitat shifts. The clustering of key retinal genes according to life stage, suggests that Atlantic cod with its sequenced genome may be an important resource for identification of underlying factors required for development and function of photopic and scotopic vision.

C5-04 Photoreceptors of a polychaete with a very long pelagic phase

Kumar, Suman (Sars Centre, Bergen, NOR)

Annelids are a diverse group of animals suited for studies of recent and long evolutionary adaptations. Malacoceros fuliginosus is a sedentary annelid with a very long pelagic larval phase and to thrive in this habitat their sensory abilities may be well adapted. Notably, the larvae develop several kinds of eyes. The larvae are phototactic within 24 hours post fertilization and possess a single pair of eyespots, while two other eyespots develop within the next 24 hours. Ultrastructural studies show that two of them have a typical rhabdomeric structure as it is common in polychaetes, but the third has a ciliary organization which is unusual for eye photoreceptors in this taxon. How such an additional eye integrates with the overall eye circuitry, how is it related to photoreceptors of other animals and what is it used for are intriguing questions. The head region of the larvae is quite compact and the close proximity of all the eyespots allow for a detailed mapping of the eye circuitry. Gene expression analysis so far hints to a possible evolution of color vision within annelids. In situ hybridization and custom-made antibodies have shown the expression of two r-opsins in distinct photoreceptor cells of the rhabdomeric eyespots suggesting subfunctionalization of photoreceptor cells along with r-opsin duplication in annelids. A broad approach analyzing wavelength specific behavioral responses, molecular characteristics and eye electrophysiology are followed to further characterize function and evolutionary origin of the different eyes.

16.10 – 17.10

Contributed Session C6: Epigenetics, inheritance and Evo-devo

SAL B

Chair: Carlos Guerrero-Bosagna

C6-01 Neuronal reprogramming of the germline

Zuoco, Giuseppina (University of Warwick, GBR); Pires da Silva, Andre (University of Warwick, GBR)

Developmental plasticity evolved as an adaptation to survive in unpredictable environments. Recent research indicates that some developmental plastic phenotypes are inherited in a non-Mendelian fashion. Here we report cross-generational plasticity in the nematode Rhabditis sp. strain SB372, in which genetically identical individuals can become females or hermaphrodites depending on factors experienced by the mother. SB372 hermaphrodite mothers, when cultured in isolation, produce only females (and a few males). However, when these mothers are exposed to chemicals produced by conspecific nematodes, they produce progeny that go through a non-feeding larval stage (dauer) that later become selfing hermaphrodites. We identified the sensory cue as being a small chemical named ascaroside (ascr#18). When the maternal sensory neuron ADF is killed with a laser microbeam, the production of hermaphrodite progeny is abolished even when the mother is in contact with ascr#18. These results indicate that neuronal signals reprogram the germline. SB372 may provide a good model for how environmental information experienced by the maternal soma can be transmitted across a generation. Our results indicate that ascarosides trigger a neuronal signaling cascade that epigenetically reprogram the germline to produce hermaphrodites instead of females.

C6-02 Allele-specific whole genome sequencing during mouse embryonic development

Marcho, Chelsea (University of Massachusetts – Amherst, USA); Mager, Jesse (University of Massachusetts – Amherst, USA)

Appropriate epigenetic regulation of gene expression during lineage allocation and tissue differentiation is required for normal development. One example of epigenetic regulation is genomic imprinting, defined as mono-allelic gene expression in a parent-of-origin manner. Imprinting is established largely due to epigenetic differences arriving in the zygote from sperm and egg haploid genomes. In the mouse, there are approximately 150 known imprinted genes, many of which are coordinately regulated in imprinted gene clusters. We have shown that the imprinted cluster Igf2r/Airn undergoes changes in imprinted expression and epigenetic modifications during specific stages of mouse gastrulation. In order to determine if other imprinted genes have similarly dynamic imprinted expression patterns and identify novel imprinted genes, we performed allele-specific RNA sequencing during gastrulation. Additionally, we per-

formed whole genome bisulfite sequencing (WGBS) to assay DNA global methylation changes and identify epigenetic regulation corresponding with imprinted expression. These data have led to the identification of several novel imprinted loci that have transient allele-specific expression during gastrulation. This suggests an epigenetic mechanism separate from the canonical gametic methylation regulating imprinted expression at these sites. Taken together with global and locus-specific methylation, these data help to define the epigenetic dynamics during mammalian gastrulation.

C6-03 Phenotypic variation in Drosophila melanogasteris caused by expression changes in a microRNA

Kittelmann, Sebastian (Oxford Brookes University, GBR); Arif, Saad (Oxford Brookes University, GBR); Almudi, Isabel (CABD, Sevilla, ESP); Nunes, M. Daniela S. (Oxford Brookes University, GBR); McGregor, Alistair P. (Oxford Brookes University, GBR)

Genetic variation between closely related groups of organisms can translate into morphological variation. We use phenotypic differences in Drosophila melanogaster to identify the underlying genetic variation and the resulting differences in developmental processes. Core questions we try to answer include: how many mutations accumulate to alter a given phenotype; are mutations more prevalent in coding or non-coding DNA; are there hotspots in gene regulatory networks where evolution acts recurrently? I use trichome patterns on the leg as a model system. Trichomes are short, non-sensory, hair-like structures formed by actin protrusions of the epidermis that largely cover the insect cuticle. A region on the femur of the second leg of Drosophila species is free from trichomes and is hence called the „naked valley". Naked valley size differs between strains of D. melanogaster. The underlying genetic variation was mapped to a 25 kb region on the third chromosome explaining up to 91 % of the variation. One of the protein-coding genes in this region, jigr1, contains a gene encoding a micro-RNA, miR-92a, in one of its introns. miR-92a interferes with expression of the protein-coding gene shavenoid, and thus blocks trichome development. Ectopic expression of miR-92a leads to a larger naked valley, and knockout of miR-92a is sufficient to drive trichome formation in the naked valley. Expression of miR-92a is stronger in second legs of large naked valley strains. This implies that genetic variation within D. melanogaster leads to expression differences of miR-92a which in turn leads to differences in shavenoid expression and thus naked valley size. Currently we are using a combination of ATAC-seq, genetic mapping, and CRISPR/Cas9 to elucidate where exactly the underlying genetic variation is located within the 25 kb locus and if it affects an enhancer or a promoter of miR-92a or its host gene.

C6-04 Analyses of gene expression and epigenetic differences in brains of Red Junglefowl selected for tameness

Bélteky, Johan (University of Linköping, SWE)

Domestication, an accelerated evolution driven by man, puts pressure on organisms to adapt to their new environment. This has generated a large variety of phenotypes in a short time-span, as seen in a number of domestic animals including the domestic chicken. Our hypothesis is that domestic phenotypes may to have developed partly as correlated responses to early selection for tameness. By reenacting early selection pressure on a population of wild-type animals we can study the associated phenotypic and genetic changes. We have bred three lines of the wild ancestor of the domestic chicken, the Red Junglefowl (Gallus gallus). By selecting solely for the trait fear of humans, we have two lines displaying high or low fear, and one unselected showing intermediate fear levels. Currently five generations of offspring have been bred within each line, and several phenotypic changes, correlated to the selection trait, can be observed: low fear birds gain weight faster, show higher feeding motivation and more aggressive behaviour, while the high fear birds show significantly more avoidance behaviour. Low fear birds also display higher dominance ranking, lay larger eggs with heavier chicks, and have better plumage condition. We performed genetic analysis by means of transcription microarray and PCR on hypothalamus and cerebral hemisphere from selected animals. Whilst the unselected group did not differ from the original parental population, the high and low fearful groups in generation S5 differed from each other significantly for a number of genes in both tissues. Amongst the differentially expressed genes, we detect functions ascribed to immunology, weight and behaviour. We also detected a number of transcripts previously annotated with sperm-associated functions. The results support the hypothesis that domesticated phenotypes may evolve because of correlated effects related to reduced fear of humans. To further investigate differences, methylated DNA Immunoprecipitation was also performed on the hypothalamus of high and low fifth generation birds, as well as SNP sequencing via GBS in order to give a more complete picture of the effects of the selection effects

16.10 – 17.10

Contributed Session C7: Life cycle evolution

SAL C

Chair: Mark Cock

C7-01 **Genetic regulation of the haploid-diploid life cycle of the brown alga Ectocarpus**

Cock, J. Mark (Station Biologique de Roscoff, FRA); Arun, Arok (Station Biologique de Roscoff, FRA); Godfroy, Olivier (Station Biologique de Roscoff, FRA); Scornet, Delphine (Station Biologique de Roscoff, FRA); Bourdareau, Simon (Station Biologique de Roscoff, FRA); Peters, Akira F.

(Bezhin Rosko, Santec, FRA); Coelho, Susana M. (Station Biologique de Roscoff, FRA)

The brown algae are members of the supergroup chromalveolata, and as such are very distantly related both to animals and to green plants. This group of seaweeds evolved complex multicellularity independently of animals and green plants and is one of only a small number of eukaryotic groups that has acquired this level of developmental complexity. The life cycle of Ectocarpus involves an alternation between two independent multicellular organisms, the sporophyte and the gametophyte. We have shown that the identities of the two generations are not determined by ploidy, but rather are determined genetically. Several life cycle mutants are currently being studied, including the ouroboros and samsara mutants, which both exhibit complete conversion of the sporophyte generation into a gametophyte. The ouroboros and samsara mutations not only correspond to key developmental regulators but also represent a new class of homeotic mutant in which there is a switch between developmental programs at the level of the whole organism rather than at the organ or tissue level. Characterisation of Ectocarpus life cycle mutants at the molecular level is providing insights into how multicellular development programs may have been built on to pre-existing regulatory networks controlling life cycle progression.

C7-02 **Marchantia MpRKD regulates the gametophyte-sporophyte transition by keeping egg cells quiescent in the absence of fertilization**

Rövekamp, Moritz (University of Zurich, CHE); Bowman, John L. (Monash University, Clayton, Melbourne, AUS; UC Davis, Davis, USA)

Unlike in animals, the life cycle of land plants alternates between two multicellular generations, the haploid gametophyte and the diploid sporophyte. In early land plants, including liverworts, the gametophyte represents the dominant generation, whereas it is reduced to just a few cells in flowering plants. Differentiation of the gametes initiates the transition from the gametophyte to sporophyte generations and, upon maturation, the egg cell establishes a quiescent state that is maintained until fertilization. This quiescence represents a hallmark of the gametophyte-sporophyte transition, however, the underlying mechanisms are complex and remain largely unknown. Intriguingly, ectopic expression of members of a clade of RKD (RWP-RK Domain) containing transcription factors, which are absent from animal genomes, can induce an egg cell-like transcriptome in sporophytic cells of Arabidopsis thaliana. Yet, to date, loss-of-function experiments have not produced phenotypes affecting the egg cell, likely due to genetic redundancy and/or cross-regulation among the five RKD genes of A. thaliana. To reduce genetic complexity, we explored the genome of Marchantia polymorpha, a liverwort belonging to the basal lineage of extant land plants. Based on sequence homology, we identified a single M. polymorpha RKD gene,

MpRKD, which is orthologous to all five A. thaliana RKD genes. Analysis of the MpRKD expression pattern and characterization of lines with reduced MpRKD activity indicate that it functions as a regulator of gametophyte development and the gametophyte-sporophyte transition. These lines show defects in thallus growth and gemma cup formation and, interestingly, unfertilized egg cells fail to establish and/or maintain the quiescent state of the egg cell and divide, resulting in sexually sterile females. The data show a fundamental role of RKD factors in gametophyte development, and particularly, a direct effect in establishing and/or maintaining the developmental program of the egg cell.

C7-03 Medusozoan genomes and the origin of a jellyfish body plan

Khalturin, Konstantin (Okinawa Institute of Science and Technology, JPN); Khalturina, Maria (Okinawa Institute of Science and Technology, JPN); Fujie, Manabu (Okinawa Institute of Science and Technology, JPN); Koyanagi, Ryo (Okinawa Institute of Science and Technology, JPN); Goto, Hiroki (Okinawa Institute of Science and Technology, JPN); Satoh, Noriyuki (Okinawa Institute of Science and Technology, JPN)

Cnidarians are the most ancient animals with complex life cycles. In Medusozoa (Scyphozoa, Hydrozoa, Cubozoa) there are three successive life stages - planula larva, polyp and jellyfish whereas in Anthozoa (corals, sea anemones) only planula and polyp stages are present. The phylogenetic position of Cnidaria provides an opportunity to explore the ancestral characteristics of the life cycle regulating machinery and to address a number of fundamental questions. How does one genome control and regulate the development of several morphologically and physiologically distinct forms? Which molecular pathways are responsible for the transition from a planula larvae into a polyp and then into a medusa? What was the ancestral pre-Bilaterian body plan and how polyp and jellyfish stages are related to each other? In order to address these questions we sequenced genomes of Aurelia aurita (Scyphozoa) and Morbakka virulenta (Cubozoa). Combined with comparative analysis of gene expression profiles in planula, polyp and jellyfish stages our data provide insights on the origin of complex life cycles and body plan evolution within Cnidaria.

C7-04 Co-option of germ layers related TFs shows regionalized expression during two non-embryonic developments

Tiozzo, Stefano (Sorbonne Université, Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA)

Colonial ascidians (Tunicata) are characterized by complex life cycle and multiple ways of development. These features make them good models to study alternative mechanisms of developmental and tissue plasticity in chordates. Particularly, in Botryllus schlosseri it is possible to compare embryonic, asexual (palleal budding, PB), and regenerative (vascular

budding, VB) developmental pathways in the same species. Non-embryonic developmental processes, such as budding or whole body regeneration, lack the familiar temporal and spatial cues classically associated with embryogenesis, like maternal determinants, or gastrulation. In our laboratory we genearated transcriptomic datasets covering the early steps of blastogenesis and vascular budding. Then we combined gene differential expression analyses with morphological approaches and we identified early regenerative structures during VB and then followed the fate of differentiating tissues during non-embryonic developments (PB and VB). In particular we observed expression of genes known to play key conserved functions in germ layer specification during solitary ascidian embryogenesis. We analized the expression patterns of FoxA1, GATAa, GATAb, Otx, Bra, Gsc and Tbx2/3 during both PB and VB. We found that the majority of these transcription factors were expressed during both non-embryonic developmental processes, revealing a regionalization of the palleal and vascular buds. Knockdown by siRNA in palleal buds confirmed that preventing the correct development of one of these regions blocks further tissue specification. Our results indicate that during both normal and injury-induced budding, a similar alternative developmental program operates via early commitment of epithelial regions.

16.10 – 17.10

Contributed Session C8: Palaeobiology and deep time

K3/K4

Chair: Javier Ortega-Hernández

C8-01 Cambrian ecdysozoans: a microscopic perspective

Harvey, Thomas H. P. (University of Leicester, GBR); Butterfield, Nicholas J. (University of Cambridge, GBR)

The rich record of Cambrian fossil ecdysozoans contributes crucial data for constraining phylogenetic hypotheses, resolving changes in diversity and disparity over time, and documenting the origins of modern-type phyla. In particular, Burgess Shale- and Orsten-type assemblages preserve diverse non-biomineralizing arthropods and worms, and therefore complement the more widespread record of biomineralizing groups, notably trilobites. Even so, each category of fossil assemblage is subject to inherent preservational biases, and cannot tell the whole story. Here, we describe microscopic fossils which have previously been overlooked but offer a novel, more biological perspective. The fossils occur as isolated body parts or near-intact cuticles, and preserve unprecedented anatomical detail. Pancrustacean appendages with diverse arrays of strongly differentiated spines and setae point to the early diversification of particle-handling and sensory roles. Cuticular components of priapulid-like worms include introvert scalids and pharyngeal teeth with

fine-scale adaptations that approach - or perhaps exceed - the diversity seen in modern priapulids. Cuticles of an extinct introvertan group, the palaeoscolecids, exhibit a fibrous cuticle structure shared (perhaps convergently) with modern nematoids, alongside scalidophoran-type sensilla. We also report on a fossil Cambrian loriciferan with the miniature body size (300 Âµm) and specialized scalid morphologies of modern representatives - the first in the fossil record. Overall, this microscopic view of Cambrian ecdysozoans reveals the early origination and subsequent conservation of various fine-scale cuticular adaptations and a miniaturized, meiofaunal body plan. By revealing anatomies that might previously have been considered „unfossilizable", the new microfossils offer additional characters for resolving ecdysozoan phylogeny and for tracking diversity and disparity over time, and a test of prevailing narratives which are biased towards macroscopic characters and organisms.

C8-02 An embryological perspective on the arthropod early fossil record

Chipman, Ariel D. (Hebrew University of Jerusalem, ISR)

Our understanding of the early evolution of the arthropod body plan has recently improved significantly through advances in phylogeny and developmental biology and through new interpretations of the fossil record. However, there has been limited effort to synthesize data from these different sources. I use current knowledge on the development of extant arthropods, together with published descriptions of fossils, to reconstruct hypothetical germband stages of a series of key taxa leading from the arthropod lower stem group to crown group taxa. These reconstruction highlight the main evolutionary transitions that have occurred during early arthropod evolution. The reconstructions suggest several novel homology hypotheses - e.g. the lower stem group head shield and head capsules in the crown group are all hypothesized to derive from the embryonic head lobes. The homology of anterior segments in different groups is resolved consistently. The transition between „lower-stem" and „upper-stem" arthropods is highlighted as a major transition with a concentration of novelties and innovations, suggesting a gap in the fossil record. A close relationship between chelicerates and megacheirans is supported by the embryonic reconstructions, and I suggest that the depth of the mandibulate-chelicerate split should be reexamined.

C8-03 Development and evolution of the synarcual in Placoderms and the Elephant shark

Chevrinais, Marion (Université du Québec à Rimouski, CAN); Johanson, Zerina (Natural History Museum, GBR); Trinajstic, Kate (Curtin University, AUS); Long, John (Flinders University, Adelaide, AUS); Morel, Catherine (Université du Québec à Rimouski, CAN)

During the evolution of vertebrates, the transition between jawless to jawed vertebrates occurred approximately 425 Ma with morphological

and developmental changes. These evolutionary novelties include jaws, paired pelvic fins and endoskeletal girdles, and reproductive intromittent organs. The presence of these novelties in the most phylogenetically basal jawed group, the placoderms, suggests that developmental mechanisms (e.g., lateral plate mesoderm formation responsible for the development of paired appendages) allowing such changes could have been already present in jawless. However, our most recent interpretation of a jawless anaspid-like fish, Euphanerops, from the Upper Devonian, challenged the evolutionary origin of some of the so-called jawed vertebrate synapomorphies. We describe, for the first time, pelvic girdles and intromittent organs in this jawless, associated with morphologically differentiated regions of the axial skeleton. Appendicular and axial skeleton novelties occur simultaneously in Euphanerops. Morphological differentiation of the anterior axial skeleton is also described for the first time in the extant jawless Sea lamprey Petromyzon marinus. Euphanerops and Petromyzon should have shared genetic pathways responsible for the development of the appendicular (abaxial domain of gene expression determining the lateral plate mesoderm development) and the axial (primaxial domain of genes coding for somite development) skeletons. In jawed vertebrates, the presence of the lateral somitic frontier suggests that the abaxial and primaxial domains are independent. But, recent studies on lamprey median fins show that these fins develop from somitic mesoderm suggesting that the origin of paired appendages could be associated with a re-deployment of this mechanism in lateral plate mesoderm. This suggests a dependence of abaxial and primaxial domains at least during some vertebrate ontogenetic stages. Euphanerops and Petromyzon ontogeny indicates that a modification of postcranial skeleton occurred earlier in vertebrate history than previously recognized.

C8-04 The new organizers hypothesis for chordate origins

Sato, Noriyuki (Technology Graduate University, Onna, JPN)

The origin and evolution of chordates is one of the most mysterious and intriguing phenomena in evolutionary developmental biology. Chordates are animals characterized by possession of a notochord, a dorsal neural tube, somites, and pharyngeal gill slits. They consist of three taxa, cephalochordates, urochordates (or tunicates), and vertebrates. Chordates belong to a supraphyletic group of deuterostomes, together with echinoderms and hemichordates, and are thought to have been derived from the common ancestor(s) of deuterostomes. Here I wish to propose the new organizers hypothesis for chordate origins by emphasizing following points; (1) the origins of chordates should be interpreted within deuterostomes, discussion with protostomes giving us less insights into this problem, (2) the origin of chordates is profoundly associated with the modification of developmental mode to form larvae or the occurrence of fish-like larvae, (3) most of the chordate-specific characters

including the notochord and somites developed with this larval form changes, and (4) each of the three chordate groups should be treated as phylum in future studies.

Satoh, N. (2016) Chordate Origins and Evolution. Academic Press, in press.

17.20 – 18.00
ROOMS C1&2

Keynote Lecture (K2)

Evo-devo of iterative body axis patterning; of mice and plants

Kerstin ten Tusscher
(University of Utrecht, NLD)

Chair: TBA

Animal body axis segmentation is an important subject for evo-devo research. Given that overt segmentation only occurs within the annelid, arthropod and vertebrate clades, an important question is whether segmentation evolved once in the bilaterian ancestor, or rather arose many times in parallel. Differences in segmentation mode deployed between different but also within the same organisms have taken as argument for parallel convergent evolution of segmenation. But what about convergence across kingdoms? In most segmented animals, segments are generated in a periodic anterior-posterior fashion, and this repetitive patterning arises from the coupling of oscillatory activity and polarised growth of the body axis that occur both from a posterior growth zone. In plant roots, growth also occurs in a polarised fashion from the root meristem, and lateral roots are generated sequentially in a shootward to rootward fashion. Even more intriguingly, prepatterning of groups of cells that become competent to form future lateral roots occurs through oscillations just above the root meristem. In this talk I will discuss similarities and differences in clock and wavefront animal segmentation versus plant lateral root patterning, and the extent to which these processes can be considered as convergent solutions to a similar developmental patterning „problem".

18.00 – 20.00
FLOOR 6

Poster Session 1
(even numbers)

09.00 – 10.40 Symposium S9:
Phenotypic plasticity driving evolution? Evidence from skeletal elements

STORA SALEN

Organizers: Antonio Cordero and Nathalie Feiner
Chairs: Antonio Cordero and Nathalie Feiner

S9-01 **Developmental evolution, plasticity and integration of the avian beak**
Abzhanov, Arkhat (Imperial College, London, GBR)

The astonishing variation in the shape and size of bird beaks reflects a wide range of dietary specializations that played an important role in avian diversification. Bird beak morphology is a result of a complex interplay of genetic and environmental factors acting during ontogeny. While developmentally responsive the beak shape is also genetically regulated but the exact contribution of intrinsic versus extrinsic and environmental controls may differ dramatically from species to species. Ancient integration mechanisms, such as bone mechanotransduction, may be co-opted to alter the level of jawbone plasticity, which evolves to reflect demands of natural history of the species.

S9-02 **Developmental evolution of - and through - phenotypic plasticity: case studies on horned beetles and beetle horns**
Moczek, Armin (Indiana University, Bloomington, USA)

Interactions between developmental processes and environmental conditions can affect the type and magnitude of selectable phenotypic variation, with the potential to constrain, bias, or facilitate the emergence of novel traits and functions. Our work utilizes horned beetles in the genus Onthophagus to explore the relative significances of diverse types of developmental plasticity, from trait-specific growth responses to nutritional variation to parental care and host-microbiome interactions to the origins of novelty and diversity. In this presentation I highlight our most significant findings to date.

S9-03 **Developmental modules in the diversification of the turtle shell**
Moustakas-Verho, Jacqueline (University of Helsinki, FIN)

The origin of the turtle shell over 200 million years ago greatly modified the amniote body plan, and the morphological plasticity of the shell

has promoted the adaptive radiation of turtles. The shell, comprising a dorsal carapace and a ventral plastron, is a layered structure formed by basal endochondral axial skeletal elements (ribs, vertebrae) and plates of bone, which are overlain by keratinous ectodermal scutes. Scutes develop as ectodermal appendages from placodal signaling centers and are patterned by reaction-diffusion dynamics. The experimental inhibition of Shh, Bmp, or Fgf signaling results in a disruption of the placodal pattern and, in the case of Shh and Bmp signaling, recapitulates the loss of scutes seen in softshell turtles. A computational model shows how two coupled reaction-diffusion systems reproduce both natural and abnormal variation in turtle scutes, and experimental evidence is used to test the hypothesis that abnormal growth or a shift in reaction-diffusion dynamics may be a consequence of environmental conditions during incubation. These placodal signaling centers, therefore, are hypothesized to be developmental modules that are responsible for the evolutionary plasticity and diversification of the turtle shell's scute patterns.

S9-04 Questioning the „early equals important rule" in ontogenetic processes: case studies from amniote ossification

Werneburg, Ingmar (Museum für Naturkunde Berlin, DEU)

The „early equals important rule"suggests that the earlier an element occurs in ontogeny, the larger and/or the more complex it becomes in adults. Amniote embryos, for example, often show a very early appearance of ossification centers related to jaw bones. They have a long time to develop and, consequently, upper and lower jaw elements are among the largest in the adult. In several case studies, we have analyzed the developmental timing of cranial and postcranial elements in mammals and sauropsids. We related changes in the sequence of ontogenetic characters to evolutionary aspects. In mammals, for example, the early appearance of the supraoccipital bone in ontogeny shows a significant correlation to the evolution of brain size. Among squamates, the stepwise evolutionary delay in the ossification of selected limb elements finally resulted in the loss of those bones in the ancestor of snakes as basis for their unique limb-less morphotype. In a further study, the evolution of adult morphological characters in squamate reptiles was directly compared to the evolution of developmental ossification sequences in the same group. For many aspects, the „early equals important rule"could be validated. However, in a number of cases, no clear correlation or even the opposite pattern was observed. Those exceptions can be explained, for example, as follows: 1. Altering growth speeds of different elements result in different adult shapes. 2. Some elements are embryologically important but lose their initial function in adult anatomy. 3. Mechanical loads through embryonic movements can shape an element. 4. Some embryonic elements are connected to each other and develop as a module. In conclusion, the „early equals important rule"is a frequent mode

of development; however, notable exceptions exist. Those are of great phylogenetic, functional, and ontogenetic importance, and need to be studied in a comprehensive morphological research program.

09.00 – 10.40

Symposium S10: Old questions, young approaches

SAL B

Organizers: José Martín-Durán and Bruno Vellutini
Chair: Bruno C. Vellutini

S10-01 Microbiome research and the eco-immunity of holobionts

Chiu, Lynn C. (University of Bordeaux, FRA)

Advances in top-down and bottom-up microbiome research allow us to raise deeper questions about the nature of „us", the host + resident microbiota („holobionts"). One aspect of the holobiont is the host immune system, which shapes and is shaped by host-microbial interactions. In our research group, we argue that it is important to take an eco-immunology perspective (Schulenburg et al 2009, Martin et al. 2011, Sadd and Schmid-Hempel 2009) of „holobiont immunity," that is, to understand holobiont immunity in its internalized and external microbial eco-evolutionary context. I distinguish between two eco-immunological approaches that falls respectively under the two major approaches of evo-devo research. Evo-devo, broadly construed, is concerned with both (1) the evolution of developmental systems ("evo-devo") and (2) the impact of these systems on organismal evolution ("devo-evo") in a complex interactive environmental context ("eco-devo-devo") (Müller 2007). The primary focus of the field eco-immunology is the first, „evo-devo." The general concern is the eco-evolutionary past and the trade-offs that resulted in the immune system as an evolutionary product. In this talk, I will discuss how advancements in microbiome research contribute new questions to the second approach, „devo-evo." I review supporting evidence that the eco-evolutionary conditions of the immune system are constructed by itself as it prunes, cultivates, stabilizes, and transmits ecological stimuli of its own development and function.

S10-02 Tiny changes, big effects: the impact of microexons on neuronal differentiation, function and evolution

Irimia, Manuel (Centre for Genomic Regulation, Barcelona, ESP)

One of the major challenges for the emergence of complex multicellular organisms is to generate an enormous diversity of cell types from a single genomic sequence. In the simplest scenario, the different cells would have the exact same protein complement available during embryo development to achieve their distinct functions and morphologies, often as divergent as those of a neuron or an erythrocyte. Therefore, how could neurons, for instance, tweak the structures and properties

of this common set of proteins to optimize their specific and distinct neuronal functions without jeopardizing those in other cell types? A well-known evolutionary mechanism to overcome this challenge is gene duplication and functional subfunctionalization of the copies. However, a less well established - and yet probably more flexible and widespread - mechanism with similar consequences is alternative splicing (AS). Through differential processing of introns and exons, AS can produce cell type-specific protein isoforms that allow optimization of their specific cellular functions. One of the most striking examples of this is provided by microexons in neurons. These tiny exons, which can encode as little as one or two aminoacids, are switched on during neuronal differentiation and show the highest evolutionary conservation of all AS types. They are often located in structured domains of proteins, where they subtly sculpt their interaction surfaces thereby modulating protein-protein interactions in a neuronal-specific manner. Although we are still beginning to unveil their biological functions, we already know they crucial for proper neuritogenesis, axon guidance, and neuronal function. The remarkable example of microexons illustrates how a co-regulated program of cell type-specific AS can diversify proteins sequences to generate novel molecular functions as well as optimize ancestral ones for complex cell type-specific tasks.

S10-03 Early animal evolution – Insights from exceptionally preserved Cambrian fossils

Ma, Xiaoya (Natural History Museum, London, GBR)

The Cambrian Explosion, marked by the sudden appearance of all major animal phyla in the fossil record, remains one of the most enigmatic evolutionary events in the history of life on Earth. This event is best evidenced by the exceptionally preserved Cambrian biotas around the world. Until recently these biotas were mainly investigated using the traditional techniques of describing palaeontological specimens. However, with the increasing development of new techniques and methods, as well as increasing integration among disciplines, these ancient fossils are giving up more of their secrets and contributing significantly to our understanding of early animal evolution. The Ecdysozoa (e.g. arthropods, nematodes, priapulids etc.) has the greatest biodiversity of any group of animals, their fossil record can be traced back to the earliest Cambrian period and has dominated the Earth ever since, which makes them a model group for investigating the early diversification of major animal phyla. This talk will introduce several recent breakthroughs in gaining a more detailed understanding of internal organ systems of Cambrian panarthropods and their evolutionary implications. The discovery of exceptionally preserved central nervous systems (CNS) of Cambrian panarthropods revealed that by the early Cambrian, arthropods had acquired complex brains; the two main CNS configurations observed in

living mandibulates and chelicerates had already diverged; anomalocaridid frontal appendages are pre-protocerebral and pre-ocular, as characters of the last common ancestor of euarthropods and onychophorans. The oldest cardiovascular system was also discovered from the Cambrian arthropod Fuxianhuia protensa, showing close association with its CNS. ïœ¨ Systematic reviews on Cambrian arthropod eyes demonstrated that some animals had acquired high visual capacity, which is also well supported by their CNS and cardiovascular systems. These internal anatomic details provide crucial information for understanding the phylogeny, physiology and ecology of early panarthropods.

S10-04 The Evolution of pleiotropy and modularity

Melo, Diogo (University of São Paulo, BRA); Marroig, Gabriel (University of São Paulo, BRA)

Evolution can only happen in the presence of variation, and in complex systems composed of multiple parts, the pattern of shared covariation is fundamental for understanding the evolutionary process. Genetic associations between traits can facilitate or alter evolutionary response, and without a robust theory of covariation we can not make sense of natural diversity. In this context, we can ask how genetic associations evolve, and how these changes are related to the genotype-phenotype map. We use experimental and computational approaches to understand how covariation changes under selection, how modular patterns can evolve, and how covariation and the genotype-phenotype map are related.

09.00 – 10.40

Symposium S11: Ancestral reconstruction of proteins, networks and genomes in plants and animals

SAL C

Organizers: Jerome Salse and Koen Geuten
Chair: Jerome Salse

S11-01 Ancestral complex and network evolution of MADS domain proteins and the origin of flowering plant lineages

Geuten, Koen (University of Leuven, BEL)

MADS-domain transcription factors are key regulators of plant development. They control identity transitions of plant meristems by timed and localised gene expression and complex formation in specific combinations of proteins. Ancient whole genome duplications have amplified the range of MADS-box genes present in extant plants. To understand the role of their evolution in the origin of flowering plant lineages, we inferred ancestral sequences of MADS-domain proteins at key transitions in plant evolution: the origin of flowering plants and the origin of core eudicots. By resurrecting the inferred sequences and expressing them heterologously, we characterised their protein interaction capacities in vitro and in vivo. Based on the observed protein interaction specificities,

we propose a model for the origin of bisexuality of the extant flower and describe how the properties of a protein interaction network originates.

S11-02 Lineage-specific radiations and the evolution of the genetic tool-kit
Brockington, Sam (University of Cambridge, GBR)

Comparative genomic analysis has revealed a significant fraction of genes that occur only in defined organismal lineages, and which have been variously termed orphan genes, taxonomically restricted or lineage-specific genes. Several studies have demonstrated that lineage-specific gene radiations can contribute to unique evolutionary changes and novel phenotypic adaptation. Here, exceptional taxon sampling, in conjunction with phylotranscriptomics has considerable power to reveal the complexity of gene family evolution and the extent of lineages specific radiations. Here we will examine the role of lineage specific gene radiations in the context of the evolution of key developmental modulators – the PIN auxin transporters. Within the PIN gene family, we demonstrate a remarkable degree of paralogous gene radiation across the major land plant organismal lineages, concomitant with convergent evolution of structural change. I will discuss the implications of these findings on our exploration of the evolution of morphological novelty, the implications for the concept of gene orthology in evolution and development, and the role of bioinformatics in the detection of novel developmental regulators.

S11-03 Reconstruction of the ancestral repertoire of proteins domains suggests modern genomes are deprived of building blocks
Bornberg-Bauer, Erich (Westfälische Wilhelms-Universität, DEU)

Modularity is a hallmark of molecular evolution. In signalling, regulatory and metabolic networks the recycling of their autonomous modules in different molecular contexts can expedite evolutionary innovation. Similarly, protein domains are structurally independent modules of proteins on which evolution acts, and modular domain rearrangements can create a vast diversity with few genetic operations, allowing for swift changes to an organisms' functional repertoire. This process is well amenable for large data sets given the strength of profile-based homology-inference and the lower rates of rearrangements. Accordingly, the wealth of available data presents an unrivaled opportunity to study the functional importance of modular molecular innovations by comparative genomics at a surprising accuracy. By comparing genomes from 30 insects, 25 plants and 50 fungi, we find the rates of gain and loss of domains and domain arrangements differ between clades but their relative ratios are remarkably similar. Thousands of domains are completely lost from genomes along every lineage since the roots while around two orders of magnitude fewer domains are gained, thus depriving modern genomes of their building blocks. Novel domains arise either as their own genes

or terminally, by extension of existing reading frames. Most strikingly and remniscent of the tenet that paralogs evolve fastest shortly after their reation, novel domains spread faster within their genomes than more established domains. Domain turnover occurs at lower rates than gene family turnover and the emergence of novel domains is foremost associated with abiotic stress response, biotic defence, development and reproduction. By comparing extant proteins and inferred ancestors we find novel single domains are more ordered, domains arisen by extension of reading frames are less ordered than established domains. These results raise further important issues regarding the physical nature of novel domains and proteins: if thetem from „"random"" DNA, how can they fold, function and be ultimately be selected for function?

S11-04 Paleogenomics in plants and animals to unveil evolutionary forces

Salse, Jerome (INRA, FRA)

During the last decade, technological improvements in sequencing technologies (NGS) led to the development of large sets of genomic resources permitting the emergence of high-resolution comparative genomic studies in both plant and animal lineages. Paleogenomics research, aiming at reconstructing ancestral genomes of modern living species, allowed us to propose a model in which the plant and animal genomes have evolved from a common ancestors with respectively a basic number of 5 to 13 chromosomes through whole genome duplications (i.e. paleopolyploidization) and translocations followed by lineage specific segmental duplications, chromosome fusions and translocations. These data demonstrates how extant animal and plant genomes are the result of inherently different rates and modes of genome evolution resulting in relatively stable animal and much more dynamic and plastic plant genomes. The established plant and animal ancestral genome, in term of chromosome structure and gene content, offer the opportunity to perform high resolution translational research from models and species of agronomic/medical interest. Efficient genomic transfer, based on accurate paleogenomics data, between mouse and Human as well as Arabidopsis/Brachypodium and cereals will be presented as case examples.

09.00 – 10.40 Symposium S12:
Process thinking for evo-devo

K3/K4

Organizer: Johannes Jaeger
Chair: Johannes Jaeger

S12-01 Process Thinking for Evo-Devo: an Introduction

Jaeger, Johannes (KLI, AUT)

Sometimes, an important aspect of the world is so obvious that we simply take it for granted. The processual nature of reality—that it is fundamentally a sequence of interconnected occurrences or events—is

one such aspect: we continually experience change, but tend instead to explain the world in terms of static things (lists or networks of genes, for example). This is particularly important for evo-devo, which consists of the study of developmental processes within evolutionary process. In this brief overview, I will introduce a bit of the history and the aim of process philosophy, and will present a number of concepts and tools that may be useful to think about evo-devo in process terms.

S12-02 Explanatory idealization and developmental processes

DiFrisco, James (KLI, AUT)

This talk provides an overview of some of the main motivations and advantages of adopting a process-centered perspective in the context of evo-devo research. I begin by discussing the role of conceptual habits in scientific research. One deeply entrenched conceptual habit - arguably itself an evolved outcome - fixates upon static and easily identifiable objects to the neglect of complex dynamics. It involves key idealizations that are useful simplifying assumptions in certain explanatory contexts, but that create problems when the idealizations are not recognized as such. I discuss a few examples of harmful idealizations that can and should be overcome by process-centered thinking in evo-devo research. These include genetic causal determinism, the static character of the genotype-phenotype map, the view of evolution as changing allele frequencies, and the identification of the organism with the adult stage in development. Process-based thinking leads to the view that whole life-cycles, or developmental processes, are more fundamental units of analysis than either genotypes or specific phenotypic stages.

S12-03 Inheritance of Process: A dynamical systems view of development and evolution

Monk, Nick (University of Sheffield, GBR)

Evolution and development are two aspects of the same dynamic process. Although they are both fundamentally processual, approaches to understanding their dynamics are typically based around â€œstaticâ€ entities. A key challenge in developing a process-based mechanistic understanding is the specification of a natural mathematical framework to explore dynamic structures. I will describe how the basic elements of a dynamical system - phase space, trajectories, attractors, basins, and separatrices - act as systems level descriptors for the logic of genotype-phenotype maps and their evolution.

S12-04 A damped oscillator drives posterior gap gene expression in Drosophila melanogasters

Verd, Berta (KLI, AUT)

„During insect development, segments either form sequentially (short-germband) or simultaneously (long-germband). In dipteran insects (flies, midges and mosquitoes), where the long-germband mode of segmen-

tation is used, the gap genes are activated by maternal gradients and cross regulate each other to form the first zygotic regulatory layer of the segmentation gene hierarchy. A precise data-driven mathematical model revealed that two distinct dynamical regimes govern anterior and posterior trunk gap gene patterning in Drosophila melanogaster . Stationary domain boundaries in the anterior rely on multi-stability whilst the observed anterior shifts of posterior gap gene domains can be explained as an emergent property of an underlying regulatory mechanism implementing a damped oscillator. Majour features of both regimes are recovered by a three-gene motif embedded in the gap gene regulatory network. Interestingly, this sub-network, known as the AC/DC motif, can also sustain oscillations. Oscillations are not found in the gap gene system but are characteristic of short-germband segmentation, suggesting that both modes share more than previously thought. Studying the evolution of gene regulatory networks can help us understand how oscillations arise or cease, and this will shed some light on how long-germband segmentation could have repeatedly and independently evolved from the ancestral short-germband mode."

11.10 – 12.25

Contributed Session C9:
Phenotypic plasticity driving evolution? Evidence from skeletal elements

STORA SALEN

Chair: Philipp Mitteroecker

C9-01

Allometry and sexual dimorphism in the human pelvis

Fischer, Barbara (KLI, AUT); Mitteroecker, Philipp (University of Vienna, AUT)

The sexual dimorphism in the human pelvis has evolved in response to several jointly acting selection regimes that result from the pelvis"multiple roles in locomotion and childbirth, among others. Because human males are on average taller than females, some aspects of sexual dimorphism in pelvis shape might result from allometry, the association between stature and pelvis shape across individuals. In this study, we aim to disentangle the two components contributing to pelvic sex differences: the allometric component, which emerges as a consequence of dimorphism in stature, and the remaining non-allometric sexual dimorphism component. We conducted a morphometric analysis of a dense set of 3D landmarks, measured on 99 female and male adult individuals. While pelvis size was similar in both sexes, pelvis shape differed substantially, with almost no overlap between females and males in shape space. Pelvis size and shape were similarly associated with stature in both sexes. Sexual dimorphism in the height-to-width ratio of the pelvis, and in the orientation of the iliac blades, was largely allometric, whereas the dimorphism in the subpubic angle and the relative size and distance of the acetabula was largely non-allometric. We conclude that,

in contrast to the overall pelvic proportions, sexual dimorphism in the birth-relevant pelvis dimensions are mainly of non-allometric origin and are likely mediated via steroid hormone secretion during puberty.

C9-02 Climate change will impact biodiversity through multiple forms of phenotypic plasticity

Campbell, Calum (University of Glasgow, GBR); Parsons, Kevin (University of Glasgow, GBR)

Climate change is expected to cause dramatic changes that will alter both natural selection and developmental conditions. Understanding interactions between development and temperature within the context of evolvability could be useful for making informed decisions about how to mitigate biodiversity loss. We hypothesised that temperature would alter bone development during key periods of ossification which in turn would alter levels of phenotypic plasticity. To test this we incubated Arctic Charr (Salvelinus alpinus) embryos at two different temperatures (5Â°C and 9Â°C to partially mimic an expected global temperature increase). We sampled embryos at two distinct developmental stages (pre-hatch and first-feeding) and performed cartilage and bone staining as well as staining for osteoblast (bone forming) and osteoclast (bone resorption) activity. We then measured variation in levels of staining to determine the impact of temperature. Additionally, a subset of fish from different temperatures were divided and subjected to benthic and limnetic prey to test for interactions between diet and temperature during ontogeny. Putative results suggest that embryos at 5Â°C exhibited higher levels of cartilage and bone development at stages equivalent to 9Â°C fish. Similarly, bone metabolism showed increased activity under 9Â°C, which may explain the increased levels of morphological plasticity found under warmer temperatures. We currently aim to assess performance traits in response to temperature, but our preliminary results suggest, 1) morphological plasticity corresponds to bone metabolism, 2) temperature interacts with diet in morphological plasticity, and 3) climate change will impact evolvability through increases in phenotypic plasticity. Studies such as this which place evo-devo into a conservation context have the potential to address the impact of climate change on biodiversity and evolvability in novel manners.

C9-03 Balance of natural selection and development in the origin of snakes

Oliveira da Silva, Filipe (University of Helsinki, FIN); Di-Poï, Nicolas (University of Helsinki, FIN)

Snakes evolved from lizards and show unique skeleton morphologies among vertebrates, including large vertebral counting, leading to unique body length, and highly-flexible skulls with bone morphologies adapted to unidirectional feeding of large preys. Despite centuries of anatomical and phylogenetic research, the ecological and developmen-

tal origins of snake skull remain amongst the most controversial topics in vertebrate evolution. Using multidimensional geometric morphometric and comparative methods as well as phenotypic trajectories of skull shape and developmental data of external skull traits, we provide here novel integrative insights into the morphology, ecology, development, and evolutionary history of early and modern snakes. First, based on the significant correlations observed between snake skull shape and habitat ecologies of extant and fossil species of lizards and snakes, we reconstruct the crown snake ancestor as a fossorial species that evolved from a terrestrial lizard. Those ecological estimations challenge the current adaptive hypotheses for origin of snakes that is focused on either a marine or fossorial lizard ancestry, and indicate an alternative ecological scenario at the origin of snakes. Second, our comparative developmental analyses of skull shape and morphogenesis between lizards and snakes demonstrated for the first time peramorphosis through acceleration in snake development. Finally, our data parallel the fastest somitogenesis rate among amniotes previously reported for snakes, strongly suggesting that snake head and body evolved in parallel. We demonstrate a balance of natural selection initially favoring fossoriality and developmental mechanisms producing faster developmental rates in snake evolution.

C9-04 Geometric morphometrics of developmental modularity and phenotypic integration in pinniped skull and teeth

Savriama, Yoland (University of Helsinki, FIN)

Modularity and integration are major concepts in evolutionary developmental biology and are used to describe the organization of biological systems. Modules can be broadly defined as connected units that are internally strongly coherent (integration) and relatively independent from other parts of the system. The empirical detection of modules have shown promising results for other biological systems and I had shed new light on the developmental processes that produce the traits and the role of morphological integration in the evolutionary diversification of clades. In mammalians, several studies have reported the compartmentalization of the skull into distinct morphological modules mainly separating a cranofacial ensemble from a neurocranial one, as opposed to the mosaic of modules identified for the teeth. Here, we explore and test hypotheses of modularity and integration in the skull and teeth of two species of pinnipeds Grey seal (Halichoerus grypus) and Ringed seal (Pusa hispida) that are morphologically distinct. We use landmark-based geometric morphometric methods for the shape and size analysis of the skull and teeth, completed with computational models that allow the simulation of hybridizations between disparate individuals and species. Preliminary analyses suggest that Grey seals show a higher degree of modularity between the face and neurocranium than Ringed seals that

reflect a strong sexual dimorphism located in the snout of Grey seals. These results are consistent with other studies of cranial modularity and integration in Carnivora.

C9-05 Diverse gene networks underlie development of convergent morphologies in turtles

Cordero, Gerardo Antonio (Lund University, SWE); Liu, Haibo (Iowa State University, USA); Wimalanathan, Kokulapalan (Iowa State University, USA); Weber, Rachel (Iowa State University, USA); Quinteros, Kevin (Iowa State University, USA); Janzen, Fredric (Iowa State University, USA)

Convergent evolution is often attributed to change in the underlying genetic architecture of similar traits in unrelated lineages. Even so, how genes interact during embryogenesis to ultimately converge upon strikingly similar adult morphologies is rarely examined. Thus, convergent evolution might be the result of predictable change in intricate gene networks that govern embryonic development. To test this hypothesis, we compared developmental transcriptomes of a novel shoulder blade morphology in two turtles that independently evolved complex shell-closing systems. As expected, developmental strategies unique to embryos of these unrelated lineages were congruent with gene expression divergence from a common ancestral state. Nonetheless, seemingly convergent developmental processes exhibited surprising diversity, thus dynamics of underlying gene networks were not completely identical. Our systems biology approach revealed lineage-specific variation in gene interactions that orchestrate morphogenesis and differentiation in divergent turtles with remarkably similar traits. In agreement with „developmental system drift" theory, we demonstrate that convergent trait evolution does not entirely arise via predictable change in developmental gene networks.

11.10 – 12.25 Contributed Session C10:
Old questions, young answers

SAL B

Chair: Kevin Pang

C10-01 Mapping the chemical connectome in the marine worm Platynereis dumerilii

Williams, Elizabeth A. (Max Planck Institute for Developmental Biology, Tübingen, DEU); Jékely, Gáspár (Max Planck Institute for Developmental Biology, Tübingen, DEU)

How did nervous system signaling evolve? Recent advances in high-throughput technologies are now allowing us to address this question through largescale studies of animal nervous systems. Connectomics is the reconstruction of an organism's neural circuits based on synaptic connections between neurons. This approach enables the generation of

maps of information flow through the nervous system that can provide mechanistic explanations of an organism's behavior. However, connectome maps based on synaptic connectivity alone give an incomplete understanding of nervous system function, as they fail to provide details of the signaling molecules involved in communication between different neurons. By combining connectome data with information from spatially resolved single cell RNA-Seq and high-throughput matching of signaling molecules to their specific receptors, we can incorporate details of molecular signaling into synaptic connectivity maps. Here, I demonstrate this approach using the larvae of the marine worm, Platynereis dumerilii, to create maps of chemical connectivity. Mapping the chemical connectome provides further insights into different signaling mechanisms operating in the nervous system of the larva, such as combinatorial peptidergic signaling and neuronal autoregulation. We used calcium imaging of live larvae to test hypotheses of nervous system signaling generated through the chemical connectome to demonstrate the predictive power of this approach. The addition of chemical neuromodulatory maps to synaptic connectivity maps should lead us to a more holistic understanding of the animal nervous system. The Platynereis dumerilii chemical connectome, which incorporates several evolutionarily conserved neuronal signaling molecules, will provide an important framework for future comparative studies.

C10-02 A single 3D chromatin compartment in amphioxus reveals stepwise evolution of vertebrate Hox bimodal regulation

Maeso, Ignacio (Universidad Pablo de Olavide, Seville, ESP); de la Calle-Mustienes, Elisa (Universidad Pablo de Olavide, Seville,ESP); Bertrand, Stéphanie (Université Pierre et Marie Curie, Paris, FRA; Observatoire Océanologique de Banyuls-sur-Mer, FRA); Diaz, Sergio G. (Universidad Pablo de Olavide, Seville, ESP); Aldea, Daniel (Université Pierre et Marie Curie, Paris, FRA; Observatoire Océanologique de Banyuls-sur-Mer, FRA); Aury, Jean-Marc (Commissariat à l'Energie Atomique (CEA), Institut de Génomique (IG), Genoscope, Evry, FRA); Mangenot, Sophie (Commissariat à l'Energie Atomique (CEA), Institut de Génomique (IG), Genoscope, Evry, FRA); Holland, Peter W. H. (University of Oxford, GBR); Devos, Damien P. (Universidad Pablo de Olavide, Seville, ESP); Escrivá, Hector (Université Pierre et Marie Curie, Paris, FRA; Observatoire Océanologique de Banyuls-sur-Mer, FRA); Gómez-Skarmeta, José L. (Universidad Pablo de Olavide, Seville, ESP)

Evolution of animal morphology largely depends on changes in the expression patterns of developmental genes. These genes are controlled by a large number of cis-regulatory elements that are distributed in extended genomic territories and are organized in 3D chromatin structures. However, it is currently unknown how these 3D chromatin compartments originate and evolve and how changes in their architecture

may have impacted the evolution of animal body plans. The HoxA and HoxD gene clusters of jawed vertebrates are organized into bipartite 3D chromatin structures that separate long-range regulatory inputs coming from the anterior and posterior Hox neighboring regions. This architecture is instrumental in allowing vertebrate Hox genes to pattern disparate parts of the body, including limbs. To understand how these 3D topologies originated, we performed an extensive 4C-seq profiling of the Hox cluster in embryos of amphioxus, an invertebrate chordate. We find that, in contrast to vertebrates, the amphioxus Hox cluster is organized into a single chromatin interaction domain that includes long-range contacts mostly from the anterior side, bringing distant cis-regulatory elements into contact with Hox genes. We infer that the vertebrate Hox bipartite regulatory system is an evolutionary novelty built by combining ancient long-range regulatory contacts from DNA in the anterior Hox neighborhood with new regulatory inputs from the posterior side.

C10-03 Transcriptomic signatures shaped by cell proportions shed light on differences in serial organ morphogenesis

Sémon, Marie (Ecole Normale Supérieure de Lyon, FRA); Guéguen, Laurent (Université de Lyon, Villeurbanne, FRA); Petit, Coraline (Ecole Normale Supérieure de Lyon, FRA); Lambert, Anne (Ecole Normale Supérieure de Lyon, FRA); Renata Peterkova (Institute of Experimental Medicine,Prague, Czech Republic); Pantalacci, Sophie (Ecole Normale Supérieure de Lyon, FRA)

„Understanding how differences in phenotype arise from differences in gene expression is a key question in evo-devo. Most transcriptomic studies comparing developing embryos or organs start with global patterns of variation in transcriptomes, which are typically extracted by multivariate analysis and identify different species or organs through developmental time. Surprisingly, it is poorly known i) what kind of expression differences shape these patterns and ii) what can be learned from these patterns on the developmental differences underpinning different morphologies. We compared time-course RNA-seq transcriptomes during development in two morphologically distinct serial organs, the upper and lower first molars in mouse. We found that these teeth largely share the same gene expression dynamics. Three major transcriptomic signatures distinguished the two teeth, all shaped by differences in the relative abundance of different cell types. First, lower/upper molar differences maintained throughout morphogenesis. These stem from differences in the relative abundance of mesenchyme, and in gene expression within tissues, established since tooth specification. Second, time-shift differences were patent in the transcriptomes. These differences could be reproduced in a simple model predicting the relative abundance of crown cusp tissue in the tooth primordia. Third, upper/lower transcriptomes differ most at early-mid crown morphogenesis, corresponding to

transiently exaggerated morphogenetic processes in the upper molar (less mitotic cells, more migrating cells). From these findings, we formulate specific hypotheses on the mechanisms enabling the two molars to reach different phenotypes. Gene expression in a complex tissue reflects not only transcriptional regulation but also abundance of different cell types. Our study shows that this simple fact, often overlooked, can be used to get valuable insights on the cellular processes underpinning differences in organ development."

C10-04 Understanding the origin of an evolutionary novelty: the male-specific turbanate eyes of the mayfly Cloeon dipterum

Almudi, Isabel (CSIC-Univ. Pablo de Olavide. 41013, Seville, ESP); Martín-Blanco, Carlos (CSIC-Univ. Pablo de Olavide. 41013, Seville, ESP); Davie, Kristofer (University of Leuven, BEL); Aerts, Stein (University of Leuven, BEL); Alba-Tercedor, Javier (University of Granada, ESP); Casares, Fernando (CSIC-Univ. Pablo de Olavide. 41013, Seville, ESP)

Evolutionary innovations are biological revolutions: new organs are critically associated with the emergence of new species and their exploitation of new niches. Despite their importance in the history of life, how morphological novelty arises and evolves is a long-standing question in Evolutionary Biology. How the genetic network associated to the new structure appears? How this new structure is functionally and anatomically integrated into the pre-existing body plan? One of the most striking examples of a sexually dimorphic novel structure occurs in males of the mayfly species Cloeon dipterum. Cloeon males develop, in addition to the compound eyes (shared by males and females), an extra pair of extremely large dorsal, turban-shaped eyes. Thus, by comparing males versus females, this mayfly species provides a privileged system to understand the origin and integration of new structures. To answer these questions, first, we have successfully established a C. dipterum culture in the lab. Next, we describe the development of the eye and its integration with the optic lobes of male and female Cloeon nymphs using X-ray microtomography (micro-CT). Furthermore, we compare sex-specific gene expression in nymphal heads, with a special focus on genes of the highly conserved Retinal Determination Network (RDN), to show how RDN elements could have played a role in the origin of this novel sexually dimorphic visual organ.

C10-05 Nervous system patterning in the Acoelomorpha

Pang, Kevin (Sars Centre, Bergen, NOR); Hejnol, Andreas (Sars Centre, NOR)

The Acoelomorpha is a group of small, acoelomate worms that are comprised of the Acoels and Nemertodermatids. These morphologically simple animals have recently attracted more attention due to their phylogenetic position, together with the enigmatic Xenoturbella, as sister

group to the remaining Bilateria. Within the Acoelomorpha, there is a wide diversity of neural structures, ranging from a basiepidermal nerve plexus like that found in Nemertodermatids and Xenoturbella, to more complex structures, including a brain and neurite bundles, found in Acoels. Here, we investigate the patterning of the nervous systems in the nemertodermatids, Meara stichopi and Nemertoderma westbladi, and the acoel, Isodiametra pulchra. M. stichopi possesses a basiepidermal nerve net, along with a dorsal pair of neurite bundles extend along the anterior-posterior axis, while N. westbladi has two pairs of neurite bundles (lateral and ventral). In contrast, I. pulchra has a bilobed brain and four pairs of neurite bundles (two ventral, one lateral, one dorsal). While the neurite bundles in M. stichopi and N. westbladi are at the base of the epidermis, the brain and neurite bundles of I. pulchra are located subepidermally, below the musculature. Using a candidate gene approach, we look at the expression of genes that may be involved in the development and maintenance of nerve condensations. We examined genes that are involved in the anterior-posterior and dorsal-ventral patterning of the nervous systems. Despite the differences in neural architecture, overall neuroectodermal patterning in the Acoelomorpha remains conserved. It is possible that an ancient neuroectodermal coordinate system predates the evolution of bilaterian nerve condensations.

11.10 – 12.25

Contributed Session C11:
Ancestral reconstruction of proteins, networks and genomes in plants and animals

SAL C

Chair: Jordi Paps

C11-01 Reconstructing the genome of the first animal: the impact of novelty in the origins of metazoans

Paps, Jordi (University of Essex, GBR); Holland, Peter W. H. (University of Oxford, GBR)

The Animal Kingdom displays a stunning diversity, result of millions of years of evolution. How did single cell microbes become animals with multiple cells? How was the transition from animals such as sponges, with a topside and downside but no front and back, to creatures as us with a front and a back end and an upside and downside? Nowadays the plethora of new genomic data can be exploited to tackle these critical questions on the genesis and evolution of metazoans. We have compared more than 60 genomes belonging to 13 animal phyla and 8 eukaryotic outgroups. This dataset and the analyses performed pay special attention to the taxon sampling, selection of outgroups, and the automatic assignment of gene homology. Moreover, we developed new bioinformatic tools to trace back the origins of genes in the gnarls of the Tree of Life of animals. We show how this pipeline is able to pinpoint

genes playing a major role in the dawn of animals, most of them tightly related to classical hallmarks of the origins of multicellularity, but others pointing to unforeseen functions that might be vital to our understanding of the rise of the Animal Kingdom. Some of the genes found have been previously related with the beginnings of animals, proving the predictive power of our approach. However, we also find other genes not related before with the origins of Metazoa, but that hold biological functions that make a huge biological sense in the context of that transition.

C11-02 TopAnat enrichment of anatomical expression patterns shows that selection on expression in nervous tissues is a major determinant of duplicate gene retentions

Robinson-Rechavi, Marc (University of Lausanne, CHE); Roux, Julien (University of Lausanne, CHE); Liu, Jialin (University of Lausanne, CHE)

The evolutionary history of vertebrates is marked by three ancient whole-genome duplications: two successive rounds in the ancestor of vertebrates, and a third one specific to teleost fishes. Biased gene loss of 80-90% of duplicates leads to the enrichment of the genome in certain functions, such as transcription factors, but this selective retention is not fully understood. Especially that there appears to be a complex relation between retention, evolutionary rate, and essentiality. We used a new method of anatomical ontology enrichment analysis, TopAnat, applied to gene expression data from in situ hybridizations of thousands of genes from two vertebrates: zebrafish and mouse. TopAnat (http://bgee.org/?page=top_anat) is similar to GO enrichment analysis, but calculates anatomical enrichment based on the Uberon ontology of bilaterian anatomy and on mapping of genes to anatomy by expression patterns. This is possible thanks to the integration of curated wild-type healthy gene expression data into the Bgee database, where RNA-Seq, microarray, EST and in situ hybridization data are transformed to comparable present / absent calls, mapped to detailed anatomy and development.We found that expression in the nervous system drives retention of duplicates after whole-genome duplication. Further analysis showed that selection against protein misfolding has stronger constraint on sequence evolution of genes expressed in nervous system, which could lead to lower chance of pseudogenization caused by relaxed purifying selection and result in a biased retention.

Bgee team: Mathieu Seppey, Komal Sanjeev, Valentine Rech De Laval, Philippe Moret

SIB WebTeam: Panu Artimo, Severine Duvaud, Vassilios Ioannidis, Heinz Stockinger“

C11-03 Comparative genomics of an adaptive radiation: transposable elements in Hox gene clusters correlate with patterns of diversification

Feiner, Nathalie (Lund University, SWE)

The processes underlying adaptive radiations have puzzled naturalists ever since the Galapagos Finches caught Darwin's attention, and novel technologies allow us to revisit this old question. Adaptive radiations occur when groups of distinctive yet closely related species evolve rapidly from a common ancestor. Transposable elements (TEs) may play important roles in this process. In an active state, these mobile genetic elements can insert elsewhere in the genome and cause changes to genome structure and gene regulation, thereby linking rapid reproductive isolation through genomic incompatibility with the origin of novel phenotypic variation. This study addresses the impact of TE activity on the adaptive radiation of Anolis lizards. In a comparative framework, I analyzed the distribution and accumulation of TEs in Hox gene clusters, genomic regions that regulate development of the morphological adaptations that characterize habitat specialists in these lizards. Unlike other vertebrates, including closely related lizard taxa, Anolis lizards have high numbers of TEs in the genomic regions of Hox clusters. Here I show that following a burst of TE activity in the lineage leading to extant Anolis, TEs have continued to accumulate during speciation events, resulting in a positive relationship between TE density and rate of speciation. These results suggest that TE activity may facilitate adaptive radiation by promoting speciation. Several of the TEs are actively transcribed and hence may be functional, but there was no evidence that the density of TEs is associated with ecological morphology. Nevertheless, an unusually high density of TEs in Hox clusters suggests that transposition could have been a rich source of phenotypic variation that may have facilitated the rapid parallel morphological adaptation to microhabitats we see in extant Anolis lizards.

C11-04 Using the Physcomitrella pseudochromosomal genome assembly as a tool to probe the duplication history of this plant's MADS-box gene family.s

Ashton, Neil W. (University of Regina, Saskatchewan, CAN); Barker, Elizabeth I. (University of Regina, Saskatchewan, CAN)

Plant MADS-box genes are known best for their roles in floral organogenesis. However, they are amply represented in vascular and non-vascular cryptogams. They are classified as type I or II with type II subdivided into MIKCC and MIKC* genes. Assembly of the sequenced genome of the moss, Physcomitrella patens, into 27 mega-scaffolds (pseudochromosomes) confirmed the major predictions of our earlier model of expansion of the MADS-box gene family in the Physcomitrella lineage. Additionally, microsynteny has been conserved in the immediate vicinity of some recent duplicates of MADS-box genes. However, comparison of non-syntenic MIKC MADS-box genes and neighbouring genes indicates that chromosomal rearrangements and/or sequence degeneration have destroyed shared synteny over longer distances (macrosynteny) around

MADS-box genes despite subsets comprising two or three MIKC genes having remained syntenic. In contrast, half of the type I MADS-box genes have been transposed creating new syntenic relations with MIKC genes. This implies conservation of ancient ancestral synteny of MIKC genes and of more recently acquired synteny of type I and MIKC genes may be selectively advantageous. Our revised model predicts the birth rate of MIKC genes in Physcomitrella is higher than that of type I genes. However, this difference is attributable to an early tandem duplication and an early segmental duplication of MIKC genes prior to two polyploidisations that account for most of the expansion of the MADS-box gene family in Physcomitrella. The early segmental duplication spawned two chromosomal lineages: one with a MIKCC gene, belonging to the PPM2 clade, in close proximity to one or a pair of MIKC* genes and another with a MIKCC gene, belonging to the PpMADS-S clade, characterised by greater separation from syntenic MIKC* genes. Our model has evolutionary implications for the Physcomitrella karyotype. It can also guide the choice of functionally redundant genes in multiple gene knockout experiments.

C11-05 Neofunctionalization of a duplicate dachshund gene underlies the evolution of a novel leg segment in arachnids

Turetzek, Natascha (Georg-August-University Göttingen, DEU); Pechmann, Matthias (Universität zu Köln, DEU); Schomburg, Christoph (Georg-August-University Göttingen, DEU); Schneider, Julia (Georg-August-University Göttingen, DEU); Prpic, Nikola-Michael (Georg-August-University Göttingen, DEU)

The acquisition of a novel function, or neofunctionalization, protects duplicated genes from redundancy and subsequent loss, and is a major force that drives adaptive evolution. Neofunctionalization has been inferred for many duplicated genes based on differences in regulation between the parental gene and its duplicate. However, only few studies actually link the new function of a duplicated gene to a novel morphological or physiological character of the organism. Here we show that the duplication of dachshund (dac) in arachnids (spiders and allies) is linked with the evolution of a novel leg segment, the patella. We have studied dac genes in two distantly related spider species, the entelegyne spider Parasteatoda tepidariorum and the haplogyne spider Pholcus phalangioides. Both species possess two paralogous dac genes that duplicated before the split between entelegyne and haplogyne spiders. In contrast to the evolutionarily highly conserved dac1, its duplicate dac2 is strongly expressed in the patella leg segment during embryogenesis in both species. Using parental RNA interference in P. tepidariorum we show that dac2 is required for the development of the patella segment. If dac2 function is impaired, then the patella is fused with the tibia into a single leg segment. Thus, removing the function of dac2 experimentally reverts P. tepidariorum leg morphology into a stage before the duplication of

dac and the evolution of the patella segment. Our results indicate that the origin of the patella is the result of the duplication and subsequent neofunctionalization of dac in the arachnid lineage.

11.10 – 12.25 Contributed Session C12:
Integrating the genotype-phenotype map with concepts of evolutionary-developmental biology

K3/K4 Chair: Michael Schubert

C12-01 **Integrating developmental knowledge to quantitative genetic models: Mapping the genetic determinants of molar sizes in mice**

Navarro, Nicolas (PSL Research University, Paris, FRA; Université de Bourgogne Franche-Comté, Dijon, FRA); Maga, A. Murat (University of Washington, Seattle, USA; Seattle Children's Research Institute, Seattle, USA)

Developmental biologists have shown that posterior molars originate from successive dental laminae, extending from the preceding tooth, and containing progenitor cells initiating tooth development with the formation of the dental placodes. Previously initiated molars seem to express inhibitors balancing mesenchymal activators, a phenomenon that was coined as Inhibitory Cascade model (IC) and demonstrated for different orders of mammals including rodents. Although originally described for tooth development, IC is now generalized to any sequentially forming structure, such as limbs or vertebrae. So far the actual identification of potential candidates for those inhibitors in the IC model of molar proportions has been elusive. Thus, quantitative genetics and epigenetics of this activation/inhibition balance remain largely unknown. Our objective is to map the „"relationship QTLs""- loci that control for genetic variation in the influences of previously developed teeth - for molar sizes using quantitative genetics toolkits. For that, we use an automated segmentation and shape quantification method to capture the 3D shapes and sizes of all maxillary and mandibular molars from 400 mCT scans in a mouse backcross population.

C12-02 **Endoplasmic reticulum chaperones control developmental buffering under thermal stress**

Sato, Atsuko (Ochanomizu University, JPN); Shimeld, Seb (University of Oxford, GBR)

Organismal development is extremely robust within each species, being buffered against genetic variation and environmental perturbation. Study of laboratory model species has revealed several possible mechanisms underlying developmental buffering, yet whether these mechanism are also important in wild populations is not known. We exploit wild populations of the marine chordate Ciona intestinalis that recently split into two species adapted to different thermal environment:

type B limited to Northern Atlantic and type A lives warmer environment a such as Japan, Mediterranean Sea, and West Coast of US. By comparing developmental robustness under heat stress, we found that type B is more susceptible to thermal stress, explaining the differences in their habitat. Examining reaction after heat stress in cross hybrids, we found that level of developmental buffering is maternally inherited. Comparative transcriptomics show expression levels of genes encoding canonical chaperones such as Hsp70 and Hsp90 do not correlate with buffering levels, nor maternally inherited in hybrid embryos. However, the expression of genes encoding endoplasmic reticulum (ER) associated chaperones does correlate and also maternally inherited. By examining the ER chaperone in genome sequences from various organisms, we found that the ER chaperone is widely conserved amongst animal kingdom. To investigate the functional conservation amongst chordates, we also tested function of the ER chaperone in a model fish species, Danio rerio. MO knockdown experiments showed that the ER associated chaperones are also important in developmental buffering in fish. These results show that ER associated chaperones comprise a cellular basis for canalization, and that variation in their expression in natural populations may explain variation in the ability of embryos to buffer environmental insult. ER chaperones have been neglected by the fields of development, evolution and ecology, but their study will enhance understanding of both our evolutionary past and the impact of global environmental change.

C12-03 Genetic basis of petal number variation

Monniaux, Marie (Max Planck Institute for Plant Breeding Research, Köln, DEU); Pieper, Bjorn (Max Planck Institute for Plant Breeding Research, Köln, DEU); Hay, Angela (Max Planck Institute for Plant Breeding Research, Köln, DEU)

Petals play a major role in the reproduction of flowering plants by attracting pollinators and assisting flower bud opening; as such they constitute one of the key innovations of angiosperms and participated in their extraordinary ecological success. Petals display at the same time a tremendous inter-specific diversity, with variation in number, shape and colour across the angiosperms, and a very restrained intra-specific diversity, since floral patterning is usually highly robust within one particular species. Petal number variation in flowering plants thus represents a promising system to understand the balance between flexibility and robustness in development, and its ecological and evolutionary consequences. We study Cardamine hirsuta, a close relative to Arabidopsis thaliana, which displays flowers with a variable loss of petals. We found that the A-class MADS-box gene APETALA1 (AP1) was a key determinant of petal number variation between those two species. Subtle differences in the expression patterns of AtAP1 and ChAP1 in the flower meristem, at the stage relevant for petal initiation, suggest that regulatory differences

at the AP1 locus underlie petal number variation between these species. Interestingly, none of the quantitative trait loci (QTL) mapped in five C. hirsuta recombinant inbred line populations corresponded to AP1, showing that intra- and inter-species phenotypic variation can have a different genetic basis. However AtAP1 indirectly controls the inter-species variation by acting epistatically on the QTL, whereas ChAP1 lost its epistatic action during evolution, resulting in phenotypic variability. Finally, we are performing field experiments in order to explore the ecological consequences of petal number variation in C. hirsuta.

C12-04 **Lineage-specific duplication of amphioxus CYP26-type retinoic acid degrading enzymes resulted in sub-functionalization of patterning and homeostatic roles in the embryo**

Schubert, Michael (Sorbonne Université, Paris 06, FRA; Observatoire Océanologique de Villefranche-sur-Mer, FRA)

Tight regulation of retinoic acid (RA) availability is fundamental for normal development. In parallel to RA synthesis, a negative feedback loop controlled by RA catabolizing enzymes of the cytochrome P450 subfamily 26 (CYP26) is crucial. In vertebrates, the functions of the three CYP26 enzymes (CYP26A1, CYP26B1, CYP26C1) that arose by two rounds (2R) of whole genome duplication (WGD) have been well characterized. By contrast, outside the vertebrates, little is known about CYP26 complements and their biological roles. In an effort to characterize the evolutionary diversification of RA catabolism, we studied the CYP26 genes of the cephalochordate amphioxus (Branchiostoma lanceolatum), an animal characterized by a vertebrate-like genome that has not undergone the 2R WGD. We found that the three amphioxus CYP26 genes (CYP26-1, CYP26-2, CYP26-3) are clustered in the genome and likely originated by lineage-specific duplication. The amphioxus CYP26 cluster hence represents a useful model to assess adaptive evolutionary changes of the RA signaling system following gene duplication. The characterization of amphioxus CYP26 expression, function, and regulation by RA signaling demonstrated that, despite the independent origins of CYP26 duplicates in amphioxus and vertebrates, they convergently assume two main roles during development: RA-dependent patterning and protection against fluctuations of RA levels. Importantly, while in vertebrates these two roles are assumed cooperatively by all three CYP26 genes, amphioxus CYP26-2 is required for RA-dependent patterning, while amphioxus CYP26-1 and CYP26-3 mediate RA homeostasis. Furthermore, comparisons of the regulatory regions of CYP26 genes of different bilaterians indicated that a CYP26-driven negative feedback system was present in the last common ancestor of deuterostomes, but not in that of bilaterians. Altogether, this work revealed convergent functions for CYP26 enzymes that originated by independent duplication events and hence reveals a novel selective mechanism for the genomic retention of gene

duplicates.

C12-05 Evolutionary comparison of gene regulatory networks for organogenesis

Arnone, M. Ina (Stazione Zoologica Anton Dohrn, Naples, ITA); Andrikou, Carmen (Stazione Zoologica Anton Dohrn, Naples, ITA); Annunziata, Rossella(Stazione Zoologica Anton Dohrn, Naples, ITA); Cuomo, Claudia (Stazione Zoologica Anton Dohrn, Naples, ITA); Lowe, Elijah (Stazione Zoologica Anton Dohrn, Naples, ITA); Perillo, Margherita (Stazione Zoologica Anton Dohrn, Naples, ITA)

Comparative gene regulatory network (GRN) approaches have been proven to be very useful in studying evolution of specification processes, body parts and organs. Using the sea urchin as main model system, we are studying the GRNs that orchestrate the formation of feeding related organs: the circum-esophageal muscles, the pancreas and the posterior gut, the latter differentiating into stomach, pyloric sphincter and intestine. The comparison of these organogenesis GRNs with their putative homologs in other echinoderm (sea star), vertebrate and also protostome animals highlighted striking commonalities: except for the use of some recurrent sub-circuits (such as the hnf1-ptf1a sub-circuit controlling acinar-like cell type formation in sea urchins and vertebrates), these developmental GRNs appear to be subject of considerable rewiring even when they contain the same groups of orthologous genes. Even more prominent is the fact that these genes often display extreme conservation of topology of expression within similar cell types or body parts. This is well illustrated by the recurrent use of the ParaHox genes xlox/pdx1 and cdx in posterior gut patterning of most bilaterians. Similarly, a significant number of the same orthologous genes seem to be involved in muscle development within metazoans (foxc, foxf, myod among others). An obvious question that arises is what actually are the constraints that maintain such a strong association between the regulatory genes and the domain of their expression even when the GRNs that connect them get extensively rewired. However, the fact that the same factors are used over and over in such different animal systems indicates that their modular components are somehow required for keeping organogenesis specific activities during evolutionary time.

14.00 – 15.40 Symposium S13:
Integrating the genotype-phenotype map with concepts of evolutionary-developmental biology

STORA SALEN

Organizers: Claudius Kratochwil and Joost Woltering
Chairs: Claudius Kratochwil and Joost Woltering

S13-01 Adaptive divergence and the dynamics of the genotype-phenotype map

Parsons, Kevin (University of Glasgow, GBR)

Adaptive divergence has fascinated biologists for more than a century but has usually been studied within a framework that assumes a straightforward and stable genotype to phenotype relationship. Recent advances from genetics have reinforced this framework for unusually simple loss of function traits, but the reality is that most traits pose a far greater challenge to understand from a genotype to phenotype perspective. A developmental perspective is now shaping research that appreciates how dynamic the genotype-phenotype map is with regards to factors such as environmental variation. Here I discuss how research on adaptive divergence in fish demonstrates a dynamic and evolving genotype-phenotype map, and how these findings can be used to address core theories surrounding the role of phenotypic plasticity in adaptive divergence. These findings suggest a new paradigm is needed for genetic research that takes into account the salient ecological environment when determining genotype to phenotype relationships.

S13-02 The evo-devo and physics of skin appendages and skin colours in reptiles

Milinkovitch, Michel C. (University of Geneva, CHE)

Skin appendages and integumentary colours in terrestrial vertebrates play crucial roles in, among others, thermoregulation, photoprotection, camouflage, and visual communication. One primary goal in my laboratory is to understand how genetic variation and physical parameters affect the development of these skin traits. More specifically, we combine EvoDevo, physics and computer modelling to understand morphogenesis and patterning of skin colours (pigmentary and structural colours) and of skin appendages (scales, hairs, spines) in reptiles and mammals. Using as showcases some of our recent results in the physics of chameleon colour change and the mapping of colour trait mutations in snakes, I will argue that a careful combination of biological and physical approaches will transform a mere collection of spectacular traits into a coherent mechanistic paradigm for the evolution and development of diversity and complexity of forms.

S13-03 Molecular mechanism and evolutionary process of female-limited Batesian mimicry in Papilio butterfly.

Fujiwara, Haruhiko (University of Tokyo, JPN)

A swallowtail butterfly, Papilio polytes, has two types of females, one of which resembles the unpalatable model butterfly, Pachliopta aristolochiae. It is known that this female-limited Batesian mimicry is controlled by a single autosomal locus H which is suggested to be a „supergene", but its molecular background has been obscure for a long time. To explore this mechanism, we performed linkage mapping analysis and whole genome sequencing with next generation sequencers. The latter

data showed a single 130kb-autosomal inversion outside doublesex (dsx) between mimetic (H) and non-mimetic (h) chromosomes, which is consistent with a locus identified from the linkage mapping. These results indicate a novel and potential approach to map the responsible region for complex trait only by whole genome sequencing. We also established a new method using in vivo electroporation to analyze gene functions in butterfly wings. Using this method, we found that only dsx from H-chromosome can induce the mimetic color pattern and simultaneously repress the non-mimetic pattern in female wings. In this meeting, I would like to discuss about the evolutionary origin and process of the female-limited Batesian mimicry of Papilio species.

Nishikawa et al. (2015) A genetic mechanism for female-limited Batesian mimicry in Papilio butterfly. Nature Genetics (2015) 47, 405-409."

S13-04 Floral organ specification: evolutionarily conserved master regulatorswith variable target genes

Kaufmann, Kerstin (University of Potsdam, DEU)

Understanding the evolution of flower morphologies across angiosperms is a central question in plant evo-devo research. Floral homeotic transcription factors, which are master regulators of floral organ specification, have been identified in many model and non-model flowering plant species. Based on the characterization of mutant phenotypes, the basic functions of floral homeotic proteins in specification of the different types of floral organs appear to be largely evolutionarily conserved. This raises the question at which level(s) in the gene-regulatory hierarchy the diversity in flower and floral organ morphologies was created during evolution. Recently, we compared DNA-binding sites and potential direct target genes of the floral homeotic protein SEPALLATA3 (SEP3) in the model plant Arabidopsis thaliana and in a closely related sister species, A. lyrata, by comparative analysis of ChIP-seq data. A high level of DNA binding site divergence is observed in these two species that originated from a common ancestor about 10 MYA. Our results suggest that only a basic „core"downstream network of floral homeotic regulators is conserved across these morphologically similar species. Currently, we experimentally characterize the evolution of active regulatory regions in these two species at genome-wide scale. The data allow us to study the general molecular mechanisms of cis-regulatory diversification and their impact on the evolution of developmental gene regulatory networks in plants.

14.00 – 15.40 Symposium S14:
Progress in animal phylogeny and its impact on the evolution of organ systems

Organizer: Andreas Hejnol

SAL B Chair: Andreas Hejnol

S14-01 The role of Xenacoelomorpha in understanding the evolution of animal diversity

Cannon, Joie (Naturhistoriska Riksmuseet, Stockholm SWE); Vellutini, Bruno (Sars Centre, Bergen, NOR); Jondelius, Ulf (Naturhistoriska Riksmuseet, Stockholm SWE); Hejnol, Andreas (Sars Centre, Bergen, NOR)

Xenacoelomorpha, comprising Acoela, Nemertodermatida, and Xenoturbella, are bilaterally symmetrical marine worms that lack a number of features common to most other bilaterians, e.g. anus, excretory organs, and circulatory system. The position of Xenacoelomorpha in the tree of life has been a major question in the study of deep animal relationships. In recent years, two conflicting hypotheses have been under debate: Xenacoelomorpha is sister group to all remaining Bilateria (=Nephrozoa, i.e. protostomes and deuterostomes), or is a clade inside Deuterostomia. Thus, determining the phylogenetic position of this clade is pivotal for understanding the early evolution of bilaterian features, or alternatively as a case of drastic secondary loss of complexity. We have shown robust phylogenomic support for Xenacoelomorpha as the sister taxon of Nephrozoa. Our phylogenetic analyses based on eleven novel xenacoelomorph transcriptomes and using different models of evolution under maximum likelihood and Bayesian paradigms, strongly corroborate this result. Additionally, gene complement analyses of several key developmental gene families based on xenacoelomorph genome and transcriptome surveys will be discussed. The sister group relationship between Nephrozoa and Xenacoelomorpha supported by our phylogenomic analyses implies that the last common ancestor of bilaterians was likely a benthic, ciliated acoelomate worm with a single opening into an epithelial gut and that excretory organs, coelomic cavities and nerve cords evolved after xenacoelomorphs separated from the stem lineage of Nephrozoa.

S14-02 Ancient deuterostome origins of a cis-regulatory element involved in vertebrate forebrain patterning

Lowe, Christopher J. (Stanford University, USA); Minor, Paul (Stanford University, USA); Yao, Yao (University of Pennsylvania, USA); Pani, Ariel (University of Chicago, USA); Epstein, Douglas (University of Pennsylvania, USA)

The origins of the vertebrate brain have been a topic of debate for several centuries. Much of what we understand about the origins of our own complex body plan and nervous system has been based on comparative studies between the body plan of vertebrates and the simpler basal chordate lineages. Our work adds a new perspective to the origins of vertebrates: Hemichordates are a phylum closely related to chordates, but with a contrasting body plan and neural organization. Despite this orga-

nizational and morphological disparity, our detailed studies using both descriptive and functional approaches reveal that hemichordate and vertebrate basic axial patterning share exquisite similarities during CNS and ectodermal patterning. Surprisingly, recent transgenic approaches have revealed some of this conservation is a result of deep conservation of the underlying regulatory logic, not shared with basal chordates, despite their much closer morphological affinities with vertebrates. I will discuss the implications of our findings for early vertebrate origins, but also what our data suggests about the rather loose connection between gene regulatory network and morphological evolution.

S14-03 How small-scale meiofauna may inform on large-scale evolution, of the nervous system in Spiralia.

Worsaae, Katrine (University of Copenhagen, DEN)

Since the dawn of phylogenomics, three bilaterian lineages have consistently been recovered: Deuterostomia, Ecdysozoa and Spiralia. Within the highly diverse Spiralia, several of the understudied, small taxa have shuffled between subgroups, their phylogenetic resolution being critical for reconstructing the evolution of central animal features, such as size, brain and segmentation. In a recent phylogenomic study we assessed the interrelationships among 90 meiofaunal and macrofaunal members of Spiralia using 402 orthologs mined from genome and transcriptome assemblies. Several of these meiofaunal lineages were found to branch off early in the diversification of Spiralia, why the concept emerges of a microscopic, acoelomate, unsegmented, direct-developing ancestor of Spiralia. Whereas most of these traits are doomed highly variable across Bilateria, the nervous system is often considered more conservative, and though this evolutionary scenario is still debatable, it already leads to further questions on, e.g., the complexity and functionality of the early spiralian brain and nervous system. While highly advanced functional genomic studies are performed on model organisms representing Ecdysozoa (e.g., fruitfly, roundworms) and Deuterostomia (e.g., mouse, chicken), not even the anatomy is known for most spiralian meiofauna, let alone their development. Our detailed morphological studies of the three early branching meiofauna groups, Micrognathozoa, Gnathostomulida, and Gastrotricha as well as a miniaturized Annelida, all reveal a comparably low structural complexity of their nervous system and compact, microscopic brain. In the context of the origin of the orthogonal nervous system, our studies confirm a well-polarized nervous system in spiralian meiofauna. Yet, the multiple new data uncover a substantial structural as well as neuropeptidergic variation - even among closely related species. This questions the often-claimed evolutionary conservatism of the nervous system and suggests a greater functional division of these meiofaunal brains than what meets the eye.

S14-04 The developmental basis for the recurrent evolution of deuterostomy

and protostomy

Martín-Durán, José M. (Sars Centre, Bergen, NOR)

Generations of biology students learn that all bilaterally symmetrical animals (e.g. humans and flies) belong to either Deuterostomia or Protostomia, a fundamental grouping that was originally based on whether the primary embryonic opening, called the blastopore, becomes the mouth or the anus of the adult. This division has prevailed for over 100 years, and has influenced nearly all views on animal evolution. However, gastrulation in Protostomia is vastly variable. For instance, penis worms and chaetognaths, as well as some spiralian lineages, exhibit deuterostomic development. To identify the mechanisms underlying the recurrent evolution of these two embryonic patterns, we compared the development of two related species of brachiopods that have similar ecological and reproductive strategies, but surprisingly display deuterostomic and protostomic development respectively. The investigation of the establishment of the axial polarity and fate identity during embryogenesis demonstrated that the protostomic species undergoes an extensive re-patterning of the blastoporal rim that relates to the cooption of the blastoporal orifice into the mouth opening. The differential deployment of Wnt signaling around the vegetal pole, together with the timing and location of mesoderm formation, is sufficient to influence the differential behavior and fate of the blastopore in these two species of brachiopods. Importantly, we demonstrate that similar developmental principles may act during gastrulation in the protostomic annelid Owenia fusiformis and might also account for the variability of blastoporal behaviors seen in this animal group. Our findings leverage the current knowledge of animal embryogenesis to mechanistically explain the evolution of deuterostomy and protostomy, demonstrating that these are recurrently appeared developmental by-products (i.e. ‚spandrels'). Our study thus challenges the long-standing evolutionary emphasis on extant blastoporal behaviors to explain the origin and diversification of bilaterian animals.

14.00 – 15.40

Symposium S15:
The evo-devo of domestication

Organizers: Marcelo Sánchez-Villagra and Leif Andersson

SAL C

Chairs: Marcelo Sánchez-Villagra and Leif Andersson

S15-01

The genetic basis for crop domestication

Purugganan, Michael (New York University, USA)

The domestication of crop species is one of the seminal evolutionary transitions of life on earth, providing the basis for the rise of agriculture. Using both genomic and archaeological data, we will show that the

domestication process was protracted, taking place for several thousand years. We will review the types of genes that appear to underlie crop domestication, particularly those associated with morphological diversification, as well as show an example of evolutionary convergence in fruit color evolution.

S15-02 Genetics of animal domestication

Andersson, Leif (Uppsala University, SWE)

The domestication syndrome in animals involves a set of traits that are shared among different species. It has been argued that these have evolved as a by-product of selection for tameness due to pleiotropic effects of the genes controlling behaviour. In this presentation I will argue that the major reason for altered coat colour in domestic animals is direct selection on colour because humans care a lot about the appearance of their domestic animals. Relaxed purifying selection most likely contribute as well and it is possible that we in the future will be able to identify some examples of pleiotropic effects where a gene variant affects both behaviour and pigmentation but it will never be a major explanation for altered pigmentation in domestic animals. I will illustrate this with our recent characterization of the Dun coat colour in horses, which are caused by mutations in what appears to be a melanocyte-specific enhancer of the TBX3 transcription factor gene. The Dun story also illustrates another important finding from several of the regulatory mutations that we have identified as underlying phenotypic change in domestic animals namely their remarkable spatio-temporal specificity. I will also present our work on whole genome sequencing of wild and domestic rabbits that has given the so far best insight concerning the genetic basis for animal domestication. This analysis showed that rabbit domestication has a highly polygenic basis and that shifts in allele frequencies at many loci rather than complete fixation at few domestication loci with major effects have occurred. Furthermore, non-coding changes dominates (at least numerically) and sequences in the vicinity of genes with an established role in brain and neuronal development have been particularly targeted.

S15-03 Does paedomorphism and neoteny explain the cranial morphology of domestic animals

Dobney, Keith (University of Liverpool, GBR)

The enormous diversity of domestic plant and animal varieties that exist today bear testament to the profound changes that domestication has induced in their wild ancestral forms over the last millennia. Understanding the evolutionary mechanisms involved in the process of domestication provides crucial insights into how wild animals and plants have been shaped over time through varying degrees of human intervention and control. Identifying the phenotypic responses to domestication has, therefore, been a long-standing and important question for archaeo-

logists and evolutionary biologists alike â€“ even playing a pivotal role in Darwin's initial development of the theory of natural selection. He contrasted the process of artificial selection by humans with that of natural selection in the wild and, in doing so, highlighted the general evolutionary mechanisms that led to past and present phenotypic diversity between wild and domestic organisms. Thus, for the last 150 years, distinguishing between the phenotypic responses brought about by artificial selection induced by domestication, from those due to natural selection in the wild, has been a major challenge for both evolutionary biologists and zooarchaeologists alike.

S15-04 Skeletal growth and life history evolution in domestic dogs

Geiger, Madeleine (University of Zurich, CHE); Sánchez-Villagra, Marcelo R. (University of Zurich)

The study of skeletal and dental growth in domestic dogs shows that correlations between morphological disparity and patterns of growth are apparent, but that other aspects of ontogeny are surprisingly similar in domestic dogs and their ancestor, the wolf. First, we investigated patterns of cranial suture closure in dependence of skull morphology in domestic dogs. Comparisons of the relative amount of closing and closed sutures and synchondroses in adult individuals showed that bulldog-type domestic dogs (dorsally rotated rostrum; e.g., bulldog) have significantly higher cloÂ¬sure scores than non-bulldog-type breeds and that domestic dogs have significantly higher closure scores than the wolf. Thus, there is a correlation between patterns of suture and synchondrosis closure and skull shape in domestic dogs, although the causal relationships remain elusive. Second, a comprehensive sample on the timing of growth plate closure and permanent tooth eruption in dogs and wolves revealed that there is no alteration of the sequence of dental maturity, skeletal maturity, and sexÂ¬ual maturity due to altered environmental conÂ¬ditions during domestication. Thus, despite their great variability, domestic dogs are wolf-like in terms of the investigated processes of somatic and sexual maturation. Third, a study on postnatal cranial shape change in domestic dogs examines the conÂ¬troversial hypothesis of an association of retardation of growth with the generation of the typical skull shape in domestic dogs, with the latter being „"paedomorphic wolves'. We conducted the first geometric morphometric analysis of ontogenetic series of dogs from different historical periods of domestication, serving to provide a comprehensive test of the paedomorphosis hypothesis. We found that cranial shape in domestic dogs is neither paedomorphic nor neomorphic and the resemblance of adult domestic dogs with juvenile wolves is mainly size related, probably determined by the negative allometry of the neurocranium.

14.00 – 15.40 Symposium S16:

Branching across the tree of life

Organizers: Yoan Coudert and Hélène Adam

K3/K4

Chairs: Yoan Coudert and Thomas Harrop

S16-01 Branching in Seed Plants : facts, questions and perspectives

Edelin, Claude (French Institute of Pondacherry, IND)

„Branching is a process by which a plant increases the number of its axes. It determines the three-dimensional structure of the organism and influences the relationship between neighboring plants. Studies of branching in seed plants mainly focused on the structure and formation of the meristems that produce the new axes. They have shown that branching is due to multicellular meristems produced by stems, leaves and roots. Depending on where the meristems are born, one usually distinguishes several branching patterns such as terminal or lateral, axillary or adventitious. The location of meristems together with their modalities of elongation and differentiation underpin the diversity of plant architectures. Many aspects of branching in seed plants are poorly known. The definition of the process itself is not clear and perhaps too restrictive. The origin of the meristems involved in branching is not always as simple as usually presented. Numerous branching patterns in both stem and root systems have yet to be discovered especially in the tropical trees and herbs. As a consequence we have only little information about the morphogenetic processes that control the growth and differentiation of meristems involved in branching. Branching in seed plants is a heterogeneous process that suggests a complex phylogenetic origin. It is interesting to observe that some aspects of branching are widespread in almost every taxon while others concentrate in some groups. This subject is still little explored and, considering the huge number of morphological traits involved in branching, their use could be a powerful tool for a better understanding of the seed plants phylogeny.

S16-02 Branching in the brown alga Ectocarpus, from genetic variations to computer simulation: what do we gain?

Charrier, Bénédicte (Station Biologique Roscoff, FRA)

Brown algae are multicellular organisms distinct from land plants, metazoans and fungi. Genome analysis in brown algae showed that they share protein identities with both Opithokonts (metazoans and fungi) and Plantae, as well as with prokaryotes (by gene lateral transfer). How these organisms did select growth and developmental strategies remains largely unknown. Here, we used several approaches to tackle branching in the filamentous brown alga Ectocarpus. The sporophyte of this alga grows apically and develops filaments made of 2 distinct cell types. Position, orientation and time of branching was monitored in both wild type and mutant organisms, and linked to the overall morpho-

logy (tuft) of the adult thallus. Treatments impacting these branching patterns together with computer simulation allowed to identify several parameters controlling the overall algal morphology. Comparison of the branching pattern with other brown algae as well as interests for the seaweed aquaculture sector will be discussed.

S16-03 From networks to function - computational models of organogenesis

Iber, Dagmar (ETH, Zurich, CHE)

One of the major challenges in biology concerns the integration of data across length and time scales into a consistent framework: how do macroscopic properties and functionalities arise from the molecular regulatory networks Âand how do they evolve? Morphogenesis provides an excellent model system to study how simple molecular networks robustly control complex pattern forming processes on the macroscopic scale in spite of molecular noise, and how important functional variants can evolve from small genetic changes. Recent advances in 3D imaging technologies, computer algorithms, and computer power now allow us to develop and analyse increasingly realistic models of biological control. In my talk, I will show how data-based modelling can be used to define mechanisms for fundamental developmental processes such as the control of branching processes and the scaling of developmental pattern on differently sized embryonic domains.

S16-04 Modelling and analysis of growth and form in branching scleractininan corals

Kaandorp, Jaap A. (University of Amsterdam, NLD)

We discuss a macroscopical growth model which can be used to simulate growth forms of complex-shaped branching organisms with radiate accretive growth. This type of growth processes can be found in many different marine sessile organisms. We use scleractinian corals as an example. Using our simulation model we show how environmental factors such as nutrient distribution light availability, hydrodynamics influence growth patterns of coral colonies. To compare the simulated coral growth forms with those of real coral colonies, we quantitatively compared our modeling results with coral colonies of the morphologically variable Caribbean coral genus Madracis. Madracis species encompass a relatively large morphological variation in colony morphology and hence represents a suitable genus to compare simulated and real coral growth forms in 3D using a quantitative approach. This quantitative analysis of three-dimensional growth forms is based on a number of morphometric parameters such as branch thickness, branch spacing etc. Our results show that simulated coral morphologies share several morphological features with real coral colonies. We have measured morphological features of three closely related Caribbean coral species of the genus Madracis (M. formosa, M. decactis and M. carmabi). Morphological

differences were then compared with phylogenies of the same species based on two nuclear DNA markers, i.e. ATPSa and SRP54. Our analysis showed that phylogenetic trees based on (macroscopical) morphological properties and phylogenetic trees based on DNA markers ATPSa and SRP54 are partially similar Our present model is able to partly capture the morphological variation in closely related and morphologically variable coral species of the genus Madracis.

16.10 – 17.10

Contributed Session C13: Biomimetics – evolutionary inspired engineering

Organizer: Naomi Nakayama

STORA SALEN

Chair: Naomi Nakayama

C13-01 Evolutionary biomimetics: tracing the natural history of biological designs

Nakayama, Naomi (University of Edinburgh, GBR)

Natural selection has horned living organisms for their forms and functions. From intricate structural colourisation to biomaterials with incredible strength, biological structures and behaviours are full of inspirations for engineering. By emulating the nature's design process, we may find new levels of understanding about the making and the working of the living organs and organisms. Through the process of biomimetic exploration, we may also trace the course of evolution. Plants are wonderful sources of inspiration for biomimetic innovations for their mechanisms of movement without muscles and remarkable adaptability to changing environment. In fact, even the entire plants can be viewed as „smart" architecture equipped with various parts of environmental sensing and adaptive functionalities. Examples of ingenious natural designs and their manmade reproductions illustrate how biomimetic aspirations can deepen our understanding of living forms and their functions today, as well as the history of their becoming.

C13-02 Nature vs robotics: from plants and animals to soft robots

Mazzolai , Barbara (Istituto Italiano di Tecnologia, Pontedera, ITA)

How does Nature can improve technology? What is the link between living systems and robots? Robots today are expected to operate in a variety of scenarios, being able to cope with uncertain situations and to react quickly to changes in the environment. In this scenario a strong relationship between nature and technology plays a major role, with the winning approach of evaluating natural systems to abstract principles for new designs. Biorobotics is a worldwide known paradigm to develop new solutions for science and technology, giving way to a series of innovative robotic solutions assisting and supporting today's society. I will bring forward some examples of robots inspired from soft animals,

like cephalopods, and plants. Specifically, I will present some scientific and technological challenges and solutions coming from these living organisms. In the animal paradigm a function is often related to an organ or compartment. Instead plants are networked, decentralized, modular, redundant, and resilient. Plants are able to move, control, sense, but they do in a different way with respect animals or other living beings. I will compare ideas, biological features, and technological translations coming from the two Kingdoms and related to areas of interest in robotics: movement, sensing and control.

C13-03 Evolutionary origin of „snapping" shrimps: Crossing the gap between pinching and snapping claws

Kaji , Tomonari (University of Alberta, CAN); Anker, Arthur (Museu Paraense Emílio Goeldi, Belém, BRA); Wirkner, Christian (Universität Rostock, DEU); Palmer, A. Richard (University of Alberta, CAN)

Snapping claws, which occur in both alpheid and palaemonid shrimps, are spectacular offensive weapons that create intense cracking sounds and shockwaves toward prey and opponents. True snapping involves: a) rapid claw closure facilitated by an energy storing mechanism at the joint, b) creation of a cavitation bubble, and c) destructive shock waves induced by cavitation bubble collapse. How such an extraordinary weapon evolved from ordinary pinching claws is not known. We examined claw form in 90 species of caridean shrimp including several snapping taxa using modern visualization techniques (e.g., micro-CT, confocal microscopy). This survey revealed a unique type of energy storage mechanism in the snapping claw of basal Alpheidae and Palaemonidae: a „slide-and-cock system" similar in form to the „sliding" type joint widely shared by non-snapping caridean shrimp. To assess the relation between form and function we conducted physical experiments using remarkable, enlarged, 3D printed scale models of claws. These experiments revealed a minute yet functionally significant quantitative difference in joint structure that clearly demarcates pinching from snapping claw function. This previously unrecognized sliding-type joint in non-snapping caridean shrimp claws appears to be an evolutionary precondition for the subsequent evolution of spectacular snapping claws.

C13-04 Engineering trades-off with biology

Vincent, Julian (University of Oxford, GBR)

Biology is gradually yielding lessons and ideas for technology, but the resulting innovation is adventitious. Biology is also very complex with no underlying analytical model and cannot adequately be interrogated by technologists. A concept which can bridge this gap is the trade-off, which can lead to speciation in biology and aspects of design and problem-solving in engineering. An ontology is described which uses biological organisms as case studies and a Russian design system - TRIZ

- to define trade-offs and the factors by which they can be manipulated. One of the components of TRIZ - the Contradiction Matrix - supplies a list of problems perceived in a design (Parameters) which, taken in pairs, define a simple trade-off. It also provides a list of possible changes (Inventive Principles) which allow navigation of the space between the two defining Parameters. The ontology uses engineering terms for its interrogation. As an example it resolves the biological trade-off „speed-accuracy“ , yielding factors of Feedback (e.g. error-correction), Dynamic Response (e.g. control of thresholds), Adaptation (e.g. ability to predict) and Consolidation (e.g. stochastic accumulation). Multi-criteria analysis will allow multi-dimensional numerical models to be developed. This approach may be able to classify high-level mechanisms of evolution.

16.10 – 17.10

Contributed Session C14: Progress in animal phylogeny and its impact on the evolution of organ systems

SAL B

Chair: Katrine Worsaae

C14-01 Xenacoelomorpha and the origin of excretory organs

Andrikou, Carmen (Sars Centre, Bergen, NOR); Thiel, Daniel (Sars Centre, Bergen, NOR); Ruiz-Santiesteban, Antonio-Juan (Sars Centre, Bergen, NOR); Hejnol, Andreas (Sars Centre, Bergen, NOR)

Excretion is the process of eliminating metabolic waste products from the organism and can occur through passive diffusion or active transport. Diffusion usually takes place through the integument whilst active transport often takes place though specialized excretory organs (e.g. nephridia, malpighian tubules etc). The origin of excretory organs remains unclear. Although excretory organs show a great variation in morphology and development across bilaterians, recent studies have shown that a suite of orthologous genes are expressed in the nephridia of planarians and vertebrates as well as in the nephrocytes of flies. The phylogenetic position of the Xenacoelomorpha (Xenoturbella + (Nemertodermatida + Acoela)) as possible sister group of all remaining bilaterians and their lack of well defined excretory structures make them a key group for unravel the evolutionary origin of excretory organs. We investigated candidate genes and their putative role in excretion by characterizing their expression patterns in two xenacoelomorph species, the nemertodermatid Meara stichopi and the acoel Isodiametra pulchra. We focused on genes that have a role in nephridia development (e.g. Sall) or in shaping the terminal filtration apparatus (e.g. Neph) of vertebrates, flies and planarians. Furthermore, we studied the role of genes involved in ammonia excretion (e.g. Rh) in crustaceans, planarians, nematodes and vertebrates. We show that in nemertodermatids and acoels all excretion related genes are mainly expressed in components of the reproductive and digestive systems as well as in individual -

yet uncharacterized - parenchymal cells and epithelium. We conducted inhibitor experiments that targeted components of the active ammonia transport pathway (e.g. V-type H+-ATPase) and confirmed their participation in ammonia excretion in acoels. Our findings hint at the presence of a not yet described complex excretory mechanism in Xenacoelomorpha, which functions as an active transport system.

C14-02 Embryogenesis of the sponge Amphimedon queenslandica and the evolution of metazoan developmental hallmarks

Larroux, Claire (University of Queensland, Brisbane, AUS); Richards, Gemma (University of Queensland, Brisbane, AUS); Nakanishi, Nagayasu (University of Florida, USA); Adamska, Maja (Autralian National University, Canberra, AUS); Degnan, Bernard (University of Queensland, Brisbane, AUS)

In the last ten years, a number of articles have been published on the embryonic development of the haplosclerid demosponge Amphimedon queenslandica, which may represent the ancestral form of development for its class. Here, we analyse histological and gene expression data to infer some of the cell behaviours and molecular mechanisms underlying the embryogenesis of this sponge and place it in the broader metazoan context. Sponge development has long been cautiously set apart from all other animal phyla. In particular, there has been much debate in the literature regarding the homology of sponge processes with gastrulation and patterning in eumetazoans. In Amphimedon, cleavage first occurs at the periphery of the embryo and involves asymmetric cell division and engulfment of nurse cells. At least six cell types differentiate by the end of cleavage, as shown by morphology and gene expression. Cells then migrate to form a bi-layered embryo that soon acquires axial symmetry, likely in response to a Wnt signal. A photosensory pigment ring seems to be patterned by a complex patchwork of expression of transcription factors and other genes. Overall, these data provide increasing evidence for the homology of key developmental processes in sponges and eumetazoans. Hence, despite the plastic nature of adult sponges and the absence in their genomes of certain genes deemed crucial to gastrulation and patterning, sponge embryonic development does seem to display many metazoan hallmarks.

C14-03 Molluscan MorphoEvoDevo: The morphogenetic and molecular basis of body plan evolution in the most diverse animal phylum

Wanninger, Andreas (University of Vienna, AUT)

Mollusks exhibit an astounding diversity of body plans that includes simple, worm-shaped organisms with little regionalization along the anterior-posterior body axis (the aplacophorans) as well as animals with a more or less distinct subdivision into head, foot, and visceral mass (many conchiferans, e.g., gastropods and cephalopods). Although a

considerable body of embryological data including cell lineage studies exist for most of the eight class-level taxa, detailed studies on molluscan morphogenesis and gene expression are scarce. In our quest to unravel the evolutionary origin of body plan diversity within the phylum as well as to reconstruct the phenotype of the last common ancestor (LCA) of key molluscan assemblages such as Conchifera (all mollusks with a primarily univalved shell), Aculifera (aplacophorans and polyplacophorans), and, ultimately, Mollusca itself, we are currently performing large-scale integrative studies on various aspects of molluscan development using representative aplacophoran, polyplacophoran, gastropod, bivalve, scaphopod, and cephalopod species as models. Thereby, data on myogenesis showed that aplacophoran bodyplan simplicity is a secondary condition and that the aculiferan LCA had a complex body musculature similar to modern-day polyplacophorans. Early aplacophoran neurogenesis, cell proliferation patterns, and expression of the mesoderm marker twist show parallels to annelids and other spiralians, but traces of segmentation were not found in any of the aculiferan or conchiferan species investigated. This argues for a shared ancestral program among spiralians during early trochophore development, whereby segmentation evolved in later larval stages in annelids alone after their split from their spiralian allies. Comparative gene expression data indicate that key developmental regulators such as Hox, ParaHox, and Wnt genes evolved novel roles in various conchiferans, which was probably a major driving force in the evolution of the vast morphological diversity expressed in this molluscan subclade.

C14-04 Conserved traits of spiralian development in the cell lineage and molecular patterning of the bryozoan Membranipora membranacea

Vellutini, Bruno C. (Sars Centre, Bergen, NOR); Martín-Durán, José M. (Sars Centre, Begen, NOR); Hejnol, Andreas (Sars Centre, NOR)

Mollusks exhibit an astounding diversity of body plans that includes simple, worm-shaped organisms with little regionalization along the anterior-posterior body axis (the aplacophorans) as well as animals with a more or less distinct subdivision into head, foot, and visceral mass (many conchiferans, e.g., gastropods and cephalopods). Although a considerable body of embryological data including cell lineage studies exist for most of the eight class-level taxa, detailed studies on molluscan morphogenesis and gene expression are scarce. In our quest to unravel the evolutionary origin of body plan diversity within the phylum as well as to reconstruct the phenotype of the last common ancestor (LCA) of key molluscan assemblages such as Conchifera (all mollusks with a primarily univalved shell), Aculifera (aplacophorans and polyplacophorans), and, ultimately, Mollusca itself, we are currently performing large-scale integrative studies on various aspects of molluscan development using representative aplacophoran, polyplacophoran, gastropod, bivalve,

scaphopod, and cephalopod species as models. Thereby, data on myogenesis showed that aplacophoran bodyplan simplicity is a secondary condition and that the aculiferan LCA had a complex body musculature similar to modern-day polyplacophorans. Early aplacophoran neurogenesis, cell proliferation patterns, and expression of the mesoderm marker twist show parallels to annelids and other spiralians, but traces of segmentation were not found in any of the aculiferan or conchiferan species investigated. This argues for a shared ancestral program among spiralians during early trochophore development, whereby segmentation evolved in later larval stages in annelids alone after their split from their spiralian allies. Comparative gene expression data indicate that key developmental regulators such as Hox, ParaHox, and Wnt genes evolved novel roles in various conchiferans, which was probably a major driving force in the evolution of the vast morphological diversity expressed in this molluscan subclade.

16.10 – 17.10

Contributed Session C15: Contributions to Evo-devo

SAL C

Chair: Jannik Vollmer

C15-01 Growth control during development

Vollmer, Jannik (ETH Zurich, CHE)

„The size and shape of organs is species-specific, and even in species in which organ size is strongly influenced by environmental cues, such as nutrition or temperature, it follows defined rules. Therefore, mechanisms must exist to ensure a tight control of organ size within a given species, while being flexible enough to allow for the evolution of different organ sizes in different species. We have combined computational modeling and quantitative measurements to analyze growth control in the Drosophila eye disc and vertebrate limb. We identify growth laws that are consistent with the growth data and that would explain the extraordinary robustness and evolutionary plasticity of the growth process and thus of the final adult eye size. These growth laws correspond to very different control mechanisms and we discuss how each of these laws constrains the set of candidate biological mechanisms for growth control in the Drosophila eye disc. We furthermore find that similar growth laws also match the quantitative growth data of the developing vertebrate limb. This suggests that a mechanism independent of the specific morphogenetic programs may regulate the potentially evolutionary conserved overall decline in growth.

C15-02 Dynamics of the circulation system during development of a colonial chordate are driven by the activity of multiple vertebrate-like hearts

Gasparini, Fabio (Università degli Studi di Padova, ITA); Cognolato, Moira (Università degli Studi di Padova, ITA); Salamon, Davide (Università degli

Studi di Padova, ITA); Donaggio, Elisa (Università degli Studi di Padova, ITA); Viviani, Laura (Università degli Studi di Padova, ITA); Manni, Lucia (Università degli Studi di Padova, ITA)

Tunicates are the sister group of the vertebrates, and the only chordate taxon including species, such as Botryllus schlosseri, able to reproduce both sexually and asexually. A colony of B. schlosseri consists of several budding blastozooids embedded in a common tunic. The latter is an extracellular matrix, which propagates following colony growth. The tunic is crossed by an extracorporeal vessel network, which links zooids each other. Each zooid has an open circulatory system and a single compartment heart. Peristaltic contractions passes from one end to the other and change direction cyclically, driving periodic reversals in blood flow. Despite the tunicate heart displays peculiar anatomical and physiological properties, there is a supported evolutionary picture of cell/tissue/organ homology with the more complex multi-chambered vertebrate heart. We studied the blood flow and the heartbeat dynamics in B. schlosseri evidencing that they are in relation to the colony development. When the colony is composed of a single zooid, the circulation is driven by a single heart and its dynamic is predictable. However, the predictability is absent in typical multi-zooid colonies. The heartbeat reversal period and the heart rate result highly heterogeneous, not only among colonies, but also among coexisting zooids at the same developmental stage in a same colony. The stage influences also the presence/absence of coordination between the heartbeat of a zooid and its bud. Heartbeat reversal period and heart rate are temperature- and development stage-dependent. Moreover, heart rate results responsive to human stabilizing and stimulating drugs (such as metoprolol and caffeine, respectively) in a predictable way. In conclusion, the contemporary presence of multiple hearts in a colony renders the system particularly complex. The high heterogeneity of results indicates that, similarly to vertebrate, a chaos theory may underline B. schlosseri circulation dynamics.

C15-03 Patterns of oligomerization and carpel reduction in angiosperm gynoecia

Sokoloff, Dmitry D. (Moscow State University, RUS); Fomichev, Constantin I. (Moscow State University, RUS); Karpunina, Polina V. (Moscow State University, RUS); Nuraliev, Maxim S. (Moscow State University, RUS); Oskolski, Alexei A. (University of Johannesburg, ZAF; V.L. Komarov Botanical Institute of Russian Academy of Sciences, St Petersburg, RUS); Remizowa, Margarita V. (Moscow State University, RUS)

Angiosperm gynoecia vary in carpel number (monomerous/non-monomerous) and presence or absence of intercarpellary fusion (syncarpy/apocarpy). Non-monomerous apocarpy is plesiomorphic in angiosperms. We review issues related to discussion on monomerous and so-called pseudomonomerous gynoecia. It is widely accepted that monomery

has evolved from non-monomerous apocarpy whereas pseudomonomery - as a result of reduction of syncarpous gynoecia to retain only one fertile carpel. This idea implies that a transition from apocarpy to syncarpy is usually irreversible, but the lack of reversals in this character is not supported by molecular phylogenetics. We propose that the emphasis should be made on the occurrence of (1) an abrupt change of gynoecium merism leading directly to single carpel (monomery) or (2) a multistep process of sterilization and reduction of all carpels but one (pseudomonomery. Both pathways occurred many times in evolution of large angiosperm clades. Technical recognizing of pseudomonomery in particular groups can be problematic because of (1) possible loss of any traits of sterile carpels and extinction of intermediate forms and (2) possible misinterpreting unusual carpel features as rudiments of sterile carpels. We highlight significance of developmental and functional constraints on structure of monomerous gynoecia (e.g., against occurrence of monomerous gynoecia with long plicate zone and inferior ovary). A peculiar kind of pseudomonomery with one carpel having fertile ovule and another (or others) having receptive stigma appeared in more than one angiosperm lineage. A loss of carpel individuality in non-monomerous syncarpous gynoecia (here called „mixomery') must not be considered as pseudomonomery. The study is supported by RFBR (project 15-04-05836).

C15-04 Potential developmental constraints on vertebrate bodyplan evolution

Irie, Naoki (University of Tokyo, JPN); Hu, Haiyang (CAS-MPG Partner Institute for Computational Biology, Chinese Academy of Sciences, CHN); Guo, Song (CAS-MPG Partner Institute for Computational Biology, Chinese Academy of Sciences, CHN); Uesaka, Masahiro (University of Tokyo, JPN); Shimai, Kotaro; Lu, Tsai-Ming; Li, Fang, Fujimoto, Satoko; Ishikawa, Masato; Liu, Shiping; Sasagawa, Yohei; Zhang, Guojie; Kuratani, Shigeru; Yu, Jr-Kai; Kusakabe, Takehiro G. (EXPANDE Consortium); Khaitovich, Philipp (CAS-MPG Partner Institute for Computational Biology, Chinese Academy of Sciences, CHN)

Basic anatomical patterns of animals (such as bodyplans) are considered to be among the most conserved phenotypes throughout macro-evolution. The causes are not well-understood. The developmental hourglass model explains this conservation by „constraints" imposed by the developmental characteristics of early organogenesis stages (i.e. developmental constraints), including highly inter-dependent signaling modules. However, not much quantitative testing has been done to test this hypothesis. We have tested for quantitative evidence of developmental constraints at mid-embryonic stages that can explain bodyplan conservation. To this aim, we collected massive RNAseq data set from early-to-late embryos of 8 chordate species (~250 samples, including chicken, turtle, mouse, xenopus frogs, zebrafish, ciona, and amphioxus embryos).

We found support that specific constraints (will be discussed in the talk) can explain the conservation of vertebrate organogenesis stages. The conservation of these stages is probably involved in the conservation of the body plan of vertebrates. In addition, we found that mid-embryonic conservation cannot be observed at a chordate-wide scale. We conclude that the hourglass model can not be applied at a phylum-wide scale for species, but it is supported at a sub-phylum-wide scale.

16.10 – 17.10

Contributed Session C16: Branching across the tree of life

K3/K4

Chairs: Yoan Coudert and Thomas Harrop

C16-01 **Mechanisms underlying the parallel evolution of inflorescence phenotype during independent domestication of African and Asian rice**

Harrop, Thomas (Institut de Recherche pour le Développement (IRD), Montpellier, FRA)

During the independent domestications of African and Asian rice, artificial selection for increased yield resulted in parallel evolution of properties of inflorescence architecture that affect grain output, such as overall size and branching complexity. However, little is known about the molecular changes associated with phenotypic evolution in the domesticated species. Inflorescence traits related to grain yield were quantified in 20 accessions of wild and domesticated Asian and African rice grown under the same conditions. The accessions differ in terms of grain yield and inflorescence architecture, with parallel changes between the domesticated species and their respective wild ancestors. The molecular mechanisms underlying this phenotypic evolution are being studied using whole-transcriptome RNA sequencing of developing inflorescences in 5 accessions covering the japonica and indica varieties of Asian rice and domesticated African rice, along with their wild relatives. This will clarify the conserved and divergent molecular mechanisms that effect phenotypic variation in the context of plant domestication.

C16-02 **Gastrovascular branching morphogenesis in the jellyfish Aurelia aurita**

Cornelissen, Annemiek J. M. (CNRS & Université Paris-Diderot, FRA); Song, Solène (CNRS & Université Paris-Diderot, FRA); Gambini, Camille (CNRS & Université Paris-Diderot, FRA); Peaucelle, Alexi (CNRS & Université Paris-Diderot, FRA); Dantan, Phillipe (CNRS & Université Paris-Diderot, FRA); Balavoine, Guillaume (CNRS & Université Paris-Diderot, FRA)

Morphogenesis of living systems is controlled by a complex of processes in which also mechanical forces plays a role. Mechanical forces can contribute either on a cellular scale by impacting on the signaling pathways, or on a tissue scale affecting the cell movements and deformations (compression, extension, intercalation, and rearrangement etc). Aurelia

Aurita has a relatively simple branched gastrovascular pattern. We aim to understand how mechanical self-organized processes are involved in the morphogenesis of this typical vascular structure. The canals grow in a monolayer membrane of cells, the endoderm. We observed that as soon as the jellyfish has obtained its circular shape, canals sprout off from the ring canal and grow at the tip by accumulation and stacking of endodermal cells followed by differentiation of the endodermal cells into canal cells. We hypothesized that these processes are induced by compressive constraints in the endoderm generated during each muscle contraction of the jellyfish. In analogy with crack propagation the vessels grow to relax the highest compressive stresses. The boundary conditions, the already existing vessels define the compressive stress field generated in the endoderm. With this algorithm we can explain the typical vascular patterns seen in Aurelia. We have challenged these hypotheses with experimental and numerical studies and during my presentation I will show you the results.

C16-03 Hormonal control and evolution of branching forms in mosses

Coudert, Yoan (CNRS/Museum National d'Histoire Naturelle Paris, FRA); Palubicki, Wojtek (Adam Mickiewicz University in Poznań, POL); Bell, Neil (Royal Botanic Garden Edinburgh, Scotland, GBR); Leyser, Ottoline (University of Cambridge, GBR); Harrison, J. (University of Bristol, GBR)

Branching patterns are a primary determinant of plant architecture and strongly impact on productivity by regulating light harvesting potential and resource allocation. Plants colonized land over 450 million years ago, and underwent architectural diversification in the haploid (gametophyte) and diploid (sporophyte) genetic stages of the life cycle independently. Although similar branching mechanisms evolved in both genetic stages, our functional understanding of branching is limited to diploid flowering plant models such as Arabidopsis. To test whether the same molecular cues regulate branching mechanisms which have evolved convergently, we undertook a computational and genetic analysis of branching patterns in the haploid leafy shoot of a moss. We show that a simple model co-ordinating the activity of shoot tips across the plant can account for the branch distribution, and that three known hormonal regulators of branching in flowering plants generate the pattern. Importantly, these cues have been independently recruited in evolution to regulate branching patterns in both haploid and diploid life cycle stages, and may be integrated via a novel mechanism in moss. Our results provide a framework to explore the hormonal control of branching form evolution in the moss lineage.

C16-04 Modelling the development and diversity of leaves

Runions, Adam (Max Planck Institute for Plant Breeding Research, Köln, DEU); Prusinkiewicz, Przemyslaw (University of Calgary, CAN); Tsiantis, Miltos (Max Planck Institute for Plant Breeding Research, Köln, DEU)

„Leaves of seed plants show tremendous morphological diversity. Remarkably, different leaf morphologies may occur between closely related species, as within-species variants, or even the same plant. This lability suggests that the striking diversity of leaf shapes found in nature may result from the variation of a few key parameters in a common generative process. Furthermore, experimental results indicate that serrations, lobes or leaflets are organized by a conserved patterning mechanism operating at the leaf margin. Notably, this mechanism acts jointly on leaf shape and vasculature, patterning both marginal protrusions and corresponding veins in the blade. Inspired by this perspective, we propose a geometric model of leaf development and diversity. It simulates development as a feedback between two processes: the dynamic patterning of growth centers at the leaf margin, and control of growth directions by veins associated with these points. Conceptually, our approach is related to Zimmerman's telome theory accounting for the evolution of leaves from primitive branching structures. Restricting patterning to the leaf margin is analogous to planation, whereas webbing is captured by differing the growth of the margin compared to that of the branching structure of supporting veins. Our models show that the spatial separation of the processes patterning and directing growth facilitates the generation of a wide range of leaf forms, from simple to lobed and compound. Additionally, transitions between different forms can be controlled in a continuous manner. These transitions reproduce frequently observed, and often drastic, changes in leaf form within the same plant or between closely related species. Together, our results provide a path towards reconciling classical theories regarding leaf evolution and development with contemporary molecular studies. Furthermore, they highlight the flexible and self-organizing nature of leaf development - supporting its importance as a key system for morphogenetic studies."

17.20 – 18.00

Keynote Lecture (K3)

A trick of the light? Petal surface structures influence animal behaviour

STORA SALEN

Beverley Glover
(University of Cambridge, GBR)
Chair: TBA

Flowers and the animals that pollinate them interact at a single key point – the petal surface. It is this single layer of tissue that provides the visual surface that advertises nectar rewards. It is on this layer of tissue that pollinators land. And it is often from this layer of tissue that the scents that attract pollinators over longer ranges are released. Our recent research has focused on the optical effects of the petal surface. The majority of petal morphologies will act to support certain plant/pollinator interactions but not others, leading to greater reproductive isolation and

speciation within the flowering plants. I will present recent work on the nanoscale properties of the petal surface, taking molecular developmental, evolutionary and pollinator behavioural perspectives.

18.00 – 20.00
FLOOR 6

Poster Session 2
(even numbers)

09.00 – 10.40

Symposium S17: Evolutionary developmental genomics

STORA SALEN

Organizers: David Ferrier and Sebastian Shimeld
Chairs: David Ferrier and Sebastian Shimeld

S17-01 Identifying the triggers of animal origins: what protists are telling us

Ruiz-Trillo, Iñaki (Pompeu Fabra University, Barcelona, ESP)

How animals emerged from their single-celled ancestors, evolving into the highly-variable complex body plans we see nowadays, is a fascinating evolutionary question. We have been addressing this question by obtaining new genomic and cell biology data from several unicellular relatives of Metazoa. This data, together with data from choanoflagellates and early-branching animals, is providing insights into the nature of the last unicellular ancestor of animals. Therefore, we now know that this ancestor already had many genes and pathways that are relevant to multicellularity. However, the origin of spatial cell differentiation in animals, and the potential role of genomic regulation in animal origins still remains unsolved. To address these questions, we have focused on the filasterean Capsaspora owczarzaki, one of the closest unicellular relatives of animals, and the one with the largest repertoire of genes involved in multicellular functions (such as transcription factors). In particular, we have analyzed its genomic regulatory landscape and its proteome and phosphotrome. All together, these data point to a complex genomic regulation in C. owczarzaki and suggest potential triggers of animal multicellularity. I will not only revise all these recent fidings, but I will also provide a novel and integrative hypothesis on the origins of animals.

S17-02 Developmental genomics of sponges

Adamska, Maja (Australian National University, Canberra, AUS)

Sponges are likely to be the earliest branching animal lineage, making them key models in studies of evolutionary history of animal genomes. From the morphological and developmental perspectives, sponges combine features of single-cell eukaryotic organisms and the complex multicellular animals. Analysis of the first sequenced sponge genome (of the demosponge Amphimedon queenslandica) demonstrated a limited number of homologues of genes involved in eumetazoan development, suggesting a gradual assembly of the complex eumetazoan developmental toolkit. However, sponges are a diverse phylum, composed of four distinct lineages (Demospongiae, Hexactinellida, Calcarea and Homoscleromorpha). We have recently sequenced genomes of five calcisponges: two calcaroneans (Sycon ciliatum and Leucosolenia com-

plicata) and three calcineans (Clathrina lacunosa, C. laminoclathrata and C. coriacea), as well as a demosponge distantly related to Amphimedon (Halisarca dujardini). For some of them, we have generated extensive collections of transcriptome datasets representing embryonic and postembryonic development and regeneration. Comparisons of developmental regulatory gene (DRG) repertoires demonstrated unexpected complexity and diversity among sponges. In particular, DRG families are significantly more complex in calcisponges than in demosponges. Overall, it appears that significant gene loss occurred independently in the calcisponge and demosponge lineages. These gene losses have been followed by gene family expansions occurring independently in the calcaronean and calcinean lineages, and, to a lesser extent, in the lineage leading to Halisarca. Strikingly, conservation of gene sequence correlates with similarity of gene expression profiles across the sponge species. Overall, usage of developmental regulatory genes demonstrated deep conservation of body plan patterning and regeneration mechanisms between sponges and the eumetazoans. At the same time, the detailed picture - numbers of genes within individual families - revealed spectacular diversity among sponge species.

S17-03 Denser taxon sampling in genomics and transcriptomics allows to test hypothesis about the evolution of development and morphology

Hejnol, Andreas (Sars Centre, Bergen, NOR)

Ongoing progress in improving sequencing technologies will allow a much denser transcriptomic and genomic taxon sampling in the future. This large amount of data will allow to test hypotheses about genome evolution that have been made based on only a handful of species across the tree. An improved resolution of animal relationships will furthermore provide the backbone for evolutionary considerations. My group has started to sequence genomes of different animal species and have developed pipelines for improved analysis. One pipeline makes use of denser transcriptomic sampling to better discriminate between „hidden orthologs“and taxon specific genes. Applying this tool to different taxa we were able to detect fast evolving genes as orthologs that would have been either interpreted as absent - gene loss - or taxon specific or orphan genes.

S17-04 The genome of the medusozoan Clytia hemisphaerica and life-cycle stage dependent gene expression

Copley, Richard (CNRS, Biologie du Développement de Villefranche sur mer, FRA)

Cnidarians are the closest living relatives of bilaterians and hold a key position for understanding metazoan evolution. We have produced a draft genome assembly and a comprehensive transcriptome of the medusozoan cnidarian, Clytia hemisphaerica, using multiple RNA-seq

libraries covering the major stages of the life-cycle, representing the first comprehensive data for a cnidarian exhibiting polyp and medusoid stages. I will present an analysis of protein coding gene use across stages, integrated with an analysis of the phylogenetic conservation or novelty of these genes, with a particular focus on transcription factors that have clear orthologs in the bilateria. I will also present in situ hybridization data for key developmental genes present in the Clytia genome, conserved between cnidarians and bilaterians, which provide insight into the likely functional role of bilaterian gene orthologs in cnidarians.

09.00 – 10.40

Symposium S18: Serial homology and segmentation

K3/K4

Organizer: Rui Diogo
Chair: Rui Diogo

S18-01 A gene regulatory network perspective on homology and serial homology

Wagner, Günter P. (Yale University, USA)

While biologists have developed a reasonably coherent understanding of homology as it applies to"the same organ in different species regardless of form of function", the concept of serial homology is still controversial. One argument is that serial homology applies to different parts of the same organism, and for that reason the phylogenetic definition of homology does not fit; ergo serial homology is not homology at all. In this contribution I will present another perspective, which applies to both „special" homology (homologous parts of different species) as well as to parts of the same organism, namely the notion of genetic/developmental individualization. For the phylogenetic homology concept to be meaningful it has to be limited to the comparison of developmentally individualized body parts. However, as soon as we include the notion of developmental individuality, we are also freed from the strictures of the phylogenetic definition of homology and can consider the identity of body parts within the same body. In doing so one has to recognize that we need to distinguish between two categories of serially homologous characters: homomorph and paramorph characters. Homomorphs are simple reiterations of the same developmental program, like multiple instances of the same cell type. The term paramorph derives from the concept of a paralog gene, i.e. two body parts are paramorph if they ancestrally derive from a homomorph reiteration of the same character but each acquired developmental individuality in later evolution such that they are now two individualized body parts. The notion of paramorph characters is particularly clear in the case of cell type evolution according to the sister cell type concept. The notion of paramorph characters also implies that groups of characters have a hierarchical

structure of relatedness. Finally I will address the recent hypothesis that tetrapod fore- and hind limbs are not serially homologous.

S18-02 Surprising developmental, evolutionary, pathological and comparative perspectives on serial homology of the head and limbs/fins: from dissimilarity to derived serial similarity

Diogo, Rui (Howard University, USA); Esteve-Altava, Borja (Royal Veterinary College, London, GBR); Molnar, Julia (Howard University, USA); Ziermann, Janine (Howard University, USA)

Most evolutionary and medical textbooks state that the pectoral and pelvic appendages of fish, and therefore the fore and hindlimbs of tetrapods, are serial homologues. However, such statements are mainly the consequence of a repetition of older ideas that were formulated based on romantic ideas and/or the notion of an ‚archetype', and that were never tested against empirical data. Here we show how such statements are contradicted by regenerative studies of axolotls, developmental studies of tetrapods, and comparative and evolutionary studies of all major vertebrate groups, including recent re-analyses of the appendicular muscles of chondrichthyans, dipnoans and coelacanths contradict this old dogma, a literature review on the available paleontological data, and the use of novel, state-of-the-art systems biology methods such as anatomical network analyses. That is, the integrative analysis of the data available strongly supports the idea that the similarity of the muscles and bones of the fore and hindlimbs of tetrapods such as salamanders and modern humans is not due to serial homology, but is instead the result of independent evolutionary changes (homoplasy) occurred mainly during the origin of tetrapods due to the co-option of similar genes for the development of both limbs. In fact, contrarily to the limbs, and particularly their most distal regions, the pelvic and pectoral girdles were seemingly very different from the moment they appeared, and have remained very different from each other since then, an idea supported by recent studies of both anatomical and genetic networks. More than becoming lost on specific definitions of what is serial homology, the important take-home message is therefore that the similarity between the pectoral and pelvic fins of fish, and particularly of the fore and hindlimbs of tetrapods, is a derived - and not an ancestral, as has been dogmatically assumed for more than 250 years - similarity.

S18-03 The rise in complexity of the vertebral column

Galis, Frietson (Naturalis Biodiversity Center, NLD)

The spectacular diversification of the vertebrate body plan since the Ordovician is to an important extent due to the rise in complexity and the associated evolvability of the segmented vertebral column. Alongside the remarkable evolutionary diversification, there has also been impressive conservation. I will discuss how the rise in complexity of vertebrae and the vertebral column has affected modularity, integration

and evolvability. Examples of different vertebrate taxa, including new data on whales, will be discussed.

S18-04 A paleontological perspective on the serial homology of appendages and sexual organs

Johanson, Zerina (Natural History Museum London, GBR); Trinasjstic, Kate (Curtin University, Perth, AUS)

Placoderms (armored fossil fishes) are currently resolved as a paraphyletic group of basal jawed vertebrates, and so are crucial for interpreting the evolution of gnathostome characters, including paired appendages and reproductive structures and strategies. Placoderms preserve the earliest evidence of both paired pectoral and pelvic appendages, as well as reproductive structures (intromittent organs in males). Antiarchs (sister group of all other jawed vertebrates) are particularly important, demonstrating that copulatory structures and internal fertilization are characteristic of the most phylogenetically basal jawed vertebrates. Placoderms challenge established ideas on the evolution of reproductive complexity (internal fertilization, rather than external, representing the basal condition), as well as the evolution of the pelvic girdle and fin, and how intromittent organs relate to the pelvic girdle/fins. Evidence suggests these are separate structures along the body in placoderms, with intromittent organs comprising dermal and perichondral bone and representing a third, more posterior set of paired appendages, homologous to pectoral and pelvic fins. Placoderms show that „competent stripes"for appendage development were more extensive along the body when these appendages first evolved. Jawless vertebrates such as Euphanerops, with paired anal fins and extensive lateral fins suggest competent stripes extended from just posterior to the skull, to the caudal fin. By comparison, in sharks, intromittent organs (claspers) develop from the pelvic fin. In squamates and birds, external genitalia also develop from hindlimb buds, while in mammals these develop more posteriorly and separate from the hindlimb, related to the position of the cloaca. Recent suggestions that development of genitalia from the hindlimb represents the ancestral condition in the evolution of external genitalia are also challenged by the separate intromittent organs in placoderms.

09.00 – 10.40

Symposium S19: Evolution of plant and animal epidermal patterns

SAL C

Organizer: Beverley Glover
Chair: Beverley Glover

S19-01 Land plants recruited the ancient membrane anchored calpain DEFECTIVE KERNEL1 (DEK1) to monitor and promote epidermis cell fate

Demko, Viktor (Norwegian University of Life Sciences, Ås, NOR); Johansen, Wenche (Hedmark University of Applied Sciences, Hamar, NOR);

Ako, Eugene (Hedmark University of Applied Sciences, Hamar, NOR); Perroud, Pierre-François (Philipps-University Marburg, DEU); Owens, Ray (Harwell Science and Innovation Campus, Oxfordshire, GBR); De Moraes, Isabel (Harwell Science and Innovation Campus, Oxfordshire, GBR); Gevaert, Kris (VIB, Ghent, BEL); Olsen, Odd-Arne (Norwegian University of Life Sciences, Ås, NOR)

Plants evolved mechanism of epidermal layers formation that depends on the activity of conserved plant calpain DEK1. In angiosperms, DEK1 is essential for oriented cell divisions that lead to the specification of embryonic protoderm, L1 layer in the shoot meristem and the aleurone layer of endosperms. We used the moss Physcomitrella patens to show that DEK1 is essential for the first oriented cell divisions leading to the tetrahedral stem cell formation in meristematic buds and later during gametophore leaf and reproductive organs morphogenesis (1). We hypothesize that the multi-spanning transmembrane domain and the cytosolic Linker segment of DEK1 are involved in spatio-temporal regulation of the calpain protease which modulates yet unknown substrate. Currently, we focus on addressing the following questions: what is the the function of the conserved motifs in the DEK1 protein, the three dimensional structure of the DEK1 molecule and the nature of DEK1 calpain substrates. In the genetic studies involving trans-species complementation, we use site-directed mutagenesis in P. patens to delete and substitute predicted functional motifs in DEK1. Obtained mutant plants display phenotypes that point to the different functional requirements of the mutated sites and thus reflect various DEK1 activities required for the different stages of development. In order to obtain the structure of DEK1 calpain domain, we performed HTP expression screens in E. coli and insect cells and are currently conducting HTP crystallization screens. We are also working towards the full 240 kDa DEK1 protein expression and purification. To identify DEK1 substrates, we employ Combined Fractional Diagonal Chromatography designed to isolate amino terminal peptides. Comparative analysis of proteomes extracted from DEK1 deletion mutant and DEK1 over-expressing line has so far identified number of candidates that are currently under investigation.

1. Olsen et al. (2015) DEK1; missing piece in puzzle of plant development. Trends Plant Sci. 20(2):70-1

S19-02 The evolution of the MBW protein complex

Airoldi, Chiara (University of Cambridge, GBR); Brockington, Samuel (University of Cambridge, GBR); Glover, Beverley (University of Cambridge, GBR)

The MBW is a transcription factor multimeric protein complex composed of MYB, bHLH and WDR proteins. It displays a very wide range of functions it regulates phenylpropanoid synthesis determining flower and

fruit color, and specifies epidermal cell types. The functional role of the MBW proteins that is widespread within the angiosperms is the regulation of phenylpropanoid production, with examples described in monocots and eudicots. In Arabidopsis and in cotton (both Rosids) the MBW complex also plays a role in cellular specification of trichomes and root hairs but it is not know when this more recent function was acquired. We are using transcriptomic data from new sequencing projects to analyse the evolution of the MYB, bHLH and WDR protein families that form the MBW complex. By comparing protein-protein interaction abilities and by mutant analysis and complementation experiments we are starting to elucidate the evolution of this multimeric complex, assessing when and how it originated, and exploring the changes that have introduced novel functional roles.

S19-03 Stomatal patterning in land plants

Rudall, Paula (Royal Botanic Gardens, Kew, GBR)

Stomata are pores (openings) in the aerial plant epidermis, delimited by a symmetric pair of guard cells (GCs), sometimes with adjacent specialised epidermal cells (subsidiary cells: SCs). Stomata are present in almost all land plants, and hence represent a well-conserved feature that can be readily compared across diverse plant groups, in which the development and arrangement (i.e. patterning) of the stomatal complex (GCs plus SCs) can be highly characteristic. The developmental bases for stomatal patterning are increasingly well-understood, especially among extant taxa. One crucial factor is the presence or absence of asymmetric divisions in the cell lineage leading to the final stomatal precursor cell (the guard-mother cell: GMC). In mesogenous development, SCs result from the same epidermal cell lineage as the GMC, following one or more asymmetric divisions; in perigenous development, SCs are derived from precursor cells in neighbouring cell lineages. However, many plant groups are known only from fossils, in which it is highly problematic to infer development. Establishment of â€œfossil fingerprintsâ€ as developmental markers for the regulation of stomatal patterning is critical for understanding evolution. For example, dimorphic cell patterning in the developing leaf epidermis could indicate that both perigene and mesogene SCs are present. In paracytic stomata, which characterize some angiosperms, lateral subsidiary cells can be either perigenous or mesogenous. Development is unknown for the paracytic stomata of fossil bennettites. Non-random stomatal orientation could result either from perigenous development, as in water-lilies, or from linear pre-patterning of mesoperigenous stomata, as in monocots, many conifers and probably bennettites.

S19-04 How did the butterfly get its blue colour?

Nadeau, Nicola J. (University of Sheffield, GBR); Curran, Emma (University of Sheffield, GBR)

Some of the brightest and most striking colours found in nature are produced not by pigments but through coherent scattering of light by nano-scale structures. Despite the importance of these colours for animal and plant signalling and communication, and their application in man-made products, very little is known about their developmental control in natural systems. We are using genetically controlled within-species variation in iridescent blue structural colour in the Heliconius butterflies in order to study the genetic and developmental basis of these colours. Populations of the co-mimetic butterflies H. erato and H. melpomene on the Western slope of the Andes in Ecuador and Colombia have an iridescent blue colour that is absent from all other populations of these species. By comparing gene expression profiles between populations of each species, as well as between wing regions that differ in scale ultrastructure, we have identified genes that are upregulated during iridescent scale development. We are also integrating this information with DNA sequence data, identifying genomic regions that are divergent between populations. Together, this will allow us to identify candidate genes for producing structural colour in animals

09.00 – 10.40

Symposium S20:
Micro-evo-devo – integrating evolution, development and population genetics

K3/K4

Organizers: Sebastian Kittelmann and Nico Posnien
Chairs: Sebastian Kittelmann and Nico Posnien

S20-01 **A single nucleotide polymorphism in eyeless/Pax6 drives natural variation in eye size**

Ramaekers, Ariane (KU Leuven, BEL); Weinberger, Simon (KU Leuven, BEL); Claeys, Annelies (KU Leuven, BEL); Jan, Jiekun (KU Leuven, BEL); Wolf, Reinhard (KU Leuven, BEL); Buchner, Erich (KU Leuven, BEL); Hassan, Bassem A. (KU Leuven, BEL)

Natural variation in sensory organ morphology underlies behavioural changes and thereby potentially influences adaptation to novel ecological niches. Unraveling the mechanisms of such morphological variation requires the identification of both causal genetic alterations and associated developmental changes. As a model, we study natural variation of the number of facets in the fruit fly compound eye, which we find to be associated with changes in visual acuity. Investigating the developmental origin of such variation revealed that both between and within species, facet number variation originates from differential developmental partitioning of the head primordium between eye and non-eye tissue, suggesting the existence of constraints impinging on compound eye development. The Ey/Pax6 transcription factor is a key

determinant of eye formation across species and a key regulator of head primordium patterning. We identified a single nucleotide polymorphism (SNP) in the eye-specific regulatory sequence of ey/Pax6 correlating with facet number variation between D. melanogaster strains. Using CRISPR/Cas9 genome editing, we show that this SNP is causal to facet number variation. Thus, our study provides a multi-scale analysis of morphological variation of a complex and highly functionally-constrained structure, the insect compound eye. It demonstrates that despite this complexity, a naturally-occuring single nucleotide substitution in the cis-regulatory sequence of a key determinant of eye formation is sufficient to cause significant eye size variation.

S20-02 Evolution and development of Drosophila male genitalia

Santos Nunes, Maria Daniela (Oxford Brookes University, GBR)

Drosophila male genitalia are a powerful model system in micro-evo-devo studies due to their rapid divergence between recently split lineages. Our research takes advantage of differences in size, shape and bristle composition of secondary genital structures that evolved in the last 250,000 years between Drosophila simulans and Drosophila mauritiana to gain insight into how evolutionary changes in developmental programs gave rise to phenotypic diversity. In this talk I will be presenting our progress in mapping the genetic basis of these changes and provide an overview of our current understanding of the genetic architecture of these traits. I will also discuss how this system can be used to connect genotype, phenotype and fitness. By testing the effect of evolved changes on mating success we hope to understand how and the degree to which sexual selection contributes to differences in genital structures and reproductive isolation.

S20-03 Developmental crosstalk in root system adaptation to acidic soil

Hardtke, Christian (UNIL, Lausanne, CHE)

To understand gene action at the cellular, tissue and organism levels is the ultimate goal of developmental biology and can connect to ecological-evolutionary aspects through analysis of natural genetic variation. In our lab, we have isolated an essential regulator of root protophloem differentiation in Arabidopsis through the natural variation approach. Although this gene is generally highly conserved, corresponding loss-of-function alleles exist in nature. Their occurrence can be explained by associated systemic root phenotypes, such as proton pump hyperactivity, which confers increased fitness as compared to wild type on overly acidic soil. Soil pH is a key parameter for nutrient accessibility and some plants have evolved tolerance to acidic soil and associated abiotic stresses. Typically, this includes mechanisms to alleviate proton toxicity. Therefore, hyperactive proton secretion by the root system to counteract passive proton influx is a counterintuitive feature frequent-

ly associated with acid soil adaptation. Based on the above described precedence, we developed a tissue culture assay to efficiently detect hardwired elevated proton pumping at high throughput in Arabidopsis accessions collected across an alkaline-to-acidic soil pH gradient. Indeed, we identified numerous hyperactive proton pumpers among accessions collected from acidic soil. Initial analyses indicate that in most cases this feature is genetically determined by one to three distinct loci. This allows us to rapidly identify causative acid soil-adaptive candidate mutations through whole genome sequencing of bulked segregants. The data suggest that acid soil adaptation can evolve repeatedly through mutation of independent loci, which can also play an important generic role in root system development.

S20-04 The quest for understanding the genetic and developmental basis of morphological shape variation in the house mouse

Pallares, Luisa F. (MPI Evolutionary Biology, Plön, DEU); Tautz, Diethard (MPI Evolutionary Biology, Plön, DEU)

The evolution of morphological shape has been a long-standing interest of biologists. Morphology was, and is still used today to classify organisms, and to trace their evolutionary relationships. The link between shape and mechanical properties has given us an external explanation of why different organisms have different shapes. However, it was developmental biology that started providing some answers to what is internally driving morphological diversification in a macro-evolutionary scale. Today, thanks to development of genome-wide approaches and techniques to precisely quantify the geometry of a structure, we are ready to give the next step in understanding morphological variation. We are now able to ask which genes/variants underlie shape variation at the micro-evolutionary level (e.g. within species), how many they are, and how much do they contribute, individually and together, to phenotypic variation. By identifying causal loci, we can then address the question of how, mechanistically, are they interacting to regulate the formation of a very precise and functional shape, and at the same time allowing for variation that will be the substrate for natural selection. As a model, we use the craniofacial bones of house mouse to address the question of morphological shape variation from a micro-evolutionary perspective. Using GWAS and geometric morphometrics we have been able to determine the genetic architecture underlying variation in such complex traits. And, using traditional knockout experiments we have started to understand when in post-natal development is craniofacial shape fine-tuned, and which genes are involved in such processes.

11.10 – 12.25 Contributed Session C17:
Evolutionary developmental genomics

STORA SALEN Chairs: Sebastian Shimeld and David Ferrier

C17-01 Nemertean and phoronid genomes reveal lophotrochozoan evolution and bilaterian head origin

Luo, Yi-Jyun (Graduate University, Onna, Okinawa, JPN); Kanda, Miyuki (Graduate University, Onna, Okinawa, JPN); Koyanagi, Ryo (Graduate University, Onna, Okinawa, JPN); Hisata, Kanako (Graduate University, Onna, Okinawa, JPN); Satoh, Noriyuki (Graduate University, Onna, Okinawa, JPN)

Nemerteans and phoronids are closely related lophotrochozoans: we have little understanding about the genetics of their evolutionary origins and head structures. Here we present the draft genomes of a ribbon worm, Notospermus geniculatus, and a horseshoe worm, Phoronis australis, together with multiple transcriptomes. Our genome-based and transcriptomic phylogenetic analyses place Nemertea sister to Lophophorata (Phoronida, Ectoprocta, and Brachiopoda). We show that lophotrochozoans but not other spiralians or ecdysozoans share high number of conserved gene families with deuterostomes. Comparative transcriptomics demonstrate that phoronid and brachiopod lophophores resemble not only morphologically but also at the molecular level. Despite dissimilar from head structures, lophophores have strikingly high expression of vertebrate head organizer and neuronal markers as well as genes related to secreting machinery and immunity. Finally, we fail to find conventional muscle actins, suggesting possible independent evolution of muscle systems in these phyla. Together, our study reveals the conservation and innovation of lophotrochozoan evolution and a common origin of bilaterian head patterning.

C17-02 Functional diversity of bZIP transcription factors in the sponge Amphimedon queenslandica: insights into the ancestral animal regulatory genome

Jindrich, Katia (The University of Queensland, Brisbane, AUS); Roper, Kathrein E. (The University of Queensland, Brisbane, AUS); Lemon, Sussan (The University of Queensland, Brisbane, AUS); Yuen, Benedict (The University of Queensland, Brisbane, AUS); Degnan, Sandie (The University of Queensland, Brisbane, AUS); Degnan, Bernard (The University of Queensland, Brisbane, AUS)

What genomic innovations supported the emergence of multicellular animals, over 600 millions years ago, remains one of the most fundamental questions in evolutionary biology. Increasing evidence suggests that the elaboration of the regulatory mechanisms controlling gene expression, rather than gene innovation, underlies this transition. Since transcriptional regulation is largely achieved through the binding of

specific transcription factors to specific cis-regulatory DNA, understanding the early evolution of these master orchestrators is key to retrace the origin of animals (metazoans). Basic leucine zipper (bZIP) transcription factors constitute one of the most ancient and conserved families of transcriptional regulators. They play a pivotal role in multiple pathways that regulate cell decisions and behaviours in all kingdoms of life. Here, we explore the early evolution and putative roles of bZIPs in a representative of one of the oldest surviving animal groups, the marine sponge Amphimedon queenslandica. Phylogenetic analyses identify 17 bZIPs in Amphimedon, originating from a repertoire of 7 and 12 bZIPs in the metazoan and holozoan ancestor, respectively. As expected for regulatory molecules, most bZIPs display high temporal specificity, cell-type specific localization and are dynamically expressed throughout Amphimedon development. Specific sponge bZIPs appear to be involved in a variety of contexts, including cell fate decisions, circadian regulation and response to pathogens. Integrating these observations with ongoing ChIP-Seq experiments, we infer that many of the roles bZIPs play in bilaterians have a more ancient origin and were present in the last common ancestor of all contemporary animals.

C17-03 The evolution of developmental gene expression programs in mammals

Cardoso-Moreira, Margarida (University of Heidelberg, DEU); Kaessmann, Henrik (University of Heidelberg, DEU)

The evolution of novel phenotypes requires changes in pre-existing developmental programs. The comparison of developmental gene expression programs across species can, therefore, aid us in identifying the molecular changes that are responsible for species-specific phenotypes. We have generated gene expression profiles covering development in 6 mammals and a bird (human, macaque, mouse, rat, rabbit, opossum and red jungle fowl) for 7 major tissues (brain, cerebellum, heart, kidney, liver, ovary and testis). Our developmental time courses are dense covering most of organogenesis and later tissue development (both prenatal and postnatal, for a total of ~ 2,000 RNA-seq libraries). In agreement with the observed increase in morphological divergence with developmental time, as first described by von Baer, we find that the conservation of developmental programs decreases over time. One facet of this decrease in conservation is the increased deployment of mammalian-specific (and species-specific) genes with developmental time, thus supporting an important role for new genes in driving morphological/physiological change. The conservation of developmental programs also differs between tissues being highest for neural tissues and lowest for reproductive tissues. More broadly, the comparison of developmental programs between different mammalian lineages and between closely related species has uncovered many instances of the main types of developmental

change: subsets of genes changing expression in time (heterochrony), in tissue distribution, in amount and in type. We will describe some of the changes in detail. Overall, the developmental changes that we identified are candidates for underlying lineage- and species-specific morphological and physiological phenotypes and further help elucidate the molecular changes responsible for developmental change (and thence new phenotypes).

C17-04 Pre-metazoan origin of animal microRNAs

Bråte, Jon (University of Oslo, NOR); Neumann, Ralf S. (University of Oslo, NOR); Fromm, Bastian (Oslo University Hospital, NOR); Haraldsen, Arthur A. B. (University of Oslo, NOR); Grini, Paul E. (University of Oslo, NOR); Shalchian-Tabrizi, Kamran (University of Oslo, NOR)

microRNAs (miRNAs) are integrated parts of the developmental toolkit in animals. They have contributed to the evolution of organismal complexity and their biogenesis machinery is highly conserved even between distantly related groups. The evolutionary history and origins of animal miRNAs is however unclear, and it is not known when they evolved and on how many occasions. We have therefore investigated the presence of miRNAs in a unicellular relative of animals, the Ichthyosporean Sphaeroforma arctica, by small RNA and transcriptome sequencing. We find evidence for at least four genes that satisfy the criteria for the annotation of miRNA genes. Comparison with another ichthyosporean, S. sirkka, showed both highly conserved miRNA genes and several miRNAs with identical genome localization. Further we identify homologues of the miRNA-processing genes Drosha and Parcha. Taken together we report the first bona fide miRNA genes as well as homologues of the animal miRNA processing machinery in unicellular Choanozoa. This implies that the ancestor of animals likely possessed and had the capacity of using miRNAs and the associated protein machinery as a gene regulatory mechanism.

C17-05 Discovering the genomic basis underlying species' phenotypic differences

Hiller, Michael (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU)

The growing number of sequenced genomes allows us now to address a key question in genetics and evolutionary biology: What is the genomic basis that underlies phenotypic differences between species? We developed a computational framework called Forward Genomics that associates phenotypic to genomic differences by focusing on phenotypes that are repeatedly lost in independent lineages. Here, we present two new Forward Genomics methods that (i) control for the phylogenetic relatedness between the species of interest, (ii) control for differences in evolutionary rates and (iii) compute the significance of the association

between phenotypic and genomic differences. We systematically compare these methods on simulated and on real data and demonstrate that the new methods significantly improve the sensitivity to detect such associations. We use these methods to discover genomic loci that underlie the degeneration of the visual system in blind subterranean mammals. This genome-wide screen identifies many loci that are enriched in functions related to eye development and the perception of light as well as loci associated with eye diseases in human. In addition, we find genomic loci with a function in the circadian rhythm, which might be an adaptation to the subterranean environment. The Forward Genomics framework has broad applicability to many other phenotypic differences. The new methods presented here significantly advance our ability to discover the genomic basis underlying phenotypic differences between species, which will contribute our understanding of how nature's phenotypic diversity has evolved.

11.10 – 12.25

Contributed Session C18: Serial homology and segmentation

SAL B

Chair: Sandro Minelli

C18-01 Serial homology in plants from a evo-devo perspective

Minelli, Alessandro (University of Padova, ITA)

By discussing serial homology, we implicitly assume that we know where the series begins and where it ends, the comparison being thus restricted to an unequivocally delimited set. This is not necessarily clear in plants, witness Goethe's idealization, that in a plant alles ist Blatt, all is leaf. Serial homology in plants is indeed more intriguing when comparisons challenge conventional organ identity - such as bracts/sepals vs. (bracteo/sepalo)petals, and fertile stamens or staminodes vs. (stamina/andro)petals - or individuality - such as the presence of a stamen-sepal common primordium in Astrantia major. The main proposals thus far advanced to overcome the strictures of traditional morphology are the continuum (R. Sattler) or fuzzy Arberian (R. Rutishauser) morphology, and the dissection of homology into a positional component vs. one of special quality (e.g., L. Ronse De Craene, E. Smets). However, (1) generally speaking, the developmental processes by which position is specified are not restricted to a set of serially homologous organs, but may extend beyond it, or fail to cover the positional specification of all members in the series; (2) an organ's special quality also results from a number of partly sequential, partly overlapping developmental processes, many of which are not specific for that organ, and the notion of organogenesis reduces to an umbrella term for a temporal window of development, defined by the final product rather than by the underlying dynamics. It is suggested here to adopt a combinatorial (factorial) approach to plant homology - based on a comparison of processes rather than the

resulting morphological patterns - within which we can accommodate also the paramorphic relationships resulting from iterative processes at different scale.

C18-02 Amphioxus illuminates the origin of the vertebrates' head

Aldea, Daniel (Observatoire Oceanologique de Banyuls-sur-Mer, FRA); Escrivá, Hector (Observatoire Oceanologique de Banyuls-sur-Mer, FRA); Bertrand, Stéphanie (Observatoire Oceanologique de Banyuls-sur-Mer, FRA)

A central question in Evolutionary Developmental Biology (Evo-Devo) is to understand the origin of the vertebrate head. Thus, the appearance of new structures as the neural crest cells, placodes and an anterior unsegmented paraxial mesoderm were key point for the emergence of the head in the vertebrates. Due to its phylogenetic position and its morphological, developmental and genomic characteristics, amphioxus represents a key animal model to understand the transition between invertebrates chordates to vertebrates chordates. Additionally, comparable to the body of the hypothetical ancestor of all chordates, the body of amphioxus is segmented in its full length. Previous work in our laboratory has shown the central role of the FGF signal in the formation of the anteriormost somites in amphioxus. Thus, the loss of the anterior somites in the hypothetical ancestor of all chordates might have facilitated the emergence of new structures, for instance a new unsegmented mesoderm. In this work, using a comparative RNA-seq approach, we looked for genes controlled by the FGF signaling pathway, then using „"in situ"" hybridization we selected those genes expressed in the paraxial mesoderm that in amphioxus gives rise to the somites. Finally, in order to understand the specific role of the transcription factors Six1/2, Pax3/7 and Zic in the formation of anterior somites, we fused the Engrailed repressor or VP16 activation domains to these transcription factors. Our results show that embryos injected with the constitutive repressed form of Six1/2 and Zic lose the most anterior somites. Thus, by studying the role of different genes during early development in amphioxus we are starting to understand how anterior somitogenesis is controlled in amphioxus and how functional changes during evolution may have played a role in the origin of the head of vertebrates.

C18-03 New clues on origins of axial skeleton regionalization and appendicular skeleton: Ontogenetic evidence from fossil and extant jawless vertebrates

Chevrinais, Marion (Université du Québec à Rimouski, CAN); Johanson, Zerina (Natural History Museum London, GBR); Trinajstic, Kate (Curtin University, Perth, AUS); Long, John (Flinders University, Adelaide, AUS); Morel, Catherine (Université du Québec à Rimouski, CAN); Renaud, Claude B. (Canadian Museum of Nature, Ottawa, CAN); Cloutier, Richard (Université du Québec à Rimouski, CAN)

During the evolution of vertebrates, the transition between jawless to jawed vertebrates occurred approximately 425 Ma with morphological and developmental changes. These evolutionary novelties include jaws, paired pelvic fins and endoskeletal girdles, and reproductive intromittent organs. The presence of these novelties in the most phylogenetically basal jawed group, the placoderms, suggests that developmental mechanisms (e.g., lateral plate mesoderm formation responsible for the development of paired appendages) allowing such changes could have been already present in jawless. However, our most recent interpretation of a jawless anaspid-like fish, Euphanerops, from the Upper Devonian, challenged the evolutionary origin of some of the so-called jawed vertebrate synapomorphies. We describe, for the first time, pelvic girdles and intromittent organs in this jawless, associated with morphologically differentiated regions of the axial skeleton. Appendicular and axial skeleton novelties occur simultaneously in Euphanerops. Morphological differentiation of the anterior axial skeleton is also described for the first time in the extant jawless Sea lamprey Petromyzon marinus. Euphanerops and Petromyzon should have shared genetic pathways responsible for the development of the appendicular (abaxial domain of gene expression determining the lateral plate mesoderm development) and the axial (primaxial domain of genes coding for somite development) skeletons. In jawed vertebrates, the presence of the lateral somitic frontier suggests that the abaxial and primaxial domains are independent. But, recent studies on lamprey median fins show that these fins develop from somitic mesoderm suggesting that the origin of paired appendages could be associated with a re-deployment of this mechanism in lateral plate mesoderm. This suggests a dependence of abaxial and primaxial domains at least during some vertebrate ontogenetic stages. Euphanerops and Petromyzon ontogeny indicates that a modification of postcranial skeleton occurred earlier in vertebrate history than previously recognized.

C18-04 HoxD patterning of the fin-fold compartment of basal gnathostomes: Implications for the fin to limb transition

Tulenko, Frank J. (Kennesaw State University, USA); Massey, James L. (University of Colorado Boulder, USA); Davis, Marcus C. (Kennesaw State University, USA)

The morphological transition from fins to limbs during the tetrapod invasion of land is one the compelling puzzles in comparative anatomy. This transition involved several key changes in appendage anatomy, including the loss of the fin-fold and dermal skeleton, and an elaboration of the distal endoskeleton to form an autopod with digits. HoxA/D cluster genes are active during both fin and limb development, and over the last two decades, have been the focus of much work aimed at gaining insight into the evolutionary origin of limb-specific morphologies. Here we characterize the expression of HoxD genes, as well as the cluster-associ-

ated genes Evx2 and LNP, in the paddlefish Polyodon spathula, a basal ray-finned fish. Our results demonstrate a collinear pattern of nesting in early fin buds that includes HoxD14, a gene previously hypothesized to be isolated from global Hox regulation. Additionally, we show that in both Polyodon and the catshark Scyliorhinus canicula (a representative chondrichthyan) late phase HoxD transcripts are present throughout the fin-fold mesenchyme and co-localize with And1, a component of the fin-fold actinotrichia and dermal skeleton. These new data support an ancestral role for HoxD genes in patterning the fin-fold compartment of jawed vertebrates, and call for a reassessment of current models of fin/limb evolution. Furthermore, these data fuel new hypotheses about the evolution of cluster regulation and the potential downstream differentiation outcomes of distinct HoxD-regulated compartments.

C18-05 Developmental morphology of the head in sturgeons (Acipenseriformes: Acipenseridae)

Warth, Peter (FSU Jena, DEU); Konstantinidis, Peter (Virginia Institute of Marine Science, USA); Hilton, Eric J. (Virginia Institute of Marine Science, USA); Naumann, Benjamin (FSU Jena, DEU); Olsson, Lennart (FSU Jena, DEU)

The development and evolution of the vertebrate head is a classical field of study since the advent of embryology. A primary focus of study relates to the diversity in shape among vertebrate heads and to unravel the homologies of the multitude of elements involved in the composition of the head. Comparative developmental morphology is a useful method to infer homologies across taxa. We used sturgeons (Acipenseridae) as a model to study the evolution of head development within gnathostomes. Together with the paddlefishes (Polyodontidae) they form the order Acipenseriformes and have a phylogenetic position close to the base of the Actinopterygii, making them an attractive taxon to study in a large-scale evolutionary context. Also, the availability of embryonic material through hatcheries in Asia, North America and Europe makes sturgeons an accessible model. On the basis of several artificially induced spawning events we conducted a study of head development of the Russian (Acipenser gueldenstaedtii) and the Siberian sturgeon (A. baerii) from neurulation on to early juveniles. We applied SEM and histology to extend the information available from previous staging tables and further focused on the morphogenesis of the head and shoulder girdle. We applied the classical clearing and staining technique with Alizarin and Alcian for light microscopical visualization of the skeleton as well as immunohistochemistry and confocal laser scanning microscopy for imaging of cartilage, muscles, tendons and nerves. The collected data show a more precise timing of the development of the neurocranial, viscerocranial and dermatocranial elements as well as the muscles of the head. We highlight the sequence of development of elements and its

implications for the homology of structures such as the basibranchials and the cranial muscles and compare our findings in sturgeon with data from other actinopterygians.

11.10 – 12.25 Contributed Session C19:
Evolution of plant and animal epidermal patterns

SAL C

Chair: Beverley Glover

C19-01 ### How to spot a Daisy

Mellers, Greg (University of Cambridge, GBR); Glover, Beverley (University of Cambridge, GBR); Ellis, Allan (University of Stellenbosch, ZAF)

Angiosperms are the most diverse division of extant land plants, occurring in almost every environment on Earth, with estimates of around 260,000 to 420,000 species. A key element in the formation of such a speciose group is thought to be their intimate co-evolution with pollinator species. Typically such pollination syndromes are gross features such as corolla colouration or floral scent. However, it is becoming increasingly apparent that finer scale features may also attract wild pollinator species. One such characteristic is the appearance of petal spots on the corolla of some species which have previously been shown to increase reproductive success. It is hoped that formation of this feature in a heterologous crop system may confer greater pollinator interactivity and thus yield. Our study aims to investigate how petal spots develop in the model daisy species Gorteria diffusa. Previous work has found there to be multiple â€œmorphotypesâ€ of the species which represent a series of natural mutations fixed within discrete populations. These allow for comparative analyses to be undertaken with the intention of elucidating the molecular regulation of spot generation. Some evidence suggests a role for MYB genes in the spot formation process hence comparative expression analyses (Î”Ct qPCR) and heterologous expression studies are being undertaken. Furthermore, Genotyping-by-Sequencing (GBS) is also being used to acquire high SNP coverage in an attempt to understand the relationships between the aforementioned morphotypes. It is hoped that through these diverse techniques a hypothetical model for spot formation may be found and subsequently perturbed for validation.

C19-02 ### Root Hair Development in Arabis alpina

Mapar, Mona (Max Planck Institute for Plant Breeding Research, Köln, DEU)

An evolutionary developmental approach is used to compare homologous processes in closely related species. In this study, we use Arabis alpina, as a model system to compare the regulation of root hair development with that in Arabidopsis thaliana. In Arabidopsis, the genetic and molecular analysis of root hair development has enabled the dissection

into developmental steps and to the identification of the molecular pathways. Our genetic screens revealed a similar spectrum of mutants as found in Arabidopsis. Candidate genes are sequenced in the mutants to find the responsible genes. I am currently focusing on the AaSCN1 gene for which I have isolated a knockdown EMS allele.

C19-03 Sculpting the surface: understanding the development, function and evolution of nanopatterning in petals

Moyroud, Edwige (University of Cambridge, GBR)

Plants and animals often display intricate micropatterns on their surface. These minute features provide unique tissue properties: for example, flowering plants can display regular striations on their petal epidermis small enough to interfere with light and produce colours that change with the viewing angle, a phenomenon known as iridescence. However, the evolution and development of those nanopatterns remain largely unexplored. We have recently characterised the optical response of iridescent flowers distributed across the flowering plant phylogeny and our results indicate that petal striations form diffraction gratings with various amounts of disorder. Despite structural differences between species, those floral gratings produce a similar optical signal shifted towards the blue end of the spectrum and behavioural experiments reveal that this unique „"petal blue halo""effect increases bumblebee foraging speed. The apparent disorder observed in floral gratings could thus reflect a common mechanism used by plants to produce strong conspicuous signals for pollinators. In parallel, we have developed Hibiscus trionum, a species with iridescent flowers, as a new genetic model to investigate the formation of surface patterns on a living tissue. We are currently using this system with a range of techniques from molecular biology to chemical analysis and modelling to test if mechanical buckling of the cuticle could explain the formation of ordered striations on the petal epidermis

C19-04 Comparative genomics suggests evolutionary adaptations of epidermal differentiation in squamate reptiles

Eckhart, Leopold (Medical University of Vienna, AUT); Holthaus, Karin B. (Medical University of Vienna, AUT); Mlitz, Veronika (Medical University of Vienna, AUT); Strasser, Bettina (Medical University of Vienna, AUT); Tschachler, Erwin (Medical University of Vienna, AUT); Alibardi, Lorenzo (University of Bologna, Italy)

The skin has a crucial protective role for terrestrial animals and particularly for reptiles. Most critically, the outermost part of the skin, the cornified layer of the epidermis, forms a barrier that protects the body against dehydration and physical, chemical, and biological insults from the environment. Studies in mammalian model species have shown that the protein components of this layer are encoded in a specific genomic re-

gion, termed the epidermal differentiation complex (EDC). Recently, we identified the EDC in birds and turtles and provided evidence for an association of skin evolution and adaptations of EDC genes. In the present study, we determined the EDC of squamate reptiles (lizards and snakes) and developed a scenario for the evolution of the cornification proteins in snakes. Comparative genomics and screenings of transcriptome data were performed for the king cobra, the Burmese python, and the green anole lizard. We identified snake EDC genes that encode homologs of human skin barrier proteins, such as loricrin and cornulin, and antimicrobial peptidoglycan recognition protein 3. The EDC of squamates also contains genes encoding corneous beta-proteins (beta-keratins) which are skin protein specific to sauropsids. Unexpectedly, we identified multiple genes encoding short proteins with extremely cysteine contents (>40%) in the EDCs of both lizard and snakes. Cysteine-rich skin proteins were previously identified as components of hard skin appendages such as claws, hair and feathers, which are stabilized by molecular cross-linking via disulfide bonds. As snakes lack such skin appendages, our results indicate that cysteine-dependent protein cross-linking contributes to the formation of their highly resilient cornified skin surface. In conclusion, the evolution of the peculiar skin biology of snakes and other squamates was associated with duplications and sequence adaptations of EDC genes.

C19-05 Conspicuous coloration in Trachemys scripta: mechanism of ontogenetic color change and the first description of iridophores in a turtle

Brejcha, Jindřich (Charles University in Prague, CZE; National Museum, Prague, CZE); Kleisner, Karel (Charles University in Prague, CZE); Font, Enrique (University of Valencia, ESP)

Male red-eared sliders (Trachemys scripta elegans) undergo an ontogenetic shift in coloration associated with an alternative reproductive tactic: while non-melanistic males court females using elaborate ritualized displays (trailing, nosing, titillation), melanistic males achieve mating by chasing and biting females. However, despite wide interest in the behavioral and ecological implications of body coloration, there are few studies of the mechanisms of color production in any Trachemys species. Here we present the first comprehensive description of integumental coloration in a chelonian, using reflectance spectrophotometry, pigment analyses, and ultrastructural characterization of chromatophores. We used standard techniques to obtain reflectance spectra from nine body regions of T. scripta elegans (N=39 females, 10 juveniles, 30 non-melanistic males, 12 melanistic males). We found differences between the sexes in coloration. We also found that the skin coloration of melanistic males differs from that of other males in every body region measured except for the yellow chin. The ultrastructural analyses show

that the red postorbital region owes its reflectance to the presence of a continuous layer or xantophores containing carotenoid vesicles. Yellow skin, on the other hand, is characterized by the presence of iridophores containing reflecting platelets together with xanthophores containing pterinosomes. Yellow and red skin also differ in pigment composition, but both contain carotenoids and pteridines. Melanophores are present in both epidermis and dermis, the epidermal melanophores being tightly connected with keratinocytes. The ontogenetic coloration change of melanistic males involves a reduction in the number of xantophores in the postorbital patch and overall changes of distribution and abundance of melanophores. We suggest that the abundant collagen fibers found in the dermis may also play a role in the production of skin coloration. To our knowledge, this is the first report of iridophores contributing to color production in the integument of chelonians.

11.10 – 12.25

Contributed Session C20: Evolution of gene regulatory networks and the origin of novelties I

K3/K4

Chair: Pete Olson

C20-01 Wing homologs in a crustaceans

Tomoyasu, Yoshinori (Miami University, Oxford, USA); Clark-Hachtel, Courtney (Miami University, Oxford, USA); Patel, Nipam (University of California Berkeley, USA); Bellés, Xavier (Institut de Biologia Evolutiva, Barcelona, ESP); Buschbeckm, Elke (University of Cincinnati, USA)

Despite the fact that insect wings are often used as an example of morphological novelty, the origin of insect wings remains one of the principal mysteries in evolution. Over a century of debates and observations have culminated into two prominent hypotheses on the insect wing origin. One hypothesis, the paranotal hypothesis, connects the origin to the lateral outgrowth of the tergum, the paranotal lobe. The second hypothesis, the exite hypothesis, connects the origin to ancestral proximal leg structures (pleurites) and the branches (exites) stemming from these segments. Despite accumulating efforts to unveil the origin of insect wings, neither hypothesis has been able to surpass the other. To approach this conundrum from an evo-devo perspective, we have been analyzing the function of vestigial (vg), a critical wing gene initially identified in Drosophila, in various organisms. Our investigation in the Tribolium beetle led to the identification of two vg-dependent tissues in the â€œwinglessâ€ first thoracic segment. Intriguingly, these two tissues may actually be homologous to the two proposed wing origins. This observation, along with our Hox analysis, has led to a combinational wing origin hypothesis, namely, insect wings have a dual origin, and that the merger of two unrelated tissues has been a key step in developing

this morphologically novel structure during evolution. We are currently testing this hypothesis by investigating the vg function in a crustacean, Parhyale. Intriguingly, through expression analyses and CRISPR/Cas9-based genetic modification, we found that vg is important for the development of both tergal and proximal leg tissues in Parhyale, suggesting that these tissues may be crustacean wing homologs. These results may further support a dual origin of insect wings. The morphological comparison of the wing (serial) homologs in various organisms will allow for the construction of a more complete history of the evolution of insect wings.

C20-02 Evolution of gene regulatory networks and the origin of novelties

Clark, Erik (University of Cambridge, GBR); Akam, Michael (University of Cambridge, GBR)

There have been two major evolutionary transitions in arthropod segmentation. The first is the evolution of pair-rule patterning, which occurred independently in insects and centipedes. The second is the evolution of long-germ segmentation, which occurred multiple times in holometabolous insects. Most of what we know about arthropod segmentation comes from Drosophila, a long-germ, pair-rule insect. We will present new findings about the gene network controlling segmentation in Drosophila. Broadly-expressed but temporally-regulated factors control the timing of segmentation, while one of these factors mediates the transition from double-segment to single-segment periodicity. These findings have significant implications for the evolution of arthropod segmentation.

C20-03 Evolution of gene regulatory networks and the origin of novelties
Investigating origins of butterfly eyespots via gene regulatory network co-option

Connahs, Heidi (National University of Singapore, SGP); Das Gupta, Mainak (National University of Singapore, SGP); Monteiro, Antonia (National University of Singapore, SGP)

How organisms evolve novel traits has emerged as one of the most fascinating yet challenging pursuits for evolutionary developmental biologists. A fundamental question concerns the nature and tempo in which these novelties arise. Do traits evolve gradually in a stepwise fashion or by co-option of pre-existing gene regulatory networks facilitating rapid evolutionary change? Butterfly eyespots are stunning examples of morphological novelties and an excellent system to address the evolution of novel traits. Eyespots arose once within the family Nymphalidae ~90 mya concurrently with a small cluster of genes expressed during early eyespot development. The question then arises whether eyespots derive from unique networks wired de-novo one gene at a time, or evolved via co-option of pre-existing networks involved in other developmental processes. One approach in testing these hypotheses is

to identify whether cis-regulatory elements (CRE's) of eyespot-associated genes are pleiotropic or function uniquely in eyespot development. We used FAIRE-seq to identify putative CRE's of genes expressed in Bicyclus anynana wing tissues with eyespots (distal hindwing) versus no eyespots (proximal hindwing), and between forewing (FW) and hindwing (HW) distal margins, which vary in eyespot number. We also compared CRE's in Bicyclus anynana with Danaus plexippus, representing a sister lineage without eyespots. Our analysis identifies the first putative CRE's for butterfly wings revealing differences in open chromatin between FWs vs. HWs and proximal vs. distal regions, with eyespot tissues possessing the largest number of CRE's. Very few CRE's are shared between FW and HW margins. We also observed differences in chromatin profiles between the two butterfly species. Thus, CRE's uniquely associated with B. anynana and eyespot wing tissue may regulate eyespot development. Future CRISPR/transgenic experiments will identify whether these putative CRE's are involved in eyespot development and display pleiotropic functions, further testing alternative hypotheses of eyespot GRN evolution."

C20-04 A phylogenetic framework for the carpel development regulation: mixing and matching old with new

Becker, Annette (Justus-Liebig-University Giessen, DEU); Pfannebecker, Kai C. (Justus-Liebig-University Giessen, DEU)

A major evolutionary innovation in the plant lineage is the angiosperm carpel, their unifying character and most complex plant organ, composed of many clearly distinct tissue types to ensure reproductive success. However, the origin of the carpel is unknown, but many components of the gene regulatory network (GRN) governing carpel development and their genetic interactions are described in Arabidopsis thaliana. To unravel the evolution of the carpel GRN and to discriminate between â€œearlyâ€ and â€œlateâ€ steps in carpel evolution we calculated thorough phylogeny reconstructions based on sequenced genomes such that orthologs of the major A. thaliana carpel GRN are now placed in their phylogenetic context. We find that the carpel GRN components are of various ages, and identify especially high retention rates for carpel development genes in Brassicaceae leading to Brassicaceae-specific interactions of carpel GRN members. Further, our data indicate that developmental processes present already in the most recent common ancestor of seed plants, such as reproductive meristem termination or adaxial/abaxial polarity specification requires few interacting transcription factors, which are not retained in duplicates after whole genome duplications (WGD). In contrast, developmental processes associated with derived carpel characters, such as the transmitting tract require larger numbers of interacting transcription factors which were retained as duplicates after WGD.

C20-05 From planarians to parasitism: Wnt/Hedgehog signalling controls AP

patterning during larval and strobilar development in tapeworms
Jarero, Francesca (Natural History Museum, London, GBR); Koziol, Uriel (Universidad de la República, Montevideo, URY); Olson, Pete (Natural History Museum, London, GBR)

Wnt/Hedgehog signalling in free-living planarians is responsible for mediating head/tail decision making during early development and in regeneration. More broadly, canonical Wnt signalling has been found to underlie AP axis formation in animals generally. We show that AP specification during larval metamorphosis in tapeworms also involves canonical Wnt signalling, with scolex formation taking place at the site(s) of Wnt repression. Moreover, we show that the same system has been co-opted during strobilar development, with segmental boundaries expressing opposing 'stripes' of anteriorizing (SFRP) and posteriorizing (Wnt1) signals—tapeworm strobilation therefore being a form of paratomy. Expression of Hedgehog and Hox also appear linked to the system, upstream and downstream of Wnt signaling, mirroring the model of AP signalling in planarians as presently understood. Taken together, we show that parasitic and free-living flatworms share the same underlying AP patterning system despite their highly disparate body plans.

13.50 – 15.30 Symposium S21:
The evolution of gene regulatory networks and the origins of novelties

STORA SALEN

Organizers: Heidi Connahs and Antónia Monteiro
Chair: Heidi Connahs and Antónia Monteiro

S21-01 Evolution of transcription factor function in development
Hinman, Veronica (Carnegie Mellon University, Pittsburgh, USA); Cary, Greg (Carnegie Mellon University, Pittsburgh, USA); Jarvela, Alys (Carnegie Mellon University, Pittsburgh, USA); Francolini, Rene (Carnegie Mellon University, Pittsburgh, USA)

It is well documented that GRNs can evolve extensively through mutations to cis-regulatory modules. Transcription factor proteins that bind these cis-regulatory modules may also evolve to produce novelty. Coding changes, however, are considered to be more rare, because transcription factors are highly pleiotropic and hence are more constrained to evolve in ways that will not produce widespread detrimental effects. Recent technological advances have unearthed a surprising variation in DNA-binding abilities, such that individual transcription factors may recognize both a preferred primary motif and an additional secondary motif. This provides a source of modularity in function. In this talk, we will present recent work that shows that orthologous transcription factors can also evolve a changed preference for a lower affinity secondary binding motif, thereby offering an unexplored mechanism for

GRN evolution. We demonstrate that this difference may allow for greater evolutionary change in timing of regulatory control and provide a mechanism through which organisms can evolve a changed response to signaling gradients. This uncovers a layer of transcription factor binding divergence that could exist for many pairs of orthologs.

S21-02 Role of novel genes in the evolution of behavioral and physiological novelty

Johnson, Brian R. (University of California, Davis, USA)

The relative roles of coding and regulatory sequence change in the evolution of phenotypic novelty is one of biology's major unresolved questions. The field of evo-devo has shown that in early development changes to regulatory regions appear to be the dominant mode of genetic change, but whether this extends to the evolution of novel phenotypes in the adult organism is unclear. Here we conduct ten RNA-Seq experiments across both novel and conserved tissues in the honey bee to determine to what extent post-developmental novelty is based on changes to the coding regions of genes. We first show that with respect to novel physiological functions in the adult animal, positively selected tissue-specific genes of high expression underlie novelty by conferring specialized cellular functions. Such genes are often, but not always taxonomically restricted genes (TRGs). We further show that positively selected genes, whether TRGs or conserved genes, are the least connected genes within gene expression networks. Overall, this work suggests that the evo-devo paradigm is limited, and that the evolution of novelty, post-development, follows additional rules. Specifically, evo-devo stresses that high network connectedness (repeated use of the same gene in many contexts) constrains coding sequence change as it would lead to negative pleiotropic effects. We suggest that in the adult animal, the converse is true: genes with low network connectedness (TRGs and tissue-specific conserved genes) underlie novel phenotypes by rapidly changing in coding sequence to perform new specialized functions.

S21-03 Tracing the mosaic ancestry of a novel tissue organizer's regulatory circuitry

Glassford, B. (University of Pittsburgh, USA); Smith, Sarah J. (University of Pittsburgh, USA); Rebeiz, Mark (University of Pittsburgh, USA)

The evolutionary origins of complex anatomical structures such as the eye or wing remain a major puzzle in evolutionary developmental biology. The development of morphology is controlled by gene regulatory networks (GRNs) composed of transcription factors, signaling pathways, and the regulatory sequences (enhancers) they control to activate expression of structural genes that ultimately confer physical properties upon a tissue. Often, tissue organizers express signaling molecules that instruct the morphogenic changes within surrounding tissues, and such

organizers are frequently associated with novel anatomical structures. Here, we dissect the ancestry of regulatory sequences responsible for the activities of two signaling pathways activated in an organizer that patterns the posterior lobe, a recently evolved novel genital formation unique to the D. melanogaster clade. We show that the activity of these enhancers evolved by changes in cis, as well as differences in upstream trans factors. Furthermore, we find that these enhancers are pleiotropically linked to additional unrelated tissues during development. These findings illustrate how tissue organizing centers evolve, and provide evidence that networks may combine regulatory sequences from more than one tissue during their assembly.

S21-04 Gene regulatory complexity in chordate spinal patterning

Shimeld, Sebastian (University of Oxford, GBR)

The amniote spinal cord develops a complex and well-defined pattern of cell types across the dorsal-ventral axis. Ventral hedgehog signalling plays a pivotal role in the establishment of this pattern, with the gene regulatory network downstream of the signal generating zones of target transcription factor gene expression that define neural progenitor pools and hence cell type complexity. Key mediators of this process are the Gli proteins, which generate a balance of activator and inhibitor downstream from hedgehog ventrally and other signals dorsally. Duplication of the Gli genes appears to have been important in this process, with Gli1, Gli2 and Gli3 having distinct roles in patterning. Spinal cord patterning appears much simpler in invertebrate chordate lineages, which have a single Gli gene. Lampreys show many aspects that are conserved with other vertebrates, but also have some key differences; I will describe our progress in dissecting the evolution of the gene regulatory system that controls spinal pattering and its relationship to spinal complexity.

13.50 – 15.30

SAL B

Symposium S22: The vertebrate limb as an evolving dynamical system

Organizers: Gerd Müller and Stuart A. Newman
Chair: Gerd Müller

S22-01 Dynamics and phylogenomics of the two-galectin tetrapod limb patterning network

Newman, Stuart (New York Medical College, Valhalla, USA)

The chicken limb skeleton is patterned by a reaction-diffusion network incorporating the interaction of two galectins, Gal-1A and Gal-8, glycan-binding proteins that act as both morphogens and mediators of cell-cell adhesion. Gal-1A induces chondrogenic mesenchymal condensation, whereas Gal-8 interferes with this effect. Each galectin induces

the other's gene expression. Mathematical and computational modeling indicates that this network is â€œmorphodynamic,â€ in that its pattern-forming capability depends on cell movement into regions of elevated Gal-1A. Using phylogenomic methods we have traced Gal-1A back to its first appearance in the vertebrates, where it already had the protein structural motif that distinguishes skeletogenic Gal-1A from nonskeletogenic avian Gal-1B and other Gal-1s that evolved later by gene duplication. This is consistent with endoskeletal elements being present in the paired appendages of cartilaginous, ray-finned, and lobe-finned fishes, including, in the latter clade, the tetrapods. We therefore traced the evolution of Gal-8 in the jawed fishes to determine the origin of the tetrapod limb patterning network. In the lobe-finned fishes the fold-structure of Gal-8 evolved under purifying selection to converge with that of the skeletogenic form of Gal-1, and its gene acquired a conserved non-coding motif with binding sites that eventually came to be utilized by transcription factors in developing tetrapod limbs. Thus, evolution of Gal-8 in the lobe-finned fishes enabled the constitution of a reaction-diffusion mechanism like that we have described, which requires a Gal-8 under stringent quantitative regulation capable of competing with Gal-1 for common cell surface binding sites, in order to produce the characteristic array of small numbers of tandemly arranged elements of the tetrapod limb skeleton. In the ray-finned fishes, in contrast, the lack of a constraining reaction-diffusion network opened the way to positive selection of Gal-8 and a radiation of endoskeletal geometries less stereotypical than that of the lobe-fins and tetrapods.

S22-02 Development and evolution of the jerboa limb skeleton

Cooper, Kimberley (Harvard Medical School, Boston, USA)

Decades of chick embryology and mouse genetics have elucidated many of the mechanisms of limb development, yet fundamental questions remain unanswered. Mutations at genes that control long bone growth lead to the proportionate truncation of the entire skeleton. How then are the correct proportions of different bones established, e.g. our long arm bones and comparably short finger bones? Since almost every limb development gene functions in both the fore and hindlimbs, why do 92% of human birth defects affect the arms or legs but rarely both? How are the same genes used to pattern the remarkably different shapes of the human arm, the horse leg, and the bat wing? Our work leverages the unique hindlimb structure of the lesser Egyptian jerboa to understand developmental malleability. The jerboa is a desert-adapted bipedal rodent with disproportionately elongated hindlimbs, particularly the feet with their fused metatarsals, and five fingers but three toes. We have shown that differences in cell mass production produce larger chondrocytes that scaffold rapidly elongating bones compared to the small chondrocytes of those that grow more slowly. Current work is focused on

identifying the genes that control different rates of cell mass production. We also showed that the jerboa, as well as the horse and camel, reduces the number of digits in part by sculpting away digit-forming cells via apoptotic cell death. The pattern of apoptosis matches the expanded expression domains of Bmp4 and Msx2, two genes also responsible for interdigital cell death. Each of these projects is leading toward the identification of gene regulatory control modules that differ between the jerboa and mouse. Toward this end, we are developing strategies in the mouse to test the function of evolutionarily divergent gene regulatory sequences. These studies will elucidate the developmental mechanisms that shape limbs of different species, including our own.

S22-03 Changing while staying the same: Self-organized patterning allows a deeply-conserved gene circuit to produce varying skeletal arrangements during limb evolution

Sharpe, James (Centre for Genomic Regulation, Barcelona, ESP)

The limb has been a classical system for asking questions about evolution and development. It has long been proposed that digit specification was the result of a self-organizing periodic patterning process (Ede & Law, Journal of Theoretical Biology, 1975) and maybe even a Turing system (Frisch & Newman, Science, 1979). However, evidence for the molecular basis of this pattern has been hard to obtain. Over the last few years we uncovered evidence for the involvement of Hox genes and FGF signaling as key modulators of this process (Sheth et al. Science, 2012), and for Bmp and Wnt signaling to constitute the Turing system itself (Raspopovic et al. Science, 2014). Most recently, we have shown that the same core regulatory circuit is also involved in the patterning of radials in the catshark Scyliorhinus canicula (Onimaru et al. Nature Communications, 2016). Through computer simulations of realistic growing models of the mouse limb bud and the catshark fin bud, we illustrate how this single regulatory circuit can recapitulate the distal skeletal patterns of both species. These data-driven models strengthen previous theoretical proposals that limb skeletal patterns were probably quite flexible during evolution. Fundamental to this flexibility is the self-organising nature of the patterning process. It supports the view that comparing the details of skeletal arrangement across species provides only limited information about evolutionary relationships.

S22-04 Avian digit identity in light of digit formation models

Capek, Daniel (Institute of Science and Technology, Gugging, AUT); Müller, Gerd B. (University of Vienna, AUT)

Turing based models currently represent the prevailing explanation for the mechanism of digit formation. It has been shown that reaction-diffusion systems can account for the patterns formed by digital and interdigital tissue. Reduction of digit number, for instance, is a widespread

trend in vertebrate evolution and can be explained by modifications of strength or timing of signaling molecules in reaction-diffusion networks. Here we suggest that modulation of the digit formation process can influence the subsequent module of digit phenotype specification. During this second phase the respective digits process information that makes them adjust their transcriptomic and morphological features. Since the signaling that digit primordia receive depends largely on the surrounding tissue, change of relative position can conceivably alter this specification. We suggest that digit reduction can change the direction of growth of digit anlagen by simple biomechanical properties. Applying these ideas to the longstanding problem of avian digit identity, we intend to explain how digit loss caused by modulation of the digit formation network can cause the remaining digits to adopt different or chimeric phenotypes, resulting in the phenotype of modern birds.

13.50 – 15.30

Symposium S23:
The role of developmental evolution in reproductive medicine

SAL C

Organizers: Mihaela Pavlicev and Günter Wagner
Chair: TBA

S23-01 **Marsupials as biomedical models for reproduction and development**

Renfree, Marilyn B. (University of Melborne, AUS)

Marsupials are mammals, but they differ from eutherian mammals primarily in their mode of reproduction that has an emphasis on lactation rather than placentation. Despite this, or perhaps because of this, they have proven to be excellent models for biomedical research. They give birth to highly altricial young, so most of their development occurs after birth while the young are in a pouch. This makes the developing young uniquely accessible for experimental manipulation at stages that are equivalent to those that occur in utero in eutherian mammals. We have exploited this characteristic in the tammar wallaby, Macropus eugenii, a small member of the kangaroo family, which has an extended period of embryonic diapause, in which the embryo remains in a state of suspended animation for 11 months. This presentation will focus on just some of these. The first is the control of early development and the greater similarity to that seen in man rather than mouse. The second is the hormonal control of virilisation and of sexual differentiation including sex reversal, and how these studies are starting to be used to interpret medical disorders of sexual development. The third is the control of genomic imprinting and how differences in imprinting the placenta and in the mammary gland have evolved. These characteristics make the tammar a powerful model for advancing our understanding of reproduction and development in all mammals including man.

S23-02 **How do mammals beat the heat? The evolution of the inflammatory**

response in pregnancy and the origin of decidual stromal cells

Chavan, Arun R. (Yale University, USA); Griffith, Oliver (Yale University, USA); Maziarz, Jamie (Yale University, USA); Tzika, Athanasia (University of Geneva, CHE); Milinkovitch, Michel (University of Geneva, CHE); Wagner, Günter (Yale University, USA)

Decidual stromal cells (DSC) are a novel uterine cell-type that originated in the stem lineage of eutherian mammals. In mouse and human, DSC are known to perform a variety of roles during implantation as well as in the maintenance of extended gestation. In many eutherian species, however, DSC are lost soon after implantation. In order to understand this variation, we reviewed the literature on DSC in all major eutherian clades. We conclude that the ancestral function of DSC, in a stem eutherian, was limited to regulating inflammation during the invasive process of implantation. Their other functions in the maintenance of pregnancy are derived features of Euarchontoglires. To further explore the evolution of the inflammatory response during pregnancy, we undertook a comparative transcriptomic study on the uteri of two eutherians, armadillo (Dasypus novemcinctus) and tenrec (Echinops telfairi), and one marsupial (Monodelphis domestica). Our data suggest that suppression of inflammation in the uterus during pregnancy, despite extensive tissue injury, is a shared derived feature of eutherian mammals, but lacking in opossum. These data also provide a mechanistic perspective, implicating the M2-polarized macrophages in bringing about the anti-inflammatory outcome. In this talk, I will discuss the implications of these findings for understanding the evolution of extended gestation in eutherian mammals and the „immunological paradox"of pregnancy.

S23-03 Placenta transcriptomics and the evolution of obstetrical syndromes

Armstrong, Don L. (University of Illinois, Urbana-Champaign, USA); McGowen, Michael R. (Queen Mary, University of London, GBR); Weckle, Amy (University of Illinois, Urbana-Champaign, USA); Caravas, Jason (Wayne State University School of Medicine, Detroit, USA); Agnew, Dalen (Michigan State University, East Lansing, USA); Benirschke, Kurt (UC San Diego, USA); Savage-Rumbaugh, Sue (Bonobo Hope Sanctuary, Iowa, USA); Nevo, Eviatar (University of Haifa, ISR); Kim, Chong J. (WSU School of Medicine, Detroit, USA); Wagner, Günter (Yale University, USA); Romero, Roberto (WSU School of Medicine, Detroit, USA); Wildman, Derek E. (University of Illinois, Urbana-Champaign, USA)

Modes of reproduction have evolved extensively during the descent of organisms. In viviparous animals the apposition of parental and fetal tissues (i.e. placentation) has evolved several times independently, resulting in physiological exchange of nutrients, gases, and waste products. Placentation occurs in invertebrates, fish, reptiles, and most famously in mammals. The placenta in all of these species is required for proper embryonic development, and eutherian mammals rely on placental transfer

in order to promote fetal growth. Moreover, the anatomy of the placenta varies more than any other mammalian organ. In order to learn about mammalian placenta diversity we analyzed its transcriptome in thirteen eutherian and one marsupial species. We found that the placenta transcriptome is quite variable both between and within species, and we propose that this variation points to evolutionary developmental adaptations as well as neutrally diverging gene expression patterns in these species. Remarkably, when strictest filtering thresholds were used, we found that only 56 orthologous genes were expressed in the placenta of all 14 species. In humans most obstetrical syndromes have been associated with disorders of placentation in which its invasion into the myometrium is dysregulated resulting in placentation that is either too shallow or too deep. The finding of lineage specific gene expression patterns may provide clues as to why humans and other apes develop obstetrical syndromes such as preeclampsia (i.e. hypertension in pregnancy, and the leading cause of maternal mortality during childbirth). Preeclampsia has not been observed outside of this clade. Other obstetrical syndromes such as pseudopregnancy in the horse may be due to evolutionary change during perissodactyl descent. We suggest that an evolutionary understanding of placentation will be helpful in developing molecular taxonomies of all human obstetrical syndromes.

S23-04 Modularity and evolution in the placenta

Elliot, Michael G. (University of Cambridge, GBR)

It is now recognized that modularity is a crucial feature of evolvable developmental systems. The modularity of mammalian development during pregnancy is less immediately apparent than in clearly segmented creatures such as insects and crustaceans, in which developmental modules may be physically manifest in distinct body segments. Nevertheless, developmental modularity may be recognized in terms of context-insensitivity of function, for example in components of genetic networks. Some genetic modules in the mammalian placenta can be identified using this criterion. For example, a gene network involving syncytin induces syncytialization of tissue in a context-insensitive manner. However, this example is challenging in the context of evo-devo in that it appears in numerous species but is not identical by descent (rather, by lateral gene transfer from viruses). More generally, the mammalian placenta is highly context-sensitive, such that many key features (i.e, the role of uterine killer cells) are necessarily unique to this tissue. Furthermore, the placenta presents unusual cell types such as fused maternal-fetal cells which differ in genotype from both mother and offspring, generating novel context-specific behaviours that are not readily explicable in terms of context-insensitive modules. I discuss features of placentation that pose problems for evolutionary developmental biology as currently formulated and discuss potential future directions.

13.50 – 15.30 Symposium S24:
Symmetry in plants and animals

K3/K4

Organizers: Sophie Nadot, Catherine Damerval and Vincent Debat
Chairs: Sophie Nadot and Vincent Debat

S24-01 **Symmetry and asymmetry of segmentation**
Fusco, Giuseppe (University of Padova, ITA)

As a morphological feature, segmentation is the occurrence of serially homologous, repeating structures along one body axis of an organism. Depending on the taxon, segmentation can be more or less pervasive (involving more or less anatomical features), can extend over a variable portion of the axis, and the segmental series of different structures can be more or less in register with each other. From the point of view of body geometry, segmentation is a form of symmetry, called translational symmetry. As such it can be exploited for the study of different properties of the developmental system, like developmental stability, through the quantification of random non-heritable deviations from the expected symmetry, or fluctuating asymmetry. However, the elements of a segmental series are in general not expected to be perfectly identical to each other, either because affected by morphological variation at the level of the region that comprises them (e.g., variable body width along the main axis), or because presenting segment-specific morphological features. While for bilateral symmetry, random fluctuations can be relatively easily separated from constitutive left-right asymmetry (directional asymmetry), random fluctuations in translational symmetry can be separated with more difficulty from constitutive morphological variation between the elements of a segmental series (constitutive segmental heteronomy). Far for being just a technical difficulty, the search for a solution to this problem invites to a more profound understanding of segmental patterns, in particular in relation to the developmental processes that generate them. Starting from the results of a recent study on size and shape translational fluctuating asymmetry in a group of multi-segmented arthropods, the geophilomorph centipedes, this nodal questions will be explored in a wider context, showing the necessity of a developmentally-based approach to the study of organism symmetry.

S24-02 **From chiral shells to chiral cells**
Davison, Angus (University of Nottingham, GBR)

While components of the pathway that establishes left-right asymmetry have been identified in diverse animals, from vertebrates to flies, it is striking that the genes involved in the first symmetry-breaking step remain wholly unknown in the most obviously chiral animals, the gastropod snails. Previously, research on snails was used to show that left-right signalling of Nodal, downstream of symmetry-breaking,

may be an ancestral feature of the Bilateria. Now, we have found that variation in a cytoskeletal protein is perfectly associated with symmetry-breaking in the pond snail, creating either right (dextral) or left (sinistral) coiling snails. Contrary to expectations, we discovered asymmetric gene expression in very early (2 cell) snail embryos, preceding morphological asymmetry, and that the same gene has a similar function in frogs. Taken together these results overturn the thinking that diverse species initiate left-right patterning differently, and are instead consistent with the view that animals, from invertebrate snails to vertebrate frogs, may derive their asymmetries from the same intracellular chiral elements.

S24-03 Evolution of floral symmetry in Lamiales

Zhong, Jinshun (University of Vermont, Burlington, USA); Kellogg, Elizabeth A. (Donald Danforth Plant Science Center, Creve Coeur, USA)

Bilaterally symmetrical corollas have evolved independently many times from radially symmetrical ancestors and are thought to increase pollination efficiency and thus promote speciation. However, evolutionary losses of bilateral symmetry have occurred sporadically in different lineages. CYC2 clade and RAD-like are genes needed for the normal development of bilateral symmetry in snapdragon corollas. However, exactly what and how changes in the floral symmetry genes correlate with the origin and loss of floral bilateral remains poorly known. To address this question, a densely sampled phylogeny of CYC2 clade genes across the order Lamiales was inferred and calibrated, and the expression patterns of these genes in early diverging and higher core clades were also examined. We found duplications and losses of CYC2 and RAD-like genes were common, but did not necessarily correlate with a corresponding transition in floral symmetry. The expression patterns of CYC2 clade and RAD-like genes have evolved in a stepwise fashion. CYC2 clade and RAD-like genes were detected broadly in the floral meristem in early diverging Lamiales lineages, but were restricted to adaxial and lateral regions in the core Lamiales. Specifically, CYC2 clade gene is expressed only very early in development in Oleaceae, while prolonged expression of CYC2 clade in corollas originated in the common ancestor of Tetrachondraceae and core Lamiales. CYC2 and RAD-like paralogs showed differential expression, and asymmetrical expression of individual CYC2 and RAD-like genes in adaxial corollas correlated with the independent origins of floral bilateral symmetry in core Lamiales. We also compared three species of core Lamiales with radially symmetrical corollas and found that each reaches radial symmetry in a different way.

S24-04 Characterization of CYCLOIDEA-like genes in Proteaceae, a basal eudicot family with multiple shifts in floral symmetry

Damerval, Catherine (CNRS, Gif/Yvette, FRA); Citerne, Hélène (Université Paris-Sud, FRA); Reyes, Elisabeth (Université Paris-Sud, FRA); le Guilloux, Martine (Université Paris-Sud, FRA); Delannoy, Etienne (CEA, Saint-Paul-

lez-Durance, FRA); Simonnet, Franck (Université Paris-Sud, FRA); Sauquet, Hervé (Université Paris-Sud, FRA); Weston, Peter H. (Royal Botanic Garden, Sydney, AUS); Nadot, Sophie (Université Paris-Sud, FRA)

The basal eudicot family Proteaceae (81 genera, >1700 species) shows considerable variation in floral symmetry but has received relatively little attention in studies of evolutionary development at the genetic level. To provide a framework for understanding the shifts in floral symmetry in Proteaceae, we reconstructed ancestral states of this trait on an updated phylogeny of the family, and characterized homologues of CYCLOIDEA (CYC), a key gene for the control of floral symmetry in both monocots and eudicots. We estimate that zygomorphy has evolved 10 to 18 times independently from actinomorphic ancestors, with at least four reversals to actinomorphy, making Proteaceae a remarkable family in terms of number of transitions in floral symmetry. We find a single duplication of CYC-like genes prior to the diversification of Proteaceae, with putative loss or divergence of the ProtCYC1 paralogue in more than half of the species sampled. ProtCYC genes are expressed in developing flowers of both actinomorphic and zygomorphic Grevillea species, with late asymmetric expression in the perianth of the latter. CYC-like genes therefore appear to be good candidates for playing a role in the establishment of floral symmetry in Grevillea.

16.00 – 17-00

Contributed Session C21: Evolution of gene regulatory networks and the origin of novelties II

STORA SALEN

Chair: M. Ina Arnone

C21-01 Evolution of early acting events in development: Regulation and evolution of complex gene networks

Cridge, Andrew G. (University of Otago, Dunedin, NZL); Permina, Elizabeth (University of Otago, Dunedin, NZL); Dearden, Peter K. (University of Otago, Dunedin, NZL)

Our aim is to understand how conserved genes change their role in the evolution of the insect segmentation network, how the network buffers change, and how that might constrain, or confer diversity of body plan. Antibodies to the early segmentation transcription factors caudal, hunchback and orthodenticle were developed for Drosophila melanogaster, Apis mellifera and Acyrthosiphon pisum. Chromatin Immunoprecipitation (ChIP)-seq was performed on embryonic tissue to identify regions enriched for transcription factor binding. These regions were analyzed to identify unique cis-regulatory motifs (CRMs) and regulated genes. The ChIP-seq study identified multiple CRMs and gene targets for the three transcription factors in each insect species studied. Bioinformatic analysis allowed confident prediction of biologically important CRMs

and transcription factor binding motifs. We identified the conserved core evolutionary genes regulated by each transcription factors in all three insects. We also identified genes that are regulated in only one species. These genes represent mechanisms that buffer changes in the regulation of our key transcription factors but still allow conserved segmentation output. By continuing to study these genes we will learn how genes become co-opted into developmental networks, how such co-opted genes integrate with the rest of the network, and if these genes act to buffer regulatory changes in the transcription factors themselves. This also identifies the level of genetic robustness on which embryonic selection can act. This data has provided us, for the first time, with an understanding of how the targets of key transcription factors change over evolutionary time, effectively a measure of evolutionary change in a complex transcription factor network.

C21-02 Convergent cis-regulatory modification leads to the evolution of mimetic wing patterns in Heliconius butterflies

Hanly, Joe (University of Cambridge, GBR); Supple, Megan (Smithsonian Tropical Research Institute, PAN); Jiggins, Chris (University of Cambridge, GBR)

Heliconius butterflies display one of the most striking and extensive examples of pattern mimicry in nature, in combination with geographical wing pattern variation within species. Red wing pattern elements are controlled by the Transcription Factor optix, which acts as a switch gene. All variation in red pattern elements can be explained by regulatory modifications to the expression domain of optix, in both H. melpomene and the co-mimietic species H. erato, though the common ancestor of these species did not share these mimetic patterns, meaning each red pattern element has evolved at least twice within this radiation. Recent work by Wallbank et al (2016) has established that wing patterns in H. melpomene are linked to discrete cis-regulatory modules of optix. Here, we used population-level variation to identify additional modules in the species H. melpomene, and illustrated that mimetic pattern elements in H. erato are similarly modular. These regulatory modules are contained within a co-linear regulatory region which is deeply conserved throughout the Lepidoptera. The pattern elements have evolved in the same order in both species. In the case of the dennis module, novel regulatory function has been gained in neighboring conserved sequence implying its origin lies in a conserved ancestral set of regulatory modules, whereas the other pattern elements have evolved independently in non-homologous regions of conserved sequence. Thus, this highly accurate case of convergent evolution has occurred by modification to ancestrally conserved non-coding hotspot loci.

C21-03 Uncovering the development of a novel abdominal structure in Black Scavenger Flies

Rajaratnam, Gowri (National University of Singapore, SGP); Su, Kathy (National University of Singapore, SGP)

Sternites are sclerotized plates located on the ventral abdominal segments in adult insects. For most insects, the proximal abdominal regions have sternites that are flat, simple structures. However, in a group of black scavenger flies (Sepsidae: Diptera), males of certain species have modified their 4th abdominal sternite into a remarkable appendage-like brush. These spectacular brushes are used to stimulate the females during courtship and vary in shape and size across species. We trace the evolution of this sternite appendage, with a phylogenetic reconstruction from 141 species, and find this structure most likely evolved independently in Themira and Perochaeta. Using a CRISPR/Cas9 system, we attempt to unravel the gene regulatory network involved in building these elaborate 4th sternite brushes in Themira and Perochaeta. We target two genes, doublesex and Distal-less, both of which are known to be expressed in the developing sternite. From this experiment, we noticed that both doublesex and Distal-less appear to play an important role in not just sexually dimorphic sternites but in monomorphic sternite formation in sepsids.

C21-04 Global analysis of dorsoventral patterning in the wasp Nasonia reveals extensive incorporation of novelty in a regulatory network

Pers, Daniel (University of Illinois at Chicago, USA)

Gene regulatory networks are vital for developmental processes (patterning/morphogenesis). Modifications to theses networks allow for the emergence of novel developmental outputs, thus exploring how GRNs vary across phylogenies can provide insight on the evolution of development. The dorsoventral GRN that patterns the Drosophila embryo is one of the most well characterized GRNs; however, evidence shows that it is not representative of all insects. We have shown that prior to gastrulation, Nasonia has identical expression of tissue specific marker genes. However, pattern generation is quite divergent. To understand this evolutionary variation, we set out to characterize Nasonia with enough depth and resolution to conduct a meaningful comparative GRN analysis. RNAi-RNAseq was used to identify 110 genes with significant differential expression patterns along the DV axis. Comparison to patterns of Drosophila orthologs uncovered a small set of genes with conserved expression. However, the majority of the DV expressed genes uncovered are unique to Nasonia. This includes conserved fly genes with new patterns in Nasonia, genes lacking orthologs in the fly, and genes potentially derived from horizontal gene transfer events. We will dissect the functions of these genes using RNAi and CRISPR, in conjunction with live imaging. However, to get a fuller picture of the evolution of this GRN, chalcid wasp diversity will be sampled. Melittobia, a closely related wasp, and Trichogramma, a basally branching Chalcid lineage, have

sequenced genomes and well-annotated transcriptomes are in preparation. By developing molecular tools within these wasps we aim to create a powerful, highly informative model system to analyze the evolutionary history of novelty in DV patterning.

16.00 – 17.00

Contributed Session C22: The vertebrate limb as an evolving dynamical system

SAL B

Chair: Stuart A. Newman

C22-01 Regeneration and preaxial polarity in limb development in tetrapod evolution

Fröbisch, Nadia B. (Museum für Naturkunde, Berlin, DEU); Bickelmann, Constanze (Museum für Naturkunde, Berlin, DEU); Olori, Jennifer (SUNY Oswego, USA); Witzmann, Florian (Museum für Naturkunde, Berlin, DEU)

Salamanders are unique among four limbed vertebrates in showing a reversed, preaxial patterning of skeletal limb elements. Moreover, they have the highest capacity of regeneration among tetrapods, including full limb regeneration. A large body of data shows that limb development is a highly conservative process and thus the deviation from this pattern in salamanders is surprising and classically considered derived for urodeles. However, it remained unknown when in the evolutionary history of tetrapods preaxial polarity evolved and whether it is evolutionarily and mechanistically linked to the capacity of regenerating the limbs. The fossil record shows that preaxial polarity in limb development was not only present in the derived temnospondyl dissorophoid Apateon, but also in the coeval basalmost dissorophoid Micromelerpeton as well as a more distant relative, the stereospondylomorph Sclerocephalus. In addition limb regeneration was also present in Micromelerpeton, as documented by a pattern of abnormalities distinctive for irregular regeneration. Furthermore, lepospondyl fossils from the amniote stem lineage indicate that limb regeneration may also have been possible in „microsaurs"in addition to tail regeneration. The latter clearly took place via a re-patterning of caudal vertebral segments, which differs from lizard tail regeneration and is otherwise only seen in salamanders among extant tetrapods. However, contrary to temnospondyls, the lepospondyl microsaurs likely had postaxial polarity in limb ossification as the majority of modern tetrapods. These new data from the fossil record indicate that the seemingly unique way of patterning limbs in salamanders was actually more wide spread among tetrapods and evolved independently of the capacity to regenerate limbs. The occurrence of salamander-like regeneration in the temnospondyl and lepospondyl lineage as well as in modern lungfish suggests that these high regenerative capacities are likely plesiomorphic for tetrapods or even sarcopterygians and were only retained in salamanders among extant tetrapods.

C22-02 **Preaxial polarity in limb development - a comparison of larval and direct developing salamanders (Caudata) to other tetrapods**

Triepel, Sandra (Museum für Naturkunde, Berlin, DEU); Müller, Hendrik (Friedrich-Schiller-Universität Jena, DEU); Mitgutsch, Christian (Museum für Naturkunde, Berlin, DEU); Fröbisch, Nadia B. (Museum für Naturkunde, Berlin, DEU)

For decades, limb development has been used as a model to study patterning mechanisms during embryogenesis. It has been shown that it is highly conserved in amniotes and frogs in many aspects, including overall patterns of gene expression as well as of skeletal condensation. Digital cartilages condensate in a sequence of IV-V-III-II-I inside of a preformed paddle - a pattern called „postaxial polarity". However, salamanders are the only extant tetrapod clade showing an aberrant pattern. Their digital cartilages condensate in a reversed sequence of II-I-III-IV-V, a pattern called â€œpreaxial polarityâ€ . Furthermore, a striking interspecific diversity can be seen in the ontogenetic timing of limb and digit development. Most salamanders with free-swimming larvae, e.g. the Mexican axolotl, bud their digits one by one. In contrast, the direct developing plethodontid salamander Desmognathus aeneus has a paddle stage during limb development comparable to other tetrapods. Limb development in amniotes is well understood. The paddle allows expressed genes to diffuse and to establish gradients across the limb bud. These gradients create positional information and regulate the polarity of the developing limb. Nevertheless, although some classic limb developmental genes have been investigated in early limb bud stages of axolotls, it remains unclear how the positional information and preaxial polarity are established in salamanders. Moreover, limb development in D. aeneus has only been described morphologically, but gene expression has not been investigated. We morphologically described limb development of four more plethodontid salamander species. All of them have a paddle stage during limb development regardless of their developmental strategy (larval or direct development). Additionally, we compared gene expression patterns during limb development in the axolotl to expression patterns in plethodontid salamanders. The data reveal obvious differences to other tetrapods and provide new insights into mechanisms underlying preaxial polarity in salamander limb development.

C22-03 **Migrating muscle precursors contribute to the formation of appendicular muscles of cartilaginous fishes**

Tanaka, Mikiko (Tokyo Institute of Technology, JPN); Okamoto, Eri (Tokyo Institute of Technology, JPN); Kusakabe, Rie (RIKEN, Kobe, JPN); Kuraku , Shigehiro (RIKEN, Kobe, JPN); Hyodo, Susumu (University of Tokyo, JPN); Onimaru, Koh (Tokyo Institute of Technology, JPN); Kuratani, Shigeru (RIKEN, Kobe, JPN)

In amniotes, muscle precursors in head and limbs are delaminated from

ventral aspect of dermomyotome before migration, whereas interlimb abdominal muscles are derived from direct extension from the dermomyotome. Such a mechanism to form muscles by direct somatic extension has been recognized for fin muscle formation in cartilaginous catshark, and thus this system was regarded as representing a primitive state to form appendicular muscles. Curiously, however, muscle precursors that migrate to give rise to hypobranchial muscles have been recognized during embryogenesis of agnathan lampreys. To solve this apparent discrepancy, here we re-examine the behavior of muscle precursors in catshark Scyliohinus canicula embryos, and show that the population of myoblasts separate from the ventral edge of dermomyotome and migrate to contribute to hypobranchial and fin muscles. Lbx1, involved in the genetic control of limb myoblast migration, are expressed in the population of muscle precursors separated from dermomyotomes. Transcripts of Pax3 and Myod, which play important roles in muscle differentiation, are also detected in the Lbx1-positive myoblasts. Furthermore, in the ventral edge of dermomyotome at the pectoral fin bud level, as well as in the myoblasts heading toward pectoral fin buds, the epithelial signatures are lost and basal memebrane is disrupted. We conclude that migratory muscle precursors has contributed to the fin muscle prior to the divergence of Chondrichthyes and other vertebrates.

C22-04 Longshanks mice as a tool to study the cell and molecular determinants of limb length variation within populations

Marchini, Marta (University of Calgary, CAN); Rolian, Campbell (University of Calgary, CAN)

The main processes of vertebrate limb outgrowth and patterning are relatively well documented. However, the genetic and development mechanisms that produce continuous selectable variation in limb bone length within populations are still unclear, primarily due to low sample variance and low analytical resolution issues in continuously distributed traits within natural populations. Artificial selection in a controlled environment can increase phenotypic variation, bypassing these issues. We have selectively bred two independent lines of mice for increased tibia length relative to body mass (a.k.a. the Longshanks mice). At generation F16, Longshanks mice had ~8% longer tibiae at 14 days postnatal, compared to random-bred Control from the same genetic background (CD1), and ~15% longer than Control at eight weeks. Endochondral ossification at the growth plates plays a key role in tibial elongation across postnatal development. Growth plates are comprised of three main zones: resting, proliferative and hypertrophic, each representing a distinct stage of the chondrocyte life cycle, controlled by many genetic pathways. We performed histomorphometric and gene expression analyses on the proximal tibial growth plate to define the cell and molecular processes involved in generating bone length variation. Histomorphometry and cell prolife-

ration assays show an expanded proliferative zone with more cells in both Longshanks lines compared to Control, but no differences in the height and cellularity of the hypertrophic zone, or in the size of terminal hypertrophic chondrocytes. Programmed cell death of the hypertrophic chondrocytes is likely accelerated in Longshanks. High throughput transcriptomic analyses show upregulation of several genes involved in chondrocyte proliferation, including Ifi202, epiphycan, aggrecan, and cartonectin, as well as hypertrophy, such as Runx2, Ptgs2, and Col10, but also cell death markers, such as Fas. These results give insight into the cell- and tissue-level processes that produce selectable limb length variation in mammals.

16.00 – 17.00

Contributed Session C23: Developmental evolution and reproductive medicine

SAL C

Chair: Peter Holland

C23-01

Light-induced oocyte maturation in the hydrozoan Clytia hemisphaerica

Quiroga Artigas, Gonzalo (Sorbonne Université, Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA)

To ensure succesful fertilisation and thus species survival, oocyte maturation and gamete release in all animals is controlled precisely by hormonal or environmental cues. One common regulatory feature is the emission of maturation-inducing hormones (MIHs) by somatic cells of the gonad to trigger meiotic resumption in the resting ovarian oocytes, howeverm the molcular identity of MIH is known only very few species. Hydrozoan jellyfish provide excellent models for studying this process because MIH is released directly from gonad somatic tissue following daily dark/light transitions. As members of the early-branching phylum Cnidaria, hydrozoans can also give insight into spawning regulation in early animal ancestors. We are studying the regulation of oocyte meiotic maturation and spawning in the hydrozoan jellyfish Clytia hemisphaerica, an emerging model species. Fully grown, prophase I arrested, oocytes in Clytia gonads resume meiosis when they are stimulated by a diffusible MIH, released from the gonad ectodermal tissue immediately following a light cue. Clytia gonads separated from the jellyfish continue to spawn every day, implying that all the machinery reuqired for regulating this crucial biological process is present in the gonads themselves. In collaboration with N. Takeda (Asamushi Research Center for Marine Biology) and R. Deguchi (Miyagi University of Education, Sendai), we have identified Clytia endogenous MIH as several structually-similar amidated neuropeptides, synthesized by cleaveage of two distinct peptide precursors. We have characterized the neuropeptide-secreting cells at the base of the gonad ectodermal cells by in situ hybridization and immunofluerescense analyses.

C23-02 Molecular evolution of the totipotent mammalian embryo

Holland, Peter (University of Oxford, GBR); Dunwell, Thomas (University of Oxford, GBR); Maeso, Ignacio (University of Oxford, GBR; CABD, Seville, ESP); Wyatt, Chris (CRG, Barcelona, ESP); Marletaz, Ferdinand (University of Oxford, GBR; OIST, JPN); Irimia, Manuel (CRG, Barcelona, ESP)

Many genes encoding transcription factors are highly conserved across the animal kingdom but there are exceptions. In particular, there are cases where gene duplication followed by asymmetric divergence generates a „new"gene. These cases provide rare opportunities to examine how new transcription factors get recruited for new developmental roles. We have been studying a group of genes that arose in mammalian evolution and are uniquely expressed at preimplantation developmental stages. These genes show variation between mammalian species, with primates and rodents being especially different. Such differences have implications for model systems approaches to developmental biology. Our comparative genomic analyses and functional studies are revealing the evolutionary origin and developmental roles of new mammalian genes.

C23-03 Cavefish evolution as a natural model for metabolic diseases

Rohner, Nicolas (Stowers Institute for Medical Research, Kansas City, USA); Aspiras, Ariel (Harvard Medical School, USA); Tabin, Cliff (Harvard Medical School, USA)

„Understanding the genetic basis of adaptation has broad implications not only for a basic understanding of evolution, but also for human pathologies given that many human diseases are a consequence of mis-adaptation to modern societies. The emerging model system Astyanax mexicanus has become an important fish species to address adaptation to extreme environments due to its unique ecology and the availability of genetic tools and genomic resources. Cave environments are typically dark and as a consequence nutrient deprived. We have previously shown that cavefish acquired impressive adaptations such as hyperphagia (increased appetite), starvation resistance and altered feeding behaviors to cope with these conditions. Here, we have focused on the fatty livers and symptoms reminiscent of diabetes these fish develop. Interestingly, we detected only very low insulin levels in cavefish (compared to surface fish) partially due to lower numbers of beta-insulin producing cells in the pancreas. In addition, cavefish display strong insulin resistance when administered with ectopic insulin. Despite the consequential elevated and highly fluctuating blood glucose levels, cavefish live long and healthy lives, probing the question whether they have acquired mechanisms allowing them to cope with extreme nutritional levels. Taking advantage of the newly available genome of Astyanax mexicanus, we identified mutations in the insulin receptor of cavefish most likely responsible for the observed insulin resistant phenotype. Importantly, the same mutations were found in cases of Type-II diabetic patients in human populations.

Our findings in independently derived cavefish populations suggest that cavefish are inherently insulin resistant, potentially as an additional strategy to acquire better starvation resistance. We are currently using genome editing to functionally test these and other candidate mutations in zebrafish and cavefish itself to study in detail the molecular mechanisms underlying the adaptation of cavefish to the extreme and nutrient poor environments."

C23-04 **Can human cranial developmental malformations be a model for evolutionary change?**

Rasskin-Gutman, Diego (University of Valencia, ESP); Esteve-Altava, Borja (The Royal Veterinary College, London, GBR); Sanchís García, Juan Manuel; (University of Valencia, ESP)

During the evolution of tetrapods, skull bone number has diminished drastically, from around 60 bones in early forms to about 30, or even less in humans and birds. Every major tetrapod lineage shows this number reduction trend, a generalization of Williston's Law first seen in his seminal work on reptiles. For this reduction in bone number to occur at an evolutionary scale, at least one of these two morphogenetic mechanisms must take place: loss or fusion of ancestral bones. The number of ossification centers also suffers a drastic reduction from 80 to about 20 during the development and growth of the human skull, which raises the possibility of using this as a model of change that might be extrapolated at evolutionary scales. This is especially so because cranial malformations occur often as a result of skull bone sutures early fusions, and the relationship between early suture fusion and shape changes in both synostotic and non-synostotic bones has been extensively studied. These conditions, known as craniosynostosis, manifest as drastic changes in the shape of particular bones, and can be lethal if not treated surgically. Putting these two observations together, the question we are asking is: can evolutionary shape change in cranial features be explained, and at which extent, by the pattern of bone sutures? In other words, we would like to explore the possibility that shape changes in the different tetrapod lineages could be developmentally explained by the morphogenetic processes by which ossification centers are lost or fused together to form single bones.

16.00 – 17.00 Contributed Session C24:
Micro-evo-devo – integrating evolution, development and population genetics

K3/K4

Chairs: Luke Hayden and Peter Dearden

C24-01 **Winding paths in development: the link between developmental and morphological variation in mouse molar teeth**

Hayden, Luke (LBMC, ENS de Lyon, FRA); Rubod, Alain (LBMC, ENS de

Lyon, FRA); Sémon, Marie (LBMC, ENS de Lyon, FRA); Pantalacci, Sophie (LBMC, ENS de Lyon, FRA)

The link between morphology and the developmental systems that give rise to it is a central issue in evolutionary developmental biology. Morphological variation must arise from changes in the developmental system, but how exactly does development change? How does developmental variation correspond to morphological variation? These questions are rarely addressed at the intraspecific level. We study the comparative tooth development of several mouse strains with slightly variable morphologies, focusing on elongation of the first molar. We hypothesize that tooth elongation is linked to increased persistence of the vestigial signaling centres corresponding to the premolar teeth, which are absent in mice. Using Shh expression as a marker, and with an extensive developmental sampling strategy, we have devised a quantitative approach to examine small-scale developmental variation. Our detailed and quantitative measurement of developmental variation has allowed us to build a matrix of developmental state and to infer the routes taken through developmental space by different strains and to examine the variation within each strain. Our methods have revealed considerable developmental variability in this system. In fact, inter-strain differences in tooth development are much greater than the relatively modest morphological variation would predict. The developmental differences between strains can be conceptualised as the two strains following different trajectories through developmental space. Examining intra-strain variability, we find that developmental variation is higher in the more morphologically variable strain. In contrast to the common assumption that developmental variation increases over time, an early peak in developmental variability is present. This period of developmental variability is under investigation via morphological and transcriptomic methods. The variable nature of this developmental system may create an underlying instability which guides evolutionary processes towards the repeated convergent evolution of the same elongated tooth phenoty

C24-02 Evolutionary novelty in a butterfly wing pattern through enhancer shuffling

Wallbank, Richard (University of Cambridge, GBR)

The modular diversification of cis-regulatory elements has been proposed as a mechanism that generates morphological novelty whilst circumventing deleterious pleiotropic effects. By subdividing a gene's regulation, novel enhancers can arise that encode new expression domains without interfering with existing patterns. Using population genetics we have identified two such cis-regulatory modules that program distinct components of wing colour pattern in the butterfly Heliconius. In the wild these patterns together constitute a universal warning signal

against predation and are part of an extensive multi-species Mullerian mimicry ring. Remarkably, although now in close proximity, the modules appear to have completely separate ancestry from one another and evolved independently in two different species. Only later did they combine to drive patterning of the same wing through a putative introgression exchange. The sequential evolution of this complex phenotype was therefore facilitated by the subfunctionalisation of discrete cis-regulatory modules. Population genetics has helped refine these modules to just a few kilobases and also revealed potential functional hotspots of clustered pattern-associated SNPs. Combining these data with transcription factor binding site predictions has made it possible to identify a number of candidate interacting factors, whose own expression patterns are now being examined. This work has now led to ongoing functional validation experiments, such as CRISPR genome editing, to explore the mechanics and evolution of these wing patterning enhancers in vivo.

C24-03 Origin and evolution of phenotypic plasticity in eyespot size across nymphalid butterflies

Bhardwaj, Shivam (National University of Singapore, SGP); Monteiro, Antónia (National University of Singapore; Yale-NUS College, SGP)

Phenotypic plasticity is the ability of an organism to change its phenotype in response to environmental cues. This property is often an evolved adaptation, allowing each phenotype to have a higher fitness in the environment that induced it. The origins of such adaptations, however, remain poorly understood. Here we detail the mechanism underlying eyespot size plasticity in response to rearing temperature in one species of nymphalid butterfly, Bicyclus anynana. Then we investigate how the plastic response to temperature, as well as each of the required components of the plastic response, evolved across nymphalid butterflies. Our results indicate that temperature-induced changes in titers of 20-hydroxyecdysone (20E) hormone at specific stages of development, together with localization of the 20E receptor in eyespot central cells, mediate eyespot size plasticity in B. anynana. The comparative study indicated that the pattern of response to rearing temperature identified in B. anynana is novel and derived. Mapping plastic response patterns on a butterfly phylogeny, revealed that reductions of eyespot size in response to increasing temperature is an ancestral response, whereas increases in eyespot size in response to temperature is a novel derived response. The origin of the novel plastic response, as well as origin of its required components, such as hormone titer differences and receptor localization, are currently being mapped on the same phylogeny. With this case study, we hope to clarify the evolution of adaptive phenotypic plasticity at the molecular level.

C24-04 The genetic and developmental bases of genital evolution between Drosophila species

Mendes, Claudia C. (Oxford Brookes University, GBR); Hagen, Joanna F. (Oxford Brookes University, GBR); Tanaka, Kentaro M. (Tokyo Metropolitan University, JPN); Gaspar, Pedro M. (Oxford Brookes University, GBR); Herbet, Mathew R. (Oxford Brookes University, GBR); Nunes, Maria D. S. (Oxford Brookes University, GBR); McGregor, Alistair P. (Oxford Brookes University, GBR)

External male genitalia can exhibit remarkable diversity to the extent that even closely related Drosophila species show drastically different genitalia. However, the developmental and genetic bases and the evolutionary forces underlying such variation are not well understood. In this study, we focused on two recently diverged species of the D. simulans clade, D. mauritiana and D. simulans. These two species show considerable differences in the morphology of the claspers and the posterior lobes; external genital structures which have been shown to play an important role during mating and coupling. Using high resolution introgression mapping in D. mauritiana and D. simulans together with an RNAi screen in D. melanogaster, we identified several positional and developmental candidate genes involved in male genitalia development, including Grunge (Gug) and male-specific lethal 3 (msl-3). While Gug, the sole Drosophila homolog of human Atrophins, may largely contribute to the differences in clasper size between D. mauritiana and D. simulans, msl-3, which is involved in chromatin modification, might underlie posterior lobe interspecific variation. We are currently testing these hypotheses by performing genome-editing experiments using CRISPR/Cas9 in reciprocal hemizygotes. As a complementary approach, we are using the powerful genetic toolkit in D. melanogaster to further investigate the novel role of these genes in male genitalia development. This study will provide new insights into the natural genetic variation underlying a rapid evolving morphological trait and serve as a platform to further elucidate the evolutionary processes contributing to speciation.

17.05 – 17.15
STORA SALEN

Student Poster Prizes

17.15 – 17.55
STORA SALEN

Keynote Lecture (K4)

Dear ants, what have you done for Evo-devo?

Ehab Ebouheif
(McGIll University, CAN)
Chair: Frietson Galis

Ants show a remarkable diversity in size and allometry both within and between species, so much so that Darwin considered ants a ˜climax of

the difficulty" for his theory of natural selection. For example, in colonies of the marauder ant Pheidolgeton diversus, the smallest worker stands on the head of the largest worker. The developmental mechanisms producing these extreme differences in growth, size, and allometry between workers and how this extreme variation evolved between ant species are questions that have remained largely unknown for over 150 years, puzzling some of the most notable biologists since Darwin, including Sir Julien Huxley, EO Wilson, and others. Over the last 20 years, my lab has made considerable progress in understanding this mystery by uncovering developmental and epigenetic mechanisms that work together to regulate growth, size, and allometry in ants. These mechanisms may be general features of both development and evolution of complex biological systems.

17.55 – 18.00 Conference Closing
STORA SALEN

18.10 – 19.00 EED Business Meeting
STORA SALEN

19.30 Conference Dinner (Castle, see map) - music from 19.15

Notes

Posters

P-001 Investigating the potential regulation of gap gene homologues by pair-rule genes in the red flour beetle Tribolium castaneum

Sharma, Rahul (University of Leeds, GBR); Peel, Andrew D. (University of Leeds, GBR)

A regulatory cascade of maternal determinants, gap genes, pair-rule genes, and segment polarity genes is critical for segment formation in Drosophila melanogaster. Unlike ancestral arthropods and vertebrates, all trunk segments are formed simultaneously in Drosophila. This has led researchers to study segmentation in those arthropods that have retained a more ancestral mode of segmentation, such as the beetle Tribolium castaneum, where trunk segments are added sequentially. A segmentation clock, reminiscent of that operating in vertebrates, has recently been identified in Tribolium, with the cyclic expression of pair-rule genes (even-skipped and odd-skipped) critical for sequential segment formation. In other studies on Tribolium, the functional knockdown of gap gene homologues (e.g. Tc-giant and Tc-Krüppel) does not result in canonical gap phenotypes, like those seen in Drosophila, but rather homeotic transformations and posterior germband truncations. We are studying the regulatory interactions between gap genes and pair-rule genes in Tribolium. Strikingly, a classic pair-rule phenotype was observed in Tc-odd-RNAi embryos, which contradicts published data where Tc-odd-RNAi embryos were mainly asegmental. This could be explained by a weaker knockdown of Tc-odd, suggested by our expression data, or a strain specific phenotype. Nevertheless, this reproducible phenotype has allowed us to study the regulation of gap gene homologues by a pair-rule gene, which is not possible in asegmental embryos. Only one instead of two stripes of Tc-giant expression are present in Tc-odd-RNAi embryos; either the T3 and A2 stripes are fused, or the T3 stripe is missing. A change in the expression level of Tc-knirps and Tc-Krüppel between WT and Tc-odd-RNAi embryos is also apparent, but with open interpretations. In summary, a regulatory input by the pair-rule gene Tc-odd might be critical for Tc-giant stripe formation. We are currently employing CRISPR/Cas9 technology to better understand the regulatory relationship between pair-rule genes and gap gene homologues in Tribolium.

P-002 Ediacaran developmental biology

Dunn, Frankie (University of Bristol, GBR)

The Ediacaran Period (635–541 Ma) records some of the earliest fossils of complex macroscopic organisms. Some of these fossils have been rationalised as members of early animal groups. However, since many Ediacaran organisms cannot be easily reconciled morphologically with modern metazoan clades, multiple alternative interpretations have been proposed, including algae, fungi, and foraminifera. The resolution of their biological affinities is important because they may inform the evolution of metazoan axis specification, symmetry making and breaking, and the appearance of a segmented body plan. In an attempt to reconcile among competing phylogenetic interpretations of the Ediacaran biota, we have adopted a developmental approach. The few existing developmental analyses of Ediacaran macro-organisms unintentionally conflate developmental pattern with developmental process. We compare growth patterns across populations of three iconic Ediacaran groups - the rangeomorphs, erniettomorphs and dickinsoniomorphs - revealing hitherto unrecognised ontogenetic characters, relating to the development of modularity and directionality of growth. By then considering morphogenetic process in these taxa, we tentatively reassess the phylogenetic position of the Ediacaran macro-organisms. Our findings refute several non-metazoan hypotheses, but reveal developmental features consistent with a metazoan affinity for these taxa. This work affirms the potential of developmental techniques for study of enigmatic fossil groups.

P-003 Finite element analysis of abdominal appendage development in the sepsid Themira biloba

Peterson, Tim (University of Vienna); Müller, Gerd B. (University of Vienna, AUT); Bowsher, Julia (North Dakota State University, USA)

Male flies in the family Sepsidae possess jointed appendages on the fourth abdominal segment. These abdominal appendages are not homologous to other insect appendages, and are an emerging model for the investigation of morphological novelty and innovation. However, the development of the appendages during metamorphosis has remained largely uncharacterized. This study describes the development of the abdominal appendages in the sepsid Themira biloba from the end of the last larval instar through eclosion, along with the morphology and capabilities of the structure in the adult fly. The abdominal appendages appear soon after pupation, before the adult epidermis has fused. The large bristles of the abdominal appendage develop early compared to the other, smaller, bristles of the abdomen. The functional range of motion for the large bristles in adult flies is described using finite element models. This movement is constrained by compressive stress on the medial edge of the abdominal lobe cuticle.

P-004 Analysis of Wnt genes and their embryonic expression patterns in the priapulid worm Priapulus caudatus

Hogvall, Mattias (Uppsala University, SWE); Budd, Graham E. (Uppsala University, SWE); Janssen, Ralf (Uppsala University, SWE)

Priapulids represent a group of basally branching ecdysozoans with an unsegmented body that may resemble the ecdysozoan ancestor to some extent (Budd 2001). This makes priapulid worms interesting model organisms for the investigation of ecdysozoan evolution. Wnt genes evolved very early during metazoan evolution and it has been shown that they play important roles in development. One such role is their assumed function in panarthopod segmentation. In onychophorans, for example, several Wnt genes are expressed in segment polarity gene-like fashion (Hogvall et al. 2014). We analysed the embryonic expression patterns for several Wnt genes, by whole mount in situ hybridization in Priapulus caudatus. Generally, the investigated Wnt genes are expressed in the posterior part of the embryo, a region associated with the blastopore (Martín-Durán et al. 2012). However, the expression patterns of the Wnt genes differ, suggesting that they may play a combined role in the development of the posterior part of the embryo. None of the genes is expressed at the border between the introvert and the main body, suggesting that they are not involved in the formation of this morphological border. This suggests that the Wnt genes in priapulids are not involved in border formation as in the panarthopods.

References:

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Martín-Durán, JM, Janssen R, Wennberg S, Budd GE, Hejnol A. 2012. Deuterostomic development in the protostome Priapulus caudatus. Curr Biol. 20;22(22):2161-6

P-005 A potential decapod shrimp model for getting insights into crustacean aquaculture and evolution

Chan, Ting-Fung (Chinese University of Hong Kong, CHN); Chu, Ka-Hou (Chinese University of Hong Kong, CHN); Hui, Ho-Lam; (Chinese University of Hong Kong, CHN)

The Crustacea form the largest subphylum of arthropods after the subphylum Insecta, and includes ecologically and environmentally important classes such as the Malacostraca, including decapods, isopods, amphipods, and stomatopods. The transparent cuticle of the cherry shrimp

Neocaridina denticulata provides for direct assessment of reproductive status, stage of molt, and tissue-specific expression of reporter genes, and facilitates screening of mutations affecting phenotype. We are now sequencing the genome of this potential new freshwater shrimp model, which will provide a better understanding of how the crustacean genome evolved, and will be useful for a wide range of further developmental and genetic research to improve crustacean aquaculture.

P-006 Chemically perturbed axis formation: Can experimental phenotype data help in understanding the interconnectivity of laterality establishing processes ?

Petrasko, Anne (University of Vienna, AUT)

To gain further insight into the involvement of various mechanisms that participate in the establishment of axis formation and laterality in Zebrafish, we analyzed chemically induced wavy notochord phenotypes. The connection between Retinoid metabolism and signaling that is tightly linked with the Sonic hedgehog, Nodal and FGF pathways, signals that are regulated via the MAPKinase pathway, the role of available ion levels and several key factors needed for cell adhesion and cell migration properties of tissues and forming organs, provided the theoretical frame under which chemically induced phenotypic changes were analyzed. The integration of similar phenotypes into a model that wants to refine/define/understand the multimodality and interconnectivity of pathways that lead to the same morphological outcome via different mechanisms was one major goal of this study.

P-007 Prenatal androgen exposure: Effects on human facial shape and its perception

Schaefer, Katrin (University of Vienna, AUT); Windhager, Sonja (University of Vienna, AUT); Müller, Gerd B. (University of Vienna, AUT); Mitteroecker; Philipp (University of Vienna, AUT)

The second-to-fourth digit ratio (2D:4D) is a bio-marker for prenatal testosterone exposure. 2D:4D ratios are sexually dimorphic, with men generally having lower ratios (longer index fingers) than women, suggesting greater early testosterone exposure. Human 2D:4D ratios and facial shape are covered independently in a rapidly increasing number of research studies. This might reflect their association with multiple other traits, ranging from sex and gender to physical qualities, appearance, and behavior. In adult men, aspects of facial shape that covary with perceived masculinity and dominance are aligned with those that covary with high prenatal testosterone. In order to explore the onset of this phenomenon, we collected data from 20 pre-pubertal boys from upper Austria. Facial shape correlates were assessed by Geometric Morphometrics using shape regressions (14.5% var. explained, $p < 0.05$ after 10,000

permutations). The corresponding shape patterns were visualized with thin-plate spline deformation grids, as well as image unwarping and image averaging: lower digit ratios corresponded to a relatively shorter forehead, smaller eyes, thinner lips, and a much more prominent lower jaw. The same boys were also perceived as more masculine and less cute (r = â€“0.525, p = 0.015). Thus, facial masculinity associated with low 2D:4D can be observed years before puberty already. It remains to be resolved in how far variation in prenatal androgen exposure might reflect maternal preparation for different life history strategies, depending on environmental context and social status.

P-008 Insights into changes in regulation of gastrulation during evolution

Machačová, Simona (Institute of Molecular Genetics of the ASCR, v.v.i., Prague, CZE)

Gastrulation is controlled by complex genetic program, which evolve through animal history. BMP signaling controls formation of dorso-ventral (DV) body axis in all Bilaterians. The core model of regulation comprises protein Chordin, what locally binds to BMPs and thus prevents interaction of BMPs with BMP receptor. However, broader signaling regulators differ greatly among various animal groups and therefore even their functional binding sites may differ. The position of Chordin expression is very specific and lies near to the primary mouth opening of gastrula, which correlates with position of organizer. Therefore, the expression of Chordin is relatively dependable for marking area of the organizer of gastrulation. Consequently, manipulation of Chordin clearly shows the organizer patterning. Our research focuses on similarities and differences of Chordin regulation among selected model organisms (zebrafish, amphioxus and starlet sea anemone). The presented poster focuses on using transgenic experiments in order to reveal general features of the core regulation system. The poster also emphasizes chemical manipulation of major developmental signalling pathways and their possible influence on DV patterning of the body. The evolutionary and molecular developmental perspectives are discussed."

P-009 History and philosophy of biology and the Extended Evolutionary Synthesis: theoretical and historiographical perspectives from Latin America

Fàbregas-Tejeda, Alejandro (Universidad Nacional Autónoma de México, MEX); Casanueva, Mario (Universidad Autónoma Metropolitana- Cuajimalpa, MEX); Vergara-Silva, Francisco (Universidad Nacional Autónoma de México, MEX)

We briefly examine the historical background of two traditions of academic research, namely developmental biology and evolutionary biology,

in Latin America from the reception of Darwinism in 19th century to the advent of the molecularized stage of evolutionary developmental biology (Evo-Devo). We then focus on local histories of Evo-Devo and philosophy of biology in Latin America (e.g. theoretical and conceptual contributions to the ongoing debate regarding the definition and scope of developmental constraints) and further explore the place of Evo-Devo in the Extended Evolutionary Synthesis comparing two contrasting views: (i) there is a single evolutionary theory in the 21st century bequeathed by the sustained efforts of multiple scientists, whose conceptual contributions can be, in principle, aligned with unbroken historical continuity; and (ii) diverse evolutionary theories (e.g. Niche Construction Theory, Evolution in 4 Dimensions, Evo-Devo, Modern Synthesis) coexist and interact in a complex network of conceptual relations. We argue that philosophical approaches, conjointly to the purpose of gaining understanding of the structure of Evo-Devo as a discipline, can bring valuable theoretical and conceptual advancements and, furthermore, guidance to empirical investigations (i.e. by dissolving pseudo-problems, epistemological misunderstandings and false antinomies). We conclude asking: what could a „philo-evo-devo" Latin American view offer for international philosophy of biology and evolutionary developmental biology? Possible answers are formulated using historiographic frameworks that analyze the history and modern place of Latin American science: these conceptualize science as a global and international endeavor (with contingent and continually contested and renegotiated centers and peripheries, or more adequately, as a polycentric network of knowledge co-production), without neglecting the importance of local contexts in the configurations of individual research fields.

P-010 Causality in complex archaeo-societies and the extended evolutionary synthesis: an example from the Archaic and Preclassic periods in the Tehuacán Valley (Mesoamerica)

Vergara-Silva, Francisco (Universidad Nacional Autónoma de México, MEX)

Analytical resources provided by niche construction theory (NCT) and eco-evo-devo (EED) can be applied to case studies of the evolution of past complex societies, traditionally approached from both processual and post-processual archaeological perspectives. Currently, NCT and EED are being incorporated into the inclusive framework of the extended evolutionary synthesis (EES). I have previously (Euro Evo Devo Vienna, 2014) argued in favor of using culture-oriented NCT- and EED-derived models of causality for the analysis of a well-documented case study in the archaeology of Mesoamerica: biocultural evolution in the Zapotec cultural region (current geographical location: Valley of Oaxaca, Mexico) during the Formative (or Preclassic) and Classic archaeological peri-

ods. Here, I adopt a 'cultural EES' (cEES) standpoint for the analysis of biocultural evolutionary causality in the Tehuacán Valley (currently in the Tehuacán-Cuicatlán Biosphere Reserve; geographical location: SE Puebla, NW Oaxaca, Mexico) during the Archaic and Formative periods. Placing 'cultural niche construction' and (other) NCT and EED-related concepts at the center of my cEES analysis, I use construction chains (sensu cNCT) and other NCT and EED-based schemes to describe the reciprocal interaction between plant domestication events, technological interventions on the environment related to water use, and the attainment of social complexities beyond the hunter-gatherer stage. My analysis is based on archaeological data sets from this Mesoamerican region collected and interpreted by Richard MacNeish (University of Chicago) and his colleagues during the Tehuacan Archaeological-Botanical Project (1945-1964), and by subsequent archaeological research initiatives in the area. Finally, I comment on points of contact between the cEES perspective advocated here and contemporary post-processual archaeological theory (e.g. Ian Hodder's 'entanglement theory'), potentially useful in further interpretations of biocultural evolutionary causality in other Mesoamerican regions..

P-011 Tol2 mediated transgenesis in the midas cichlid species complex (Amphilophus spp.)

Sefton, Maggie (University of Konstanz, DEU); Liang, Yipeng (University of Konstanz, DEU); Kratochwil, Claudius (University of Konstanz, DEU); Meyer, Axel (University of Konstanz, DEU)

With over 2000 described species, cichlid fish are among the most diverse and species-rich vertebrate groups; however, the molecular mechanisms underlying this diversity remain poorly understood. By adapting state-of-the-art methods such as transgenesis for use in cichlids, we can better understand the genetic and developmental basis of phenotypic diversity. The aim of this study was to establish transgenesis in cichlids of the Midas species complex (Amphilophus spp.) to facilitate future investigations of the function and regulation of genes implicated in phenotypic diversification. We report, for the first time, successful Tol2 transposon mediated transgenesis in this species. We generated transgenic fish expressing GFP under the ubiquitin promoter region, active throughout the body. The transgene was integrated into the germline and successfully passed on to the F1 generation; transgenic offspring consistently exhibit strong, widespread GFP. These offspring can be used in further experiments including lineage tracing and grafting studies, which will allow us to investigate the mechanisms underlying traits such as color patterning. A further goal of this study was to test hypotheses about the

role and regulation of specific genes throughout development. Transgenesis facilitates the functional assessment of candidate genes in vivo, which is essential to understanding the connection between genotype and phenotype. We generated transgenic Midas carrying GFP under the control of the mitfA promoter, a transcription factor duplicated in teleosts, known to be involved in melanophore development in other vertebrates including zebrafish. Preliminary results suggest that the mitfA promoter is active in xanthophores, rather than melanophores, in this species. This hints at divergence in the expression patterns of this gene among teleosts, contributing to our knowledge about functional divergence of duplicated genes. These results establish a framework for transgenesis and developmental studies in Midas cichlids, and will help elucidate the role of genetic and regulatory changes during phenotypic diversification.

P-012 Evaluation of horizontally transferred genes in ten genomes of stick insects

Jaron, Kamil S. (University of Lausanne, CHE); Bast, Jens (University of Lausanne, CHE); Schwander, Tanja (University of Lausanne, CHE); Robinson-Rechavi, Marc (University of Lausanne, CHE; Swiss Institute of Bioinformatics, Lausanne, CHE)

Horizontal gene transfer (HGT) is known to be a major driver of adaptive evolution in bacteria and archaea and it plays a significant role in evolution of fungi, but its contribution to evolutionary innovation and diversification in animals is not clear. We evaluate the contribution of HGT to genome evolution in stick insects. We generated de novo assemblies of genomes from 10 different stick insects species. Further, we quantify the amount and origin of horizontally acquired genes in past 20my, inferring whether the turnover rates of horizontally acquired genes and assess whether they contribute to species divergence. Finally, since our species set comprises both sexual and asexual species, we evaluate whether an absence of recombination affects the turnover rate of horizontally acquired genes.

P-013 Postembryonic development of the ctenophores inferred from gene expression data

Røsæg, Line L. (University of Oslo, NOR); Evenstad, Andreas (University of Oslo, NOR); Andresen, Ina J. (University of Oslo, NOR); Bråte, Jon (University of Oslo, NOR); Shalchian-Tabrizi, Kamran (University of Oslo, NOR)

The ctenophore Mnemiopsis leidyi has emerged as a novel model organism in the field of evolutionary developmental biology. Belonging to one of the earliest branching phyla in the animal tree of life, it is important for reconstruction of the developmental programs of the earliest

animal ancestors. Today, several resources are available when working with M. leidyi; a published genome; in situ hybridisation of genes important in development and a cell fate map of the developing embryo. Yet, the genetic basis of the postembryonic development of M. leidyi is not understood. Furthermore, the axis-specifying role of the Wnt pathway during development is known throughout the animal kingdom, but has not been established as responsible for this process in ctenophores. Here we are investigating the postembryonic development of M. leidyi and the potential developmental differences of the morphological transition between the cydippid larvae and the adult. Our aim is to understand the underlying genetic mechanisms involved in the morphological transition between these two stages. Our primary approach is to generate gene expression data from each of the growth stages (cydippid larvae, transition stage and adults) and from the oral and aboral parts of M. leidyi. Differentially expressed genes between each stage and along the oral-aboral axis are used to describe the genetic basis of postembryonic development. In addition, we also analyse the expression pattern of developmental genes chosen a priori, such as the canonical Wnt-catenin pathway. Comparative analyses of these data is done against similar expression data from another two other species, Beroe cucumis and Pleurobrachia bachei, in order to uncover general pattern of gene expression and evolution of gene regulatory networks in the postembryonic development among ctenophores.

P-014 Evolution of non-coding RNAs in ctenophores)

Evenstad, Andreas (University of Oslo, NOR); Røsæg, Line L. (University of Oslo, NOR); Andresen, Ina J. (University of Oslo, NOR); Shalchian-Tabrizi, Kamran (University of Oslo, NOR); Bråte, Jon (University of Oslo, NOR)

Long non-coding RNAs (lncRNAs) is a class of RNAs that can act as regulators of gene expression and are important in developmental programs of animals. Most studies of animal lncRNAs have focused on model organisms, in particular mammalian species, but little is known from the most basal metazoan lineages. In this study, we therefore investigate the repertoire of lncRNAs in the ctenophores, which together with sponges constitute the deepest branches in the metazoan phylogeny. Our approach is to use Mnemiopsis leidyi as a system and explore the postembryonic gene expression by transcriptome sequencing, and compare the data with available embryonic data as well as data from other ctenophores species. The expression data is divided into the post-embryonic oral and aboral body parts in order to infer possible roles of lncRNAs in development and maintenance of the oral-aboral body axis. We present data from these studies by mapping the lncRNA data along the phylogenetic tree of ctenophores to deduce the patterns of lncRNA evolution. Comparison with recently reported sponge lncRNA is done to

understand whether these two basal animal lineages share homologous genes and thereby get insight into the ancestral condition of Metazoa.

P-015 Investigation of the cytoskeletal dynamics during spiral cleavage

Hsieh, Yu-Wen (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU); Handberg-Thorsager, Mette (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU); Tomancak, Pavel (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU)

Spiral cleavage is the ancestral developmental mode within the Spiralia. It covers a period of the early development characterized by asymmetric divisions with alternating division angles giving the embryo a spiral looking appearance. The position and fate of the cells determined during the spiral cleavage are thus crucial for body plan formation. However, the mechanisms controlling spiral cleavage are poorly understood. To elucidate the molecular, cellular and physical mechanisms of spiral cleavage, we use the marine annelid Platynereis dumerilii as a model. We wish to unravel the role of the cytoskeleton during spiral cleavage focusing on the cytoplasmic and cortical contributions. We do this through mRNA injections of fluorescently labeled tubulin (EMTB-3XGFP) and nuclei (H2B-mCherry) into the Platynereis zygote to label cytoplasmic elements. We imaged the live embryos by selective plane illumination microscopy (SPIM), which allows us to monitor the cell divisions during early development in high-resolution, high-speed, and 3D-reconstructable manners. We processed the data with Fiji softwares (Preibisch et al., 2010, 2014, and 2015), and reconstructed this way early cell cleavages in Platynereis. Next, we extracted dynamic cellular events such as inclination of the mitotic spindles, transportation of the nuclei in the cells, and membrane deformation during cell division. Moreover, we monitored the cortical actomyosin dynamics through Lifeact-mKate2 mRNA injection and imaging by spinning-disc confocal microscopy. This different imaging strategies and physical calculations have shown us that cytoskeletal elements are highly dynamic during spiral cleavage. By inhibiting microtubule polymerization with colchicine or nocodazole, or inhibiting actin polymerization with latrunculin A, we elucidated the active roles of the cytoskeletal elements in spiralian development. This study provides physical, cellular, and molecular mechanistic insights into the spiralian development and a base to compare their degree of conservation among spiralians.

P-016 A histological study of limb regeneration of the salamander Ambystoma mexicanum

Bothe, Vivien (Museum für Naturkunde, Berlin, DEU); Mahlow, Kristin (Museum für Naturkunde, Berlin, DEU); Fröbisch, Nadia B. (Museum für Naturkunde, Berlin, DEU)

Urodele are undefeated in the field of tissue regeneration amongst vertebrates. They have great ability to repair and renew lost or damage body parts, such as tails, jaws, and limbs. However, the regenerative capacity among mammals is very limited. Hence, regeneration is a much discussed and researched topic in evolution as well as in biomedical fields. Axolotls are the most commonly used urodele amphibian in the laboratory and highly suitable model organisms. Thereby, their limbs are the best-described and studied structure of their body. In spite of numerous investigations of axolotl regeneration, only few studies compare morphological features of original and regenerated limbs. Most of these have focused on nerves or muscles and very few have provided detailed information about bones and cartilage, and the histology of these structures. Therefore, the present study provides a histological investigation of regenerated limbs to research whether regenerated body parts are exact replica of the original. For this, histological serial sections of 54 Axolotl larvae were made, in 29 of which had regenerated their extremities after biting of conspecifics, while 26 were subject to targeted amputations, in order to compare tissue structures of the original and the regenerated limbs. The amputations were performed in several larval stages (48, 52, 53) and at different limb positions (middle of humerus, above mesopod). To confirm the histological results, 3D reconstructions were additionally prepared and x-ray microtomography (microCT) scans performed. The results indicate that regenerated forelimbs show a diversity of limb and digit abnormalities which pointed to imperfect regeneration. Besides, wound healing in regenerating limbs depends in the degree of differentiation of the lost limb. Furthermore, the differences were greater in regenerated forelimbs, which were caused by natural bites than in regenerated forelimbs after amputation.

P-017 Cobalamin receptors in vertebrates: transitions to novel functions?

Ruivo, Raquel (University of Porto, PRT); Oliveira, Diogo (University of Porto, PRT); Castro, L. Filipe C. (University of Porto, PRT)

Vitamin B12, also known as cobalamin, is an essential nutrient which serves as enzyme cofactor. In humans, defects in intestinal absorption, plasma transport or intracellular metabolism result in megaloblastic anaemia and severe neurological disorders. In mammals, B12 is delivered to target cells bound to a specialized carrier, Transcobalamin II (TCNII). The TCNII-B12 complex is recognized by CD320, a membrane receptor. Structurally, CD320 is composed of two LDLR-A domains, typical of low density lipoprotein receptors (LDLR). Apart from lipids, lipoprotein receptors may also mediate the uptake of vitamins and hormones. In fact, a mouse knock down model suggested CD320 as the sole receptor responsible for B12 absorption in the CNS, whereas additional non-specific lipoprotein receptors could facilitate TCNII-B12 uptake in other organs. Synteny analysis revealed that the CD320 gene locus is well

conserved in mammals, birds, reptiles, amphibians and fish. Surprisingly, fishes and amphibians retain a gene coding for a longer receptor, with additional LDLR-A domains. Subsequent truncation events gave rise to shorter receptors in amniotes. However, birds and reptiles exhibit lower sequence and domain conservation when compared to the strikingly conserved mammalian receptor. Together, these observations suggest that the vitamin B12 specific receptor evolved from a truncated homolog of a classical lipoprotein receptor, present in all metazoan lineages. Thus, the present work aims at 1) elucidating the evolutionary origin of the B12 receptor and 2) understanding the link between receptor specialization and novelty acquisition in mammals.

P-018 A pipeline for the systematic identification of non-redundant full-ORF cDNAs for polymorphic and evolutionary divergent genomes: application to the ascidian Ciona intestinalis

Rothbächer, Ute (University of Innsbruck, AUT; CNRS/Université Aix-Marseille, FRA); Gilchrist, Michael J. (The Francis Crick Institute, Mill Hill Laboratory, London, GRB); Lemaire, Patrick (CNRS/Université Montpellier, FRA)

Genome-wide resources, such as collections of cDNA clones encoding for complete proteins (full-ORF clones), are crucial tools for studying the evolution of gene function and genetic interactions. Non-model organisms, in particular marine organisms, provide a rich source of functional diversity. Marine organism genomes are, however, frequently highly polymorphic and encode proteins that diverge significantly from those of well-annotated model genomes. The construction of full-ORF clone collections from non-model organisms is hindered by the difficulty of predicting accurately the N-terminal ends of proteins, and distinguishing recent paralogs from highly polymorphic alleles. We report a computational strategy that overcomes these difficulties, and allows for accurate gene level clustering of transcript data followed by the automated identification of full-ORFs with correct 5'- and 3'-ends. It is robust to polymorphism, includes paralog calling and does not require evolutionary proximity to well annotated model organisms. We developed this pipeline for the ascidian Ciona intestinalis, a highly polymorphic member of the divergent sister group of the vertebrates, emerging as a powerful model organism to study chordate gene function, gene regulatory networks and molecular mechanisms underlying human pathologies. Using this pipeline we have generated the first full-ORF collection for a highly polymorphic marine invertebrate. It contains 19,163 full-ORF cDNA clones covering 60% of Ciona coding genes, and full-ORF orthologs for approximately half of curated human disease-associated genes.

P-019 Life-cycle traits of marsh frog Pelophylax ridibundus can be transformed without change in locus RC08604

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Adaptations to local environments in larval growth rate of moor frog Rana arvalis may be associated with polymorphism in locus RC08604, partly located in thyroid-hormone receptor (Trî^2) gene (Richter-Boix et al., 2011). Marsh frog Pelophylax ridibundus can change life-cycle traits (first of all the age and body size at maturity) in various warm water habitats. In natural thermal ponds of Kamchatka peninsula (Lyapkov, 2014) and in a small thermal sedimental pond near Nizhny Tagil (Fominykh, Lyapkov, 2012), P.ridibundus forms numerous groups of overwintering tadpoles, moreover, these overwintering tadpoles often develop into frogs with higher fitness components (body size and reproductive characteristics. Both Kamchatka and Nizhny Tagil P. ridibundus populations were founded by few frogs, introduced from European Russia. We have found reduced diversity in microsatellite loci (Rrid059A, RlCA1b5, Rrid171A) in Kamchatka populations of P. ridibundus, and locus RC08604 displayed almost no allelic diversity at all. No evidence of selection in this locus was found in Kamchatka populations of P. ridibundus.

P-020 Long-term developmental arrest in the embryogenesis of the common toad (Bufo bufo) as a non-specific adaptation to adverse environmental conditions

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Embryos are extremely sensitive to all environmental factors at the so-called ‚critical stages' of normal development. Under an influence of various adverse factors, the maximal levels of mortality concurs with the critical stages. In our experiments with the embryos of the common toad, the stages of early neurula and tail bud were characterized as the critical once. However, once the threshold values of several adverse factors were exceeded, the stages of mid-blastula and mid-gastrula became the critical stages. If the oxygen concentration, density of embryos or toxicant concentration surpassed their threshold values, embryonic development has been arrested at the mid-blastula or mid-gastrula stages. The pattern of this reaction depended on the particular factor. In the case of high density and hypoxic conditions, development proceeded normally until the mid-gastrula stage, then stopped and embryos underwent mass mortality. Under the high copper concentrations (10, 25 and 50 mg / L) the development was slowed down at the blastula stage and arrested at the mid-gastrula stage. Developmental arrest can last for several days (up to 86h, i.e 81% of normal development, which lasts about 100h). If existing conditions were left as is, almost all embryos died (about 90%), but small fraction of embryos survived and reached the stage of hatching. The most interesting finding is that if conditions were sharply improved, the long-term developmental arrest has been cancelled. The embryos survived and managed to reach the hatchling stage much faster than in the course of normal development. We suppose that

the developmental arrest occurring at one of the critical stages can be viewed as an adaptation allowing the embryos to survive: embryos are able not to proceed to the next developmental stage (e.g. formation of neural plate) waiting for ceasing of the adverse environmental influence.

P-021 Draft genomes of two marine cladocerans

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The Cladocera represents an order of microcrustaceans or brachiopods commonly named as water fleas, and the freshwater cladoceran Daphnia pulex is the first crustacean genome being sequenced a few years ago. A surprising genomic feature found in the Daphnia is the elevated rate of gene duplication, including those in the metabolic pathways, suggesting numerous paralogues were acquired with divergent expression to encounter ecological challenges. Here, we presented the draft genomes of two marine cladocerans, and analysed the microRNAs, developmental and metabolic genes to reveal whether the elevated rate of gene duplication is freshwater cladoceran-specific or more widespread among the Cladocera.

P-022 De novo myogenesis and neurogenesis during ascidian colony propagation

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Through a highly stereotyped embryogenesis, ascidian fertilized eggs develop into a tadpole larva with a chordate body plan. After a pelagic stage the tadpole attaches to a substratum and metamorphose into a sessile juvenile form (oozoid). At this point two divergent life histories can take place: in solitary species the oozooid increase in size and become a sexually mature adult zooid. In contrast, colonial species such as Botryllus schlosseri start a life-long asexual developmental program, whereby entire new bodies, including all somatic and germline tissues, develop in a budding process called blastogenesis (or palleal budding). The gene regulatory program (GRP) driving the formation of the neuromuscular system in the tadpole and in the adult zooid is extensively studied in solitary forms. However, almost nothing is known about myo- and neuro-genesis during the non-embryonic development of colonial ascidians. In this study we started to dissect the GRP that lead to the tadpole and the post-metamorphic zooid musculature and nervous system and analyzed expression and function of key transcription factors during blastogenesis of Botryllus schlosseri. In particular, we analyzed early determination factors for myo- (Macho, Tbx6, Tbx1/10, COE) and neurogenesis (SoxB1, Otx, Pax3/7, POUIII, COE), regulatory modules (MRF, Etr/ELAV, POUIV) as well as structural factors involved in muscle (Myosin)

and neuron (preGnrH) differentiation. The preliminary data suggest that: 1) in a colony neurons and muscle are specified de novo during every budding event, 2) the specification and differentiation origin in a defined structure named dorsal tube and 3) at least for myogenesis, only the embryonic GRP responsible of the formation of zooid muscle is co-opted during blastogenesis, whereas the one responsible of larva musculature is silent.

P-023 The origin of the vertebrate stomach: insights from the catshark gut development

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The gastrointestinal tract (GIT) develops from a simple undifferentiated tube into highly differentiated regions. Each region has a specific structure and gene expression signature enabling different functions. The origin of jawed vertebrates coincides with the appearance of a novel GIT region, the stomach. This anatomical structure is characterized by gastric glands responsible for the secretion of HCl and pepsin that enables digestion. GIT regionalization and gastric gland differentiation has been reported during development in traditional model organisms. However, no comparable information is available in the living representatives of basal jawed vertebrates, such are the chondrichthyans. Here we provide the first comparative analysis of GIT development in a chondrichthyan representative, the catshark Scyliorhinus canicula. We identify a clear molecular regionalization of the embryonic gut assigned by the expression of Barx1 and Sox2 in the anterior portion of the digestive tract and by the expression of Cdx2 in its posterior portion. Moreover, we show that these expression domains relate with the formation of the stomach anteriorly and the intestine posteriorly. Finally, we provide evidences of gastric gland development close to hatching, accompanied by the beginning of the gastric proton pump H+/K+ ATPase expression. Our findings suggest that regionalization of the gut and differentiation of structures specialized in distinct stages of the digestion, involved developmental networks that emerged at the stem of gnathostome evolution.

P-024 The evolution of the piRNA pathway - insights from the starlet sea anemone

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Ulrich (University of Vienna, AUT)

Piwi interacting RNAs (piRNAs) are metazoan specific small RNAs associated with Piwi proteins required for fertility, genome integrity and transposon surveillance. While mostly expressed in the germline in model bilaterians, piRNAs and Piwis are also found in stem cells of highly regenerative animals. Cnidarians (sea anemones, hydras, corals and jellyfish) have a remarkable regeneration capacity and their phylogenetic position as bilaterian sister group makes them important for the understanding of the evolution of the piRNA pathway. We investigated the piRNA pathway in the anthozoan Nematostella vectensis. Small RNA sequencing showed that piRNAs are extremely abundant, corresponding to more than 90% of small RNA reads across all developmental stages. This presents the highest abundance of piRNAs in metazoans and is in striking contrast to bilaterians, where the proportion of piRNAs is low due to their spatial restriction. We found that Nematostella has three bona fide Piwi proteins. Piwi1, Piwi2 and a homolog of the piRNA-related helicase Vasa of bilaterians show surprisingly broad expression domains in embryos, likely indicating the multipotency of many embryonic cells. In adults however, expression of these genes is only detectable in the putative gonia and their early division products, similar to the situation in Bilateria. Immunostaining of Vasa2 reveals a distinct perinuclear localisation („nuage"), which clearly represents an ancestral metazoan feature. We conclude that during development the repertoire of multipotent cells is progressively minimised and gets restricted to the adult germline. The late and continuous segregation of germline cells from somatic cells correlates with the early broad expression and the high regeneration capacity of cnidarians. We propose that this reflects an ancestral situation maintained in the cnidarian and few other animal lineages."

P-025 Fog is rising: A signaling pathway used for morphogenesis across insects

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One of the best-studied signaling pathways regulating morphogenesis is the Drosophila Folded gastrulation (Fog) pathway. In this pathway, the ligand Fog activates a G-protein coupled receptor that induces actomyosin network rearrangements. In the Drosophila embryo, Fog signaling is active in several morphogenetic events, including internalization of the ventral mesoderm and posterior midgut during gastrulation. To understand how such a pathway evolved, a comparative approach is needed. However, it was previously thought that fog is not conserved outside the higher Diptera. In contrast, we have found that although fog is rapidly evolving, it is, in fact, present in the wasp Nasonia vitripennis, a member

of the Hymenoptera, the most basally branching lineage of the Holometabola. Both Nasonia and Drosophila share a similar, but independently evolved, mode of long-germ embryogenesis, in which all segments are patterned prior to gastrulation. The gastrulation movements of Nasonia are, however, clearly distinct from those of Drosophila. In particular, the mesoderm is not internalized via a ventral furrow and the germband undergoes very little extension. In spite of these differences, the Fog pathway is crucial in Nasonia for correct morphogenesis during gastrulation, as in Drosophila. During normal mesoderm internalization in Nasonia the ectoderm breaks its epithelial contact with the mesoderm and migrates on top of it, until the two ectodermal sheets fuse at the ventral midline. In Nasonia embryos with impaired Fog signaling, the ectoderm fails to migrate over the mesoderm. Despite this defect, presumptive mesodermal cells still become squamous and migrate away from the ventral region, creating a ventral hole in these embryos. The posterior midgut internalization of Nasonia embryos with disturbed Fog signaling fails as well, resulting in a diffuse mass of cells at the posterior.

P-026 Evolution of a Gene Regulatory Network for gut development downstream of Xlox and Cdx in two echinoderms

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The comparison of the Gene Regulatory Networks (GRNs) among different animals helps to understand the origin of each morphological character of the body plan. Our project aims to compare the gene interactions acting downstream of the two ParaHox genes, Xlox and Cdx in two echinoderms, the sea urchin Strongylocentrotus purpuratus and the sea star Patiria miniata, whose last common ancestor lived about 500 MYA. Xlox and Cdx have been demonstrated to be involved in the formation of the gut in the sea urchin and sea star larvae and the sea urchin Xlox, similarly to its orthologue Pdx1 in mouse embryo, controls the formation of the pyloric sphincter. In order to compare the two GRNs we have first generated data-sets of RNA-Seq on wild type and Xlox and Cdx knocked-down sea urchin and sea star embryos. The RNA-Seq datasets have been analyzed and a complete list of differential transcription factors, the key elements for the reconstruction of the GRN, has been generated for both animals. Among these, the sea urchin factor Meis is of great interest because of its already known interaction with Hox genes in Vertebrates and its role as oncogene. Currently we are working on the generation of differential sea urchin and sea star ATAC-Seq to reveal the different chromatin organization in the regulatory regions of these transcription factors in the wild type and perturbed conditions. The key interactions downstream of the sea urchin and the sea star Xlox and Cdx will be

validated by morpholino injection experiments assessing the effects on the level of expression of all the TFs involved in these GRNs. Moreover, to establish the direct downstream interactions of the two sea urchin ParaHox proteins ChIP experiments are being performed. Taken together these information will help us to construct the GRNs around Xlox and Cdx in sea urchin and sea star and from the comparison of the two GRNs we will identify the kernel elements that didn't change during evolution, as well as the intrinsic differences in the GRN accumulated during the evolution of the two echinoderm lineages.

P-027 The iBeetle large-scale RNAi screen reveals new genes for dorsoventral pattern formation in Tribolium castaneum

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The detailed knowledge about dorsoventral (DV) axis formation in Drosophila melanogaster provides an excellent platform for comparative studies within insects. In Drosophila, the ventral activation of Toll-receptor initiates the nuclear uptake of the transcription factor NF-kB/Dorsal resulting in a stable nuclear Dorsal gradient which regulates target genes like the mesodermal genes twist and the neuroectodermal gene short gastrulation (sog) in a concentration dependent manner. In the red flour beetle Tribolium castaneum, NF-kB/Dorsal also forms a nuclear concentration gradient. This gradient is, however, highly dynamic due to positive and negative feedback loops. Both Tc-Toll and the inhibitor Tc-cact are activated zygotically by Toll signaling. In the course of a genome wide RNAi screen in Tribolium (the iBeetle screen) we have identified another positive feedback element, a new serine protease which is likely to act upstream of Toll within the protease cascade activating the Toll ligand SpÃ¤tzle. The expression of this gene initiates ventrally during early blastoderm stage in a broad domain along the entire egg length. After knockdown, Tc-twi and Tc-cact lack early expression while they are being activated only during early gastrulation. This corresponds to a delayed formation of the Dorsal gradient. In contrast to Tc-twi and Tc-cact, the expression of Tc-sog is completely abolished in most knockdown embryos. This suggests that the new protease affects the timing of Dorsal gradient formation. Importantly, the phenotype shows that the Dorsal target genes in Tribolium have to be activated in a temporal sequence. We propose that in contrast to Drosophila where several concentration thresholds of Dorsal are read out simultaneously, the Tribolium Dorsal gradient acts by temporal shift of few (or only one) concentration thresholds coupled to a fixed sequence of target gene activation.

P-028 Dissecting the functional role of Wnt signalling in the development of Platynereis dumerilii

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Wnt signalling is a key player in development of multicellular organisms. It decides between proliferation and differentiation, specifies cells of certain tissues and body regions (e.g. posterior end of a body, lateral regions of a neural plate etc.), guides growing axons or morphogenetic movements and polarizes cell divisions. The marine polychaete annelid Platynereis dumerili is a member of the clade Lophotrochozoa, a second large branch of protostome lineage previously under-represented among model organisms. Our aim is to characterize a functional role of the canonical Wnt/Î²-catenin signalling during Platynereis larval development with a special focus on conserved regulation of body patterning genes and the development of major organ systems. To achieve this, we cultivate developing larvae in a presence of chemical activators or inhibitors of Wnt/Î²-catenin signalling in order to manipulate activity of the pathway. This manipulation changes the level and localization of Î²-catenin and transcription of known target genes showing that it efficiently alters the activity of canonical Wnt pathway. Using in-situ hybridization we visualize the expression patterns of selected transcription factors, which are crucial for patterning of the body plan, for cell specification as well as some effector genes. Expression of several genes is greatly reduced upon over-activation of Wnt/Î²-catenin signalling whereas others are not affected. Interestingly, Wnt inhibition does not always produce reversed effect but both activation and inhibition often result in very similar gene expression and morphological changes. We hypothesize that this is because Wnts are important for balance between cell proliferation and differentiation and when this balance is perturbed, in both cases less differentiated cells are produced.

P-029 Molluscan Wnt gene expression and the evolution of morphological novelties

Rodríguez Monje, Sonia V. (University of Vienna, AUT)

Wnt signaling proteins are highly conserved molecules that play key roles during metazoan development. They bind to transmembrane familiy receptors such as frizzled, LRP and tyrosine kinases and subsequently trigger the transcription of several Wnt target genes. Studies on Drosophila, Xenopus and zebrafish show, that Wnt signaling activity is involved in processes such as gastrulation and patterning of the body axis. Unfortunately, there is still a considerable gap in knowledge concerning Wnt function in one of the two protostome superphyla, Lophotrochozoa, that includes numerous diverse groups such as the annelids and the mollusks. The latter are particularly interesting due to their vast diversity of morphological phenotypes as well as life cycles they exhibit. We retrieved transcripts from members of 12 Wnt subfamilies from transcriptomes of three different mollusks: Dreissena polymorpha

(Bivalvia), Acanthochitona crinita (Polyplacophora) and Antalis entalis (Scaphopoda), and analysed their temporal and spatial expression domains during development. We found that Wnt1 is expressed in the most posterior body region in the polyplacophoran, a condition similar to other bilaterians and congruent with the notion that Wnts are primarily involved in patterning the anterior-posterior axis of bilaterian animals. To our surprise, however, we found Wnt expression being confined to specific organ systems such as the prototroch and the dorsal mantle opening in scaphopods. Unlike in bilaterians, a posterial wnt expression domain was not found in the scaphopod, raising the question as to whether Wnt genes are generally expressed differently in conchiferans, and thus may have been coopted into novel functions compared to aculiferans as well as other bilaterians.

P-030 The roles of the Wnt antagonists Axin and Lrp4 during embryogenesis of the red flour beetle Tribolium castaneums

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In both, vertebrates and invertebrates, the fine-tuning of the Wnt signalling pathway is essential for numerous processes in embryogenesis and during adult life. While in insects the roles of Wnt-agonists like the Wnt ligands and their receptors of the Frizzled family have been intensely covered, the functional analysis of Wnt-antagonists other than Axin has just started. First, we describe here additional features of the Wnt-antagonist Axin in the flour beetle Tribolium castaneum. We show that Tc-axin is dynamically expressed throughout embryogenesis and confirm itÂ´s essential role in head development. In addition, we describe novel, more extreme Tc-axin RNAi phenotypes, where missing anterior structures are replaced by posterior abdominal segments in reversed polarity and a second, ectopic hindgut at the anterior. We describe here for the first time the function of the lrp4 gene in an insect. Lrp4 that has been characterized as a Wnt-inhibitor in vertebrates is absent from the Drosophila genome. In Tribolium, the obvious Tc-lrp4 ortholog is ubiquitously expressed throughout embryogenesis. Its downregulation using RNAi results in the reduction of head-structures but not in polarity reversal. Furthermore, segmentation is impaired and larvae develop with a severe gap-phenotype. We conclude that like in vertebrates Tc-lrp4 functions as a Wnt-inhibitor during various stages of Tribolium embryogensis.“

P-031 Amphioxus SCP1: a case of retrogene replacement and co-option of regulatory elements adjacent to the ParaHox cluster

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Retrogenes are formed when an mRNA transcript is reversed transcribed and re-inserted into the genome in a genomic location unrelated to the

original locus. If this retrocopy inserts into a transcriptionally favourable locus, and is able to carry out its original function, it can, in rare cases, lead to retrogene replacement. This results in the original, often multi-exonic, parental copy being pseudogenised and lost whilst the newer, single exon, retrogene copy „replaces" the role of the ancestral parent gene. One example of this is that of Amphioxus SCP1, a gene that plays a conserved role in the synaptonemal complex of meiosis and exists as a large multi-exonic gene in most animals. AmphiSCP1, however, contains a single coding exon of ~3200bp and has inserted next to the ParaHox cluster of amphioxus and replaced its ancestral parental copy. Here, we show that AmphiSCP1 has not only replaced its parental copy, but has evolved additional regulatory function by co-opting a bidirectional promoter from the nearby AmphiCHIC gene. AmphiSCP1 has also evolved a de novo, multi-exonic 5'UTR that displays distinct regulatory states, in the form of two different isoforms, in order to make use of this promoter region and has evolved novel expression patterns during amphioxus embryogenesis in addition to its ancestral role in meiosis. The absence of ParaHox-like expression of AmphiSCP1, despite its proximity to the ParaHox cluster, also suggests that the ParaHox regulatory block is not so easily disrupted or co-opted by invasions to the surrounding ParaHox locus.

P-032 Evolution of microRNA target interactions in animals)

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MicroRNAs (miRNAs) are 21-23 nucleotides non-coding RNAs that post-transcriptionally regulate gene expression in animals. Despite the mechanism of miRNA actions are better revealed in recent years, how miRNAs can contribute to metazoan macroevolution remains poorly demonstrated. We analysed the mRNA and miRNA datasets of 32 animals that have their genomes fully sequenced. Based on the phylogenetic positions of miRNAs and the functions of their target genes, 124 miRNAs are found to be functionally constrained after their births. Differential selections on miRNAs after their birth and co-options to gene regulatory networks are found in different lineages, which provide another instrumental way to the diversification of genetic regulation and morphological complexity during animal evolution.

P-033 Whole genome duplications in two Asian horseshoe crabs

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Whole-genome duplication (WGD) results in new genomic resources that can be exploited by evolution for rewiring genetic regulatory networks in organisms. In metazoans, WGD occurred before the last common ancestor of vertebrates, and has been postulated as a major evolutionary force that contributed to their speciation and diversification of morphological structures. In a recent study, we have sequenced the draft genomes of three out of the four extant horseshoe crab species (including the two from Hong Kong), and unexpectedly found that there are multiple copies of different sets of investigated genes in all of these invertebrates, suggesting WGD also happened in the sexually reproducing invertebrates. We are now forming a consortium to investigate the different aspects of the two Asian horseshoe crabs, in light to better understand this rare event in the metazoan evolution.

P-034 A pycnogonid draft genome reveals different genomic situation to the euchelicerates

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The Pycnogonida (sea spiders) represents a phylum of long debatable phylogenetic position inside the Arthropoda â€“ it has been dubious whether it is grouped within the Chelicerata as a sister group to euchelicerates or as a sister group to all other euarthropods. The Euchelicerata comprises of the arachnids (e.g. scorpions and spiders) and the xiphosurans (horseshoe crabs); recent genomes sequencing of these two groups of animals revealed that they have undergone unusual lineage modifications, with massive gene duplication events detected in the former and genome duplication observed in the latter. Here we present the draft genome of a pycnogonid. Analysis of its different gene families and microRNAs revealed the sea spider to be a big contrast to the euchelicerates in terms of genomic structure, as the majority of these genes was present in single copies. This study provides the first evidence that the genomic content of the pycnogonid does not differ much to the other non-euchelicerate arthropods, and suggests that if the pycnogonid was a chelicerate, the genomic features observed in the arachnids and the xiphosurans would have been a result of lineage-specific modifications after the separation of pycnogonid from their last common ancestor.

P-035 The polycistronic smORF milli-pattes is essential for Rhodnius prolixus embryogenesis

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Rhonius prolixus (Hemiptera) is one of the major vectors of the Chagas

disease in America as a vector of Trypanossoma cruzi. Several classical aspects of insect physiology were originally described in this hemiptera by the seminal work of Wigglesworth. In contrast, studies of R. prolixus embryonic development have been largely neglected, with noticeable exceptions in recent years. Here, we investigate the role of the polycistronic gene mille-pattes (mlpt), as a representative of a new class of genes encoding small open reading frames (sm-ORFs) in a single transcript, an unusual feature of eukaryotic mRNA. mille-pattes name, multiple legs in french, was coined from the observation of the knockdown (RNAi) embryonic phenotype of the beetle Tribolium castaneum (Tc), which display up to six pairs of legs instead of the three pairs found in wild-type (Savard et al., 2006). Tc-mlpt regulates not only gap genes, but also some downstream Hox genes. Since mlpt function was only investigated in holometabolous insect such as T. castaneum, we sought to investigate the role of mlpt in the hemimetabolous insect R. prolixus. First, we established a new in situ hybridization protocol which enabled the detailed analysis of Rp-mlpt expression. Rp-mlpt is expressed in similar domains to its Tribolium ortholog with noticeable exceptions of a strong expression at the antennal segment in the hemiptera. Rp-mlpt parental knockdown through RNA interference (RNAi) injection lead to complete lethality during embryogenesis. Preliminary phenotypic analysis showed a large number of leg pairs after Rp-mlpt RNAi and reduction of abdominal segments, indicating that homeotic transformations have occurred. To conclude, our study indicates that the embryonic function of the polycistronic smORF mlpt was already essential at the common ancestor of Hemiptera and Holometabola.

P-036 Genetics underlying the evolution of a key morphological innovation: the propelling fan of the water walking bug Rhagovelia sp.

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The invasion of new habitats often requires the evolution of key novel traits that will facilitate the exploitation of the new environment. The origin of novel phenotypic characters is therefore a key component in organismal diversification, yet the mechanisms and selective forces underlying the emergence of such evolutionary novelties are largely unknown. In Rhagovelia sp. (genus of water-walking insects) the evolution of a highly elaborate swimming fan on the tarsus of the propelling mid-legs increases water resistance against leg movements, thereby increasing their propelling function. This novel adaptive trait allowed the Rhagovelia group to conquer and diversify on running water surfaces; a niche that is not accessible for most other water-walking insects. However, the genes underlying the differentiation of the fan during development are unknown. With next-generation sequencing it is now possible

to access transcriptomes and gene expression at unprecedented levels. Here, we report a characterization of the gene expression levels between developing mid-legs (with fan) against forelegs and hind-legs (without fan) in R. antilleana. This approach has allowed the identification of a list of 82 candidate genes potentially associated with the evolution of this strikingly novel phenotype. With this analysis, we also provide evidence that both co-option of pre-existing genes and lineage specific genes might be involved in the evolution of novel phenotypes. Furthermore, we performed a dsRNA knock-down of two of the candidate genes and showed that gdf8 (growth differentiation factor 8) is responsible for the elongation of the Rhagovelia mid-leg pre-tarsus (structure that protects the fan). The functional screen of more candidate genes is currently on going. By studying the developmental genetic and adaptive bases of this phenotype we will be able to understand the mechanisms through which spectacular morphological adaptations can arise

P-037 Investigating the evolution of the functional specificity of Wnt ligands

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In metazoans there are thirteen Wnt gene subfamilies, seven of which are present in Drosophila melanogaster. These genes are important in many developmental processes, for example, wingless (wg) regulates many processes during Drosophila development from segmentation to growth of imaginal discs and cell death. However, in contrast, the other Wnt ligands have more restricted roles, for example, loss of Wnt6 only affects the maxillary palps. Although they appear to differ in their developmental functions, wg and Wnt6 are ancient paralogues that have remained closely linked in metazoans, exhibit similarities in their amino acid sequences and show overlapping expression patterns. However it is not known how the Wg and Wnt6 proteins differ functionally neither at the molecular level nor the amino acid differences responsible. Therefore, we are testing the ability of these two proteins to rescue functions of the other and mapping the protein domains that confer differences in their functions during a range of developmental processes. This research will provide new insights into the evolution of Wnt signaling and help to better understand the molecular basis of differences among Wnt ligands that contributes to the specificity of this signaling system during developmental processes.

P-038 sp5 and nlk are expressed during tail development and regeneration in the European amphioxus.

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Amphioxus, the only extant cephalochordate & earliest diverging chordate subphylum, present a unique model system for studying the evolution of chordate traits. Their lineage is considered conservative, & a good proxy for the morphology & genomic content of the ancestral chordate. Adult amphioxus also show remarkable ability to regenerate tissues of the post-anal tail, the homologues of which regenerate poorly in many vertebrates. These include the dorsal nerve cord & the notochord, homologous to the human spinal cord & nucleus pulposus of the intervertebral discs, & muscle. This allows comparative study of the formation of these tissues during development & regeneration. This work investigates the intracellular signalling that regulates progenitor cell activity in amphioxus tail formation. Transcriptomic analysis of tail regeneration detected two signalling-related genes with known roles in tail progenitor regulation of other deuterostomes: Nemo-Like Kinase (nlk) & Specificity Protein 5 (sp5). Both have established relationships in vertebrates to Wnt & BMP signalling, two pathways previously shown as active during amphioxus tail regeneration: nlk as an upstream regulator of both pathways & sp5 as a downstream target of Wnt signalling. We present here a phylogenetic analysis of the evolution of sp5 & nlk within the deuterostomes. To characterise their roles in amphioxus tail development, & connection to Wnt & BMP signalling specifically, both wildtype B. lanceolatum embryos & embryos with pharmacologically perturbed Wnt & BMP signalling were assayed for sp5 & nlk expression, using in situ hybridisation. The responsiveness of their expression to these treatments demonstrates potential interactions with Wnt & BMP signalling, discussed here in the context of their known roles in other deuterostomes. Finally the expression levels of sp5 & nlk were compared between unamputated & regenerating adult tails using semi-quantitative-PCR. These results will ultimately provide insight into the potential roles of these genes in tail formation of the ancestral chordate."

P-039 Marine annelid larvae and evolution of Associative Learning

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The 6 days old larvae of the marine Annelid Platynereis dumerilii are active, autonomous animals, endowed with many sensory abilities. Moreover, they possess a brain structure with striking similarities to the Arthropod Mushroom Bodies, which in Insects are known to play a specific role in associative learning. This project aims at showing that Platynereis larvae are able to perform (odor) associative learning, a key bevioral innovation that may have arisen in the early Cambrian. To this purpose, we are developing microfluidic setups to be used to demonstrate learning, as well as to combine neuronal calcium imaging and laser ablations to test the potential role of Mushroom Bodies in learning. Finding that Mushroom Bodies are indeed involved in Associative Learning

would shine new light on the evolution of learning, arguing in favor of a learning center being present as far back in time as in the brain of the last common Protostome ancestor.

P-040 Evolutionary innovation in vertebrate late development

Liu, Jialin (University of Lausanne, CHE); Robinson-Rechavi, Marc (University of Lausanne, CHE)

Both the early conservation and hourglass models suggest that late development has the highest divergence at the morphological and molecular levels between species. My aim is to determine as much as possible the relative contributions of relaxation of purifying selection vs. increase in positive selection, in the observed high divergence of genes from this developmental period. In order to achieve this aim, I adopted three approaches. First, I used modularity analysis to get distinct sets of genes (modules) co-expressed specifically in consecutive stages and compared different evolutionary forces (positive and negative selection, neutral evolution) across modules. Second, I applied a modified „transcriptome age index" to measure evolutionary forces on the whole transcriptome level and compared it across development. Finally, I adapted a gene set enrichment approach to detect polygenic selection on pathways. At the single gene level, I found higher evolution rates on sequences of genes expressed during late development were determined by an interaction of weaker purifying selection, higher neutral drift and stronger positive selection. At the polygenic level, I found that pathways specific to late development have higher evidence under positive selection. Overall, all the analyses indicate that late development is both under lower evolutionary constraint and a higher rate of adaptation.

P-041 Statistical rule of variation in floral organ numbers

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Floral organ number is one of the most fundamental features to define floral morphology. Although there are some exceptions, basic floral organ number is conserved within two largest clades of angiosperms. Eudicots, the largest clade, usually have flowers with four or five petals (tetra- or penta-merous), whereas the monocots, the second largest clade, have trimerous flowers usually with three times two perianth organs. On the other hand, clades branched near the eudicot-monocot bifurcation, such as family Ranunculaceae, show diversity in floral organ numbers among species. For examples, genus Ranunculus shows high stability on five, some species in genera Anemone and Eranthis show pentamerous flowers but others have six or more perianth organs, Ficaria verna flowers have eight or higher number of petals. Moreover, Ranunculaceae flowers show considerable variation of floral organ number within

a species or even within an individual. What causes such variation, and how can we define the typical floral organ number for those species? To answer these questions, we measured and analysed statistically the variations of floral organ numbers of Ranunculaceae. We found that the standard deviation is equal to the square root of the difference between the mean and a specific number. This specific number was strictly fixed on five in Ranunculus, whereas it was varied among Anemone species, suggesting a new method to find a robust species-representative number in varied morphologies. There were four types of variations within a population: symmetric, positively and negatively skewed, and multimodal variations. To explain the former three types, we propose a model assuming the fluctuation of expression boundary of organ-fate determinants, which is consistent with recent studies focusing on flexibility of floral structure of Nigella damascena.

P-042 Elucidating the dynamics of the dorsoventral gene regulatory network in Tribolium castaneum

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The patterning of the dorsoventral (DV) axis in Drosophila belongs to the most extensive studied developmental processes. However, the gene regulatory network controlling dorsoventral axis formation has undergone radical changes during insect evolution. In Drosophila DV patterning is mainly based on Toll signaling while BMP signaling has a spatially restricted function. In more basally branching insects BMP signaling becomes more important, progressively replacing Toll's function. To gain an unbiased global understanding of the DV GNR, we performed comparative transcriptome analyses after RNAi in the short germ beetle Tribolium castaneum, an insect with more basal features of embryogenesis compared to Drosophila. We manipulated both Toll signaling, including the important Toll target gene twist, and BMP signaling. In order to identify differentially expressed genes, we compared the transcriptomic data of knockdown embryos from Tc-Toll, Tc-twi, Tc-short gastrulation and Tc-decapentaplegic to control samples. By this approach we identified > 750 genes and analyzed the expression pattern of a specific subset which showed differential expression in more than one knockdown condition. Genes with interesting expression patterns were also analyzed regarding their function. We found new genes with localized expression and showed that conserved genes frequently possess earlier and stronger phenotypes in Tribolium compared to their Drosophila orthologs. Tc-Dorsal seems to establish expression patterns in at least three different

domains within the ventral third of the Tribolium embryo. But our data indicate new subregions in which the Tribolium nuclear Dorsal gradient seems to regulate the expression of target genes. In order to visualize on the one hand, the Dorsal gradient itself and on the other hand some of its target genes we generate different reporter lines using CRISPR/Cas-9 system. This approach might help to understand the dynamics and the fine-tuned spatiotemporal regulation of the DV GRN in Tribolium.

P-043 Light perception in Amphioxus: insights into evolution of photoreception in vertebrates

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Amphioxus belongs to cephalochordates subphylum, sister group to vertebrates. Amphioxus lives in shelf seas all over the world. Amphioxus larvae are planctonic while adults are benthic. This huge change in way of live is probably acompanied with change in light perception. To address this we focus in our study on describing opsin diversity in three different species of amphioxus. The opsins are main photopigments in Metazoans and thus might provide information about light perception in different developmental stages of amphioxus. We performed detailed in silico search for opsin sequences and complete our data with expressional, functional in vitro as well as in vivo studies. Our results can provide valuable information about photoreception in amphioxus and about evolution of light perception in vertebrates.

P-044 BMP signaling regulates left-right asymmetry in amphioxus

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Left-right asymmetry in deuterostomes is regulated by the interplay of several signaling pathways that result in triggering of sidedness-determining Nodal cascade. BMP signaling has previously been shown to regulate left-right axis by either activating or inhibiting the expression of Nodal. We set out to determine the role of BMP signaling during left-right axis specification in the basal chordate amphioxus, whose larvae exhibit pronounced asymmetry in paraxial structures and in the pharynx. We performed a series of experiments affecting BMP pathway and screened the embryos and larvae for members of Nodal signaling cascade and for left- and right-sided markers. Knockdown of BMP signaling leads to the loss of Nodal expression and a concomitant loss of the left sided identity. The larvae further display right isomerism, which phenocopies the previously described effect of inhibition of Nodal signaling. Upregulation

of BMP signaling results in the loss of Nodal signaling in only about a half of the embryos while the other half shows normal expression of Nodal pathway members. We conclude that BMP signaling is necessary for the establishment of the left-right axis in amphioxus and we further propose that BMP signaling acts upstream of Nodal.

P-045 Interpreting gene regulatory information of invertebrate chordate amphioxus: an insight from transgenic studies in amphioxus and fish

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Cephalochordates, commonly known as amphioxus or lancelets, are the most basal subphylum of chordates. Cephalochordates are thus key to understanding the origin of vertebrates and molecular mechanisms underlying vertebrate evolution. The evolution of developmental control mechanisms during invertebrate- to-vertebrate transition involved not only gene duplication events but also specific changes in spatial and temporal expression of many genes. To get insight into spatiotemporal regulation of gene expression during invertebrate-to-vertebrate transition, functional studies of amphioxus gene regulatory elements are highly warranted. Here, we performed transgenic reporter studies in amphioxus, zebrafish and medaka using promoters and enhancers derived from the genome of Florida amphioxus. We found that vertebrate embryo can, at least in some cases, correctly interpret the regulatory information encoded by the amphioxus genome indicating deep evolutionary conservation. We envision that comparative transgenic analysis of gene regulatory sequences in the context of amphioxus and vertebrate embryos will likely provide an important mechanistic insight into the evolution of vertebrate body plan.

P-046 Dual-rowed dentition of the Mexican axolotl develops from a common single dental primordium

Yamazaki, Yosuke (Charles University in Prague, CZE); Soukup, Vladimir (Institute of Molecular Genetics of the AS CR, Prague, CZE); Cerny, Robert (Charles University in Prague, CZE)

pitx2 and shh are key developmental genes during odontogenesis. These genes are essential for a competent field of tooth initiation, the primary odontogenic band or dental lamina. Whereas pitx2 labels the odontogenic band, focal expression of shh is shown in initiating individual tooth germs. Therefore, a combination of pitx2 and shh expression have been used to characterize dental initiation and patterning. The aim of this study is to reveal a developmental process of double rows dentition (outer and inner dental arcades) in the Mexican axolotl in a temporal and spatial manner. Initially, the odontogenic band appeared as a single primary dental field on each jaw along jaw axis. shh marked the first

tooth germs developing within this pitx2-expressing odontogenic band. Next, the primary odontogenic band was separated into tooth fields which are named after bones of attachment; the premaxillary, vomerine and palatal tooth fields on the upper jaw and the dentary and splenial tooth fields on the lower jaw. During this separating phase, these fields were connected with the pitx2 positive epithelium transiently. At this period, shh marks newly developed tooth germs, which were added in each tooth field. Later, tooth germs on each jaw developed and were organized into two tooth row, outer and inner dental arcades. This data suggests that the outer and inner dental arcades are derived from the common primary odontogenic band. The patterning of the Mexican axolotl dentition thus reveals how a complex multi-rowed dentition is organized and it might provide a common blueprint for patterning of tetrapod dentition."

P-047 Convergent evolution of embryonic pigmentation in the Gerromorpha

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Evolutionary convergence is a common, but poorly understood, phenomenon. A key question is whether the evolution of convergent phenotypes is due to the appearance of genomic changes that are convergent themselves. To address this question, we study a trait of colouration in the embryos of semi-aquatic bugs (Hemiptera, Gerromorpha). In all species studied, a red pigment is visible in the developing eyes. Some species, however, exhibit red and yellow colouration in the antennae and legs. Based on the known phylogeny of the group, this extra-ocular pigmentation evolved several times independently and is likely a convergent trait. Our hypothesis is that the biosynthesis of eye pigments (Pteridins and/or ommochromes) is activated during embryo development in the antennae and legs. Our first step to test this hypothesis is to characterize the pigmentation pathway in one species (Limnogonus franciscanus) having this derived trait. We will use mass spectrometry to identify the precise chemical nature of the pigments. Based on the well-known Drosophila eye pigmentation pathway, we cloned several key genes and studied their embryonic expression and the effect of their inactivation using RNA interference. We are also performing a transcriptomic analysis in order to identify genes involved in the regulation of this trait. Once the network has been deciphered in Limnogonus franciscanus, we will be able to compare it with other Gerromorpha species that show a similar trait, as well as with species that do not have this feature. This model should help understand to what extent the evolution of new characters is constrained by a given genomic context, and therefore

whether it can be predicted.

P-048 Computational representation and manual curation of homology relations between anatomical structures

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Bgee (dataBase for Gene Expression Evolution) is a database to automatically compare gene expression patterns between animal species. It notably requires curating relations of historical homology between anatomical structures of different species, to be able to define which organs are comparable between species. Until recently, only species-specific anatomical ontologies were available to map homologous organs, which implied a very large curation work in order to add new species to the mappings. The Uberon ontology has been more recently developed to provide an integrated cross-species anatomy ontology, and it allows the report of homology relations with respect to taxa, and not only on a species-pair basis. The Bgee team have thus created an external annotation file, defining homology relations between anatomical structures described in the Uberon ontology. It is used to capture which structures are believed to derive from a common ancestral structure, and in which taxon this ancestral structure has appeared; homology relations can then be inferred for any species members of these taxa. The format of this annotation file is inspired from the GO annotation file format, and the procedure to provide supporting information is inspired from the guide to GO evidence codes. Each homology assertion maps some Uberon anatomical structures for a defined taxon; for each assertion, a source (such as a PMID) and an evidence code (such as „compositional similarity evidence", „developmental similarity evidence", „gene expression similarity evidence") are provided. Homology hypotheses can be explicitly negated thanks to the use of a „qualifier" column, and alternative hypothesis can be captured in different assertions. So far, the Bgee team has annotated homology relations for 1,032 Uberon structures. More information is available at https://github.com/BgeeDB/anatomical-similarity-annotations/. Bgee is accessible at http://bgee.org/. Uberon is available at http://uberon.org/.

P-049 Fluctuating asymmetry as an outcome of phenotypic plasticity: morphological responses of floral organs in Iris pumila to environmental heterogeneity

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As sessile organisms, plants are constantly exposed to the spatial and temporal variation of abiotic factors in their immediate environment. Accordingly, morphological plasticity to such environmental heterogeneity may result in the asymmetry of plant parts. To determine whether the exposure of floral organs to different intensities of environmental factors during development may lead to the morphological variation among them, we examined three functionally-distinct organs of Iris pumila: falls, standards and styles. Since the repeated floral organs are arranged around a central axis by an angle of 120°, six different orientations were determined for a total of 267 pairs of genetically distinct Iris flowers: 0° (toward the sun), 120° and 240°- for the first flower, and 60°, 180° and 360°- for the other one, from the same pot. Every orientation set of organs experienced different portion of sun radiation. To quantify the shape variation and asymmetry of floral organs we used the method of geometric morphometric. A canonical variate analysis (CVA) was employed to explore differences in shape between differently positioned floral organs in I. pumila. The statistical differences in mean shapes were assessed with a permutation test using the Mahalanobis and Procrustes distances. The ordinations of CVA plots provide a summary of patterns among orientations. For both the symmetric and asymmetric component of the total variation, some confidence ellipses are clearly separated from each other, suggesting that there are differences in the shape among differently oriented floral organs, which is consistent with the results of the permutation tests. This study is the first one, explicitly showing that phenotypic plasticity in response to environmental heterogeneity contributes to fluctuating asymmetry in plant organs.

P-050 Identification of differentially expressed genes of developing mouse and vole tooth

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One main objective of evolutionary developmental biology is to decipher how the developmental processes give rise to different phenotypes. To elucidate the molecular mechanism of these developmental processes, it is useful to compare closely or distantly related species at their equivalent developmental stages. However, well-investigated comparable developmental stages are always a prerequisite to successful explorarion of molecular mechanisms (Roux et. al. 2015). Towards this direction, previously we identified equivalent dental morphology of developing mouse and vole and have shown correlation of expression of 4 major dental genes within this two species (Jernvall et al. 2000). Nevertheless the modern high-throughput transcriptomics can enhance

our knowledge of tooth evolution. The aim of the study is to identify gene expression levels in crucial developmental stages which lead to different pheontypes of mouse and vole tooth. Therefore we measured the gene expression levels in mouse and vole tooth at embryonic day 13 and 14 through on Solid RNAseq platform. The RNA reads from both the species were aligned against Mouse genome (Refseq mm10) to quantify the gene expression. Thereafter the differentially expressed genes (DE_ genes) were identified using negative binomial distribution (R package: DeSeq2) and compared with â€œGene expression in toothâ€ -database (http://bite-it.helsinki.fi/). Further bioinformatic analysis which will be done in ongoing work, are required to find out important signals or interactions and could be validated through in vivo experiments. Overall our study and method will help us to identify more potential tooth developmental genes and their roles in diverse tooth morphology. We show using modeling how genes expressed differentially between the species could be involved in the shape differences

P-051 Evolution and development of the limbs in the gecko Hemidactylus: a new squamate non-model organism

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Geckos (Squamata: Gekkota) have the extraordinary ability to climb walls and hang upside down. Structures aiding in this specialized locomotion are found in the autopods throughout Gekkota, including the gecko Hemidactylus. First, adhesive toepads consisting of small bristle-like structures, the setae, are located subdigitally on the distal part of the digits; between these, weak intermolecular Van-der-Waals forces facilitate frictional adhesion. The second feature in the geckoâ€™s autopod are paraphalanges located laterally to the phalanges, occasionally also dorsally and/or ventrally, which are associated with the interphalangeal joints. Among Gekkota, these are either cartilaginous or ossified. Third, some phalanges are reduced to create a better angle for the claw to aid in the geckos clinging. In this study, we define the development of the gecko Hemidactylus sp. with special focus on its limbs and compare it to other vertebrate taxa. Due to the squamateâ€™s basal phylogenetic position as well as the above mentioned ecological specializations, results will broaden our understanding of the evolution and diversity of the tetrapod limb. A morphological staging table including eleven developmentally important stages is established. Specifically, the development of the limbs is monitored. Furthermore, histological staining revealed that paraphalangeal elements in Hemidactylus sp. are found in two different shapes: nubbin-like ones at the distal end of the metacarpals; and triangular ones distally of various phalanges. Paraphalanges ossify after hatching. Micro CT data analysis showed that the penultimate phalanges are reduced in digits III and IV of the manus, and in digits III, IV and V of

the pes. The evolution and development of such and alike ecological specialisations is not yet fully understood; the establishment of this new non-model organism will enable us to gain more information and to further investigate the molecular mechanisms underlying.

P-052 External gills of bichir develop by accelerated formation of all germ layers of the hyoid metamere

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The external gills are transient but key larval adaptations that are well known from amphibians or from lungfishes. Among the actinopterygian fishes, the external gills are present only in representatives of the earliest-branching group, bichirs. Interestingly, whereas bichir external gills are associated with the hyoid arch, in all other larval vertebrates these organs are located on branchial arches as a rule. The aim of this study is to examine developmental bases of the external gills in the Senegal bichir (Polypterus senegalus) in order to test their origin. We have confirmed that the bichir external gills indeed develop from the hyoid arch region, moreover, our results further identify an unexpected acceleration of all germ layers in the bichir hyoid metamere. We have revealed an early lateral expansion of the pharyngeal endoderm in the hyoid region, which was found to constitute the external gill anlage. Next, we have analysed mesodermal derivatives, and show that the very first cranial muscles are associated with the hyoid external gills. Finally, we have focused on the neural crest cells as the source of the craniofacial mesenchyme. We have found that the hyoid stream of neural crest cells provides supporting mesenchyme for the bichir external gills, and that emigration of the hyoid stream is notably accelerated when compared to the mandibular stream. This is very surprising, since according to the common vertebrate scheme, the mandibular metamere should develop prior to other more posterior metameres. We conclude that bichir external gills are indeed unique among all vertebrates in that they develop by heterochronic acceleration of all germ layers within the hyoid region of developing bichir head. We will also discuss possible homology of the external gills among vertebrate larvae.

P-053 Miniaturization and ontogeny: a paleobiological approach

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Miniaturization is a phylogenetic concept that has been defined as the

evolution of extremely small adult size in a lineage. It does not simply imply the decrease of the body size, but also involves structural modifications to maintain functional efficiency at a reduced size. Particularly, miniaturized tetrapods are characterized by novel cranial arrangements that result from the interplay between the extrapolation of the conservative negative allometry of the brain, eyes, and otic capsules in vertebrates and functional constraints on nervous and sensory systems. Because extreme size reduction may trigger profound morphological changes that represent a pool of alternate morphological designs, miniaturization has been considered as a key factor for the evolution of major clades. In particular, it has been proposed that lissamphibians originated from a clade of Permian dwarfed temnospondyls and that a suite of characters supporting the temnospondyl-lissamphibian hypothesis are features associated with miniaturization. In this work, I compare qualitatively and morphometrically the adults of these dwarfed temnospondyls with developmental sequences of larger species and show that the features previously associated with miniaturization in the clade are not consistent with the cranial novel arrangements expected from size constraints as in miniaturized extant tetrapods, but resemble the juvenile condition of larger temnospondyls. Therefore, it is the truncation of the ancestral ontogeny, and not miniaturization, the factor that played a major role in the morphological evolution of the Permian relatives of lissamphibians.

P-054 Developmental strategies of skeletogenesis in bichirs and sturgeons: comparative analysis of two disparate cranial architecturess

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Skeletal tissues exemplify the key vertebrate innovation. Among recent vertebrates, the Ray-finned fishes represent the most numerous and successful lineage and they also exhibit amazing variety of their skeletal architectures and phenotypic adaptations. Here, we present comparative developmental analyses of cranial skeletal tissues and structures in two early branching lineages of Ray-finned fishes, that differ essentially in their strategy of skeletogenesis. Whereas bichirs represent heavily armoured forms with massive exoskeleton, with thick ganoid scales and with dental structures that cover the whole oropharynx, sturgeons, on the contrary, are cartilaginous fishes with secondarily reduced skeleton and with teeth that are completely lost during larval development. Using exceptional embryonic series of the Senegal bichir (Polypterus senegalus) and the sterlet (Acipenser ruthenus), the formation and growth dynamics of their skeletal systems were described and compared. Application of morphometric approaches allowed semi-quantitative investigations of spatial expansions of individual cranial bones. Moreover,

homologous cranial elements were arranged into comparable developmental modules, what facilitated better interspecific evaluation of their transformation during craniofacial development. Our study revealed substantial differences in the initiation, number, and sequence of formation, but also in the growth dynamics of corresponding developmental modules between studied lineages. We thus suggest that these factors provide the developmental basis generating the disparate patterns of craniofacial architectures.

P-055 Evolution and development of nectar spurs

Cullen, Ellen V. (University of Cambridge, GBR)

Nectar spurs (tubular outgrowths of the petal) are hypothesized to be a „key innovation" which can lead to rapid speciation within a lineage and are important for pollinator specificity. However, there is still much to learn about nectar spur development. My PhD aims to probe both the morphological and molecular basis of nectar spur outgrowth. The species Linaria vulgaris (which has a nectar spur) and Antirrhinum majus (possesses only a nectar pouch, called a gibba) will be examined. A morphological characterisation of spur growth over time will take place and the number and size of cells in each species will be determined. Both a candidate gene and a transcriptome approach will be used to probe the molecular basis of nectar spur development. All of the above comparisons will be performed at key developmental stages of spur growth. The control of variation in nectar spur length will also be investigated, focusing on Linaria salzmannii and Linaria clementei, two closely related species which have extremely long and short spurs respectively. Preliminary results found that an increase in growth rate drives the increase in spur length at a morphological level, however cell size is not significantly different in mature spurs. Thus there must be a higher number of cells in the spur of L. salzmannii, perhaps due to increased cell division. These data add to knowledge about nectar spur development in a comparative context.

P-056 Unique variation in the active retinal peripheral zone among squamate reptiles

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The retina is a complex, layered tissue responsible for the perception of visual stimuli coming from the external environment. In contrast to mammals, the capacity for retinal regeneration in teleosts and amphibians, and to a lower degree in birds, is partly maintained by a stem cell population residing in the peripheral ciliary marginal zone (CMZ). However, little is known about morphogenesis and adult regeneration of retinal tissues in non-classical squamate models (lizards, snakes), despite both their unique regenerative capacity and great eye diversity (in terms

of size, structure, functionality). Our comparative study indicates that eye growth in squamates correlates with the maintenance of proliferative activity and expression of progenitor markers in the embryonic retinal margin. Proliferation, BrdU pulse-chase assays, and gene expression patterns at postnatal stages indicate an atypical location of putative stem cells towards the ciliary body at the retinal peripheral zone, and not in a CMZ-like region, as well as striking eye-size dependent variations in the amount of label-retaining cells in said region. Importantly, our preliminary data also show that this unique peripheral zone is active and responds to neurotoxin-induced retinal damage, strongly supporting that it contains the stem cell niche responsible for continued growth and regeneration of the squamate retina. Altogether, our study shows for the first time the existence of a putative retinal stem cell niche in adult amniotes. We expect that the integration of new animal models will lead to a better understanding of the genetic and biochemical mechanisms resulting in irreversible vision loss in humans, and our goals are to provide an evolutionary context to the key signaling pathways of regeneration.

P-057 Cells without borders: how syncytia and cells form the adult glass sponge body plan at metamorphosis

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Gastrulation involves complex morphogenetic movements that position blastomeres in the early embryo where they will form the future tissues of the adult. In sponges a „true" gut is not formed; instead gastrulation in the Porifera has been interpreted as either the formation of a bilayered ciliated larva or the development of the feeding chambers at metamorphosis. Glass sponges (Class Hexactinellida) are one of only two poriferan groups that already have clearly formed flagellated chambers as larvae. The fate of the larval chambers and of other tissues during metamorphosis is unknown. One species, Oopsacas minuta, found in submarine caves in the Mediterranean, is reproductive year round, but describing metamorphosis has been a challenge because the syncytial nature of the tissue makes it difficult to trace cell fates using conventional markers. We used three-dimensional models to describe larval tissue reorganization at metamorphosis in O. minuta. Glass sponges have a unique mix of independent cells and multinucleated syncytia that is established during embryogenesis. The identity of these components appeared to remain constant through metamorphosis. Changes included use of lipid inclusions to attach the larva anteriorly to the substrate; enlarging of flagellated chambers by production of collar flagella units; the appearance of canals between chambers, and importantly the loss of multiciliated cells that formed a belt around the larva. Larval flagellated chambers appear to be retained throughout metamorphosis becoming the kernels of the

first pumping chambers of the juvenile sponge. Importantly the ciliated cells with which the larva swims were discarded. As in the adult glass sponge there is no evidence that cellular components of the larva or settler are independently motile. In O. minuta therefore, the future feeding chambers are formed during embryogenesis and retained through metamorphosis to be the feeding epithelium of the adult sponge.

P-058 Central complex development and evolution: cellular and genetic mechanisms

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The central complex is an insect brain neuropil with higher order functions such as locomotor control or spatial orientation. Its structure is highly conserved in adult insects, but astonishingly the developmental timing differs greatly between species. For instance, in Schistocerca insects the central complex forms during embryogenesis while in Drosophila it develops postembryonically. Tribolium takes an intermediate position where the central complex forms partially during embryogenesis and is completed postembryonically. The cellular and molecular basis of such a heterochronic shift of brain development and how a conserved adult structure can show vastly different developmental schemata remains unknown. In this work we want to elucidate the cellular mechanisms and the exact developmental timing of heterochrony by comparing central complex development of Tribolium castaneum and Drosophila melanogaster. In order to mark comparable cell groups in both species, we will generate antibodies and transgenic tools (using CRISPR/Cas9 techniques) to mark cells that share the expression of the highly conserved transcription factor retinal homeobox (rx). rx is expressed in cells contributing to the central complex of both species and after knockdown a central complex phenotype is found in Drosophila as well as Tribolium. First, homology of a potential sub-group of rx-positive cells will be established in the adult brain of Tribolium and Drosophila. The developmental process will then be followed back from the adult to the embryo where rx expression starts. The detected differences will be correlated with neuroblast numbers, types, apoptosis, proliferation and cell division. This will hopefully provide insights into the cellular mechanisms underlying the heterochronic shift as well as its exact timing. We propose that the genetic marking of homologous cells and their comparison between species promises to reveal the cellular and developmental basis of brain evolution.

P-059 Role of the Nodal signaling pathway in amphioxus neural induction

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Neural induction (NI) is the process through which pluripotent cells are committed to a neural fate. This process seems to start during gastrulation in vertebrates, when the three embryonic layers are established and dorsal ectoderm becomes neuroectoderm. According to the â€œdefault modelâ€ , ectodermal cells acquire epidermal fate when exposed to Bone Morphogenetic Protein (BMP) signals that are present in the ventral region of the embryo. On the other side, lack of these signals triggers neural fate acquisition by default. This model is nowadays challenged by the presence of other molecular actors involved in NI. In fact, it has been shown that in vertebrates the dorsal organizer produces BMP antagonists, and other signals that might play an important role in this process. However, not much is known about NI in other chordates outside vertebrates and about the evolution of this process. To answer this question, we have focused our attention on the cephalochordate Branchiostoma lanceolatum. Cephalochordates (amphioxus) belong to the phylum chordata, together with vertebrates and tunicates, and constitute the earliest group that diverged in this clade. They all share several morphological characteristics such as a perforated pharynx, segmented muscles, a notochord and a hollow nerve chord. It has been previously shown by our team that, as vertebrates, the amphioxus presents an organizer (homologous to the Spemann organizer in Xenopus), the dorsal blastoporal lip. This organizer is able to induce formation of a secondary axis when grafted to a host gastrula; moreover, it also induces neural markers expression when grafted to ectodermal explants. The question is now to compare how NI is controlled at the molecular level between cephalochordates and vertebrates in order to better understand the evolutionary history of this process in chordates.

P-060 Pelvic, Pectoral, Median: The developmental basis of fin evolution

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The origin of paired appendages is a persistent problem in vertebrate evolutionary developmental biology. Unlike the forelimbs and hindlimbs of tetrapods, the pectoral and pelvic fins of non-sarcopterygian fishes have fundamental differences in morphology. This project will investigate the development of axial and appendicular structures in the paired and median fins in several basal fishes. Using contrast-enhanced microCT imaging we can make detailed visualizations of the developing morphology of the fins and their constituent tissues at different stages as a foundation for comparative 3D analysis. We are investigating the developmental timing and tissue origins of the external and internal structures of the pelvic fins, as compared with pectoral and median fins. As representatives of basal gnathostome lineages, we will examine two actinopterygian fish, namely trout (Oncorhynchus mykiss) and paddlefish (Polyodon spathula), and a cartilaginous fish, the bamboo shark (Chi-

loscyllium punctatum). Specific comparative data on the development of these structures will form the basis for further research on the pelvic girdle and fin development in fishes, and the results are expected to give more insight about the evolutionary origin of the paired appendages in vertebrates.

P-061 Exploring the biology of a three-gendered nematode

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The nematode Rhabditis sp. SB347 is a free-living species with an atypical breeding strategy, in which males, females and hermaphrodites co-exist. This mating system, named trioecy, is rare and thought to be evolutionary unstable as it would represent the transition between gonochorism (male/female) and hermaphroditism. However, trioecy and „trioecy-like"systems exist in some parasitic nematodes. For these nematodes, selfing individuals (hermaphrodites or parthenogenetic females) represent the infective/parasitic stage, while males and females are free-living. Could trioecy have been co-opted in the evolution towards parasitism? We have assembled, annotated and built a genetic map of the genome of Rhabditis sp. SB347. With these resources, along with empirical studies, we are exploring the biology of this unusual mating system. In particular, we found that the X chromosome seems to display severe segregation distortion and may play an important role in the dynamics of trioecy. Through a comparative genomics approach, we are also investigating how the evolution of mating systems can shape the genome's structure and content and what is the place of trioecy in the evolution of parasitism.

P-062 The tubular collar cord of hemichordates and the chordate neural tube: homology or homoplasy?

Kaul-Strehlow, Sabrina (University of Vienna, AUT)

Comparative gene expression analyses have revealed that the neural tube of chordate deuterostomes and the ventral nerve cord of polychaete protostomes exhibit a highly similar mediolateral architecture. On that basis, a likewise complex CNS has been proposed in the urbilaterian. Hemichordate enteropneusts, a group of non-chordate deuterostomes, possess a much less complex nervous system, yet a part of the dorsal nerve cord forms a hollow tube resembling the neural tube of chordates. Putative homology of this collar cord and the chordate neural tube is supported by ultrastructural resemblances. However, recent gene expression analyses are less conclusive and revealed contradicting results. The majority of data has been collected from Saccoglossus kowalevskii, a species showing a derived mode of development. In order to clarify this issue, we investigated the expression of neuronal regionalization genes in the indirect developing enteropneust Balanoglossus misakiensis. We focused on the development of the collar cord and

studied anteroposterior (six3/6, otx, engrailed) and mediolateral (pax6, dlx, nk2.1/2.2) patterning genes. Expression analysis shows that the tubular collar cord of B. misakiensis is positioned anteroposteriorly in a region corresponding to the vertebrate midbrain. However, mediolateral patterning of pax6, dlx, and nk2.1/2.2 is completely aberrant and has no corresponding domains in the chordate neural tube, neither in the midbrain region nor in the trunk. Under consideration of all available data (morphology, gene expression, and phylogenomic analyses), putative homology of the collar cord and chordate neural tube is evaluated.

P-063 Multiple origins of multicuspid teeth in squamate reptiles

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Strong selective pressures affect tooth complexity, which varies mainly due to the patterning of positive reliefs on the tooth surface – the cusps. Through cusp addition events, mammals have achieved considerable variation in terms of complex tooth morphologies during their evolution. At the developmental level, these events relied on the dynamics of enamel knots, the signaling structures controlling mammalian tooth growth. However, little is known about the development and evolution of teeth in other vertebrate groups. Here we present the first large-scale assessment of tooth morphologies in squamates (i.e., lizards and snakes), comprising over 450 extant and fossil species displaying a unique shape diversity. Geometric morphometrics reveal that complex tooth shapes in lizards significantly correlate with diet, since highly complex teeth with a high cusp number correlate with increased plant consumption. Lizard groups including an important proportion of herbivorous species notably show the broadest tooth shape variability. Based on the most recent phylogenetic data, ancestral character reconstructions indicate that the last common ancestor to all squamates was an insectivore with unicuspid teeth. Complex teeth then evolved multiple times independently, primarily during the Late Cretaceous. However, plant consumption evolved in current lizard groups only during the Cenozoic, substantially delayed from the initial increases in tooth complexity. Such results question the drivers of tooth phenotypic variation in lizards, as a true equivalent structure to the mammalian enamel knot system has yet to be identified. We thus provide insights on expression patterns of conserved regulatory pathways during the morphogenesis of complex teeth in different lizard species.

P-064 A comprehensive pipeline for identifiying lincRNAs on the basal-branching chordate Amphioxus

Herrera, Carlos (Universitat de Barcelona, ESP)

Among the numerous classes of RNAs, long non coding RNAs (lncRNAs) are similar in terms of expression and gene structure to the mRNAs but lack the potential to encode proteins. Over the last years, lncRNAs have been proven to play important roles in gene regulation, and have shown to be involved in many key developmental processes. However, the low sequence conservation of lncRNAs has hindered the identification of deep orthologues among distantly related species, hence the evolutionary dynamics of lncRNAs has been scarcely studied, and few data are known at evolutionary key-nodes of animal evolution. We aim to identify the lncRNA complement in the cephalocordate amphioxus, the best proxy to the key evolutionary node of the origin of chordates and vertebrates. For this, we used strand specific RNA-seq data from several adult tissues and developmental stages of Branchiostoma lanceolatum. We used first the CPAT software in order to assess the coding potential of each canonical transcript, then a selection of probably non coding, multiexonic gene structures (at least 2 exons) and a minimum length of 300 nucleotides. Transcripts were blasted using blastx against the non-redundant protein database, and the ones that did not had a significant hit were filtered again with hmmer searches to eliminate the ones with similarity to conserved protein domains upon 6-frame translation. This yielded around 1700 transcripts that were classified according to their relative position among coding genes into intergenic, antisense, intragenic or overlapping. Using the intergenic portion (lincRNAs) we have developed the scripts for finding conserved microsynteny between Branchiostoma lanceolatum, Homo sapiens, Danio rerio, and Strongylocentrotus purpuratus, and more organisms will follow soon. This approach pointed at some candidates that are being tested right now. Some of the current and future work includes In Situ Hybridization and, if possible, knock-outs with CRISPR."

P-065 **A comparative differential expression analysis approach to the study of Hox3/zen gene evolution in insects**

Gurska, Daniela (University of Cologne, DEU); Panfilio, Kristen A. (University of Cologne, DEU)

Unlike canonical Hox3 genes, which function in embryonic tissue specification along the anterior-posterior body axis in all bilaterians, the insect orthologues, known as zerknÃ¼llt (zen), have undergone multiple instances of functional divergence. To date, all known zen genes are instead involved in the development of the extraembryonic membranes (EEMs). The EEMs have a protective role allowing embryos to survive in diverse ecological niches, hence contributing to the eminent evolutionary success of insects. Key evolutionary changes in EEMs correlate with changes in zen genes; it is only within winged insects that complete EEMs are observed as a morphological innovation, and that zen concomitantly acquired a strictly extraembryonic role. However,

zen genes differ in the exact nature of their role, functioning either in early tissue specification or in late morphogenesis. Therefore, we focus on the holometabolous beetle Tribolium castaneum, as two diverged paralogues were described: one with early (Tc-zen1) and one with late function (Tc-zen2). We present the mRNA and protein expression profiles of both Tribolium zen genes during early and late embryonic development. To reveal the degree of divergence in transcriptional targets between the paralogues during early development, we knocked down (via pRNAi) the Tribolium zen genes and performed RNA-seq. Subsequent differential expression analysis suggests that indeed the paralogues do not share transcriptional targets. Additionally, principle component analysis suggests that despite the early expression of both paralogues, the impact of Tc-zen2 knockdown on early transcriptional control was significantly lower than for Tc-zen1, which is consistent with Tc-zen2 having a late function. Moreover, we confirmed the presence of Tc-Zen2 until the late developmental stages when its function takes place. Future planned RNA-seq after Tc-zen2 RNAi during late development will clarify whether the different roles of early and late zen genes arose upstream, downstream, or within the zen genes themselves.

P-066 Evolution of olfactory channels in Drosophila

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Sensory systems provide fascinating examples of exquisite developmental regulation, as well as dynamic evolutionary modifications. Olfactory systems are particularly intriguing because of the vast and ever-changing chemical space organisms are exposed to in the environment. The neural channels that are responsible for detecting odors are structurally and functionally diverse, expressing different combinations of sensory receptors, displaying distinct breadths and kinetics of odor-evoked activity, and targeting discrete regions in the brain. How new olfactory neuron classes arise during evolution is unknown. In order to identify the genes contributing to cell-specific differences between related sensory neurons, we have taken a genome-wide transcriptional profiling approach in the olfactory system of Drosophila melanogaster. We have applied TaDa (Targeted DamID) to seven populations of closely-related olfactory sensory neurons, which express different members of a clade of genes encoding organic acid-sensing Ionotropic Receptors. Our neuron-specific transcriptional profiles largely recapitulate the evolutionary history of the sensory receptor genes that they express. This suggests that the evolution of sensory neuron populations may follow a similar „duplication and divergence" path as the olfactory receptor genes that they express. These data additionally identify many differentially-regulated loci among cell classes, whose functions during development or in mature neurons we are now pursuing.

P-067 Genetic paths underlying the convergent evolution of pigmented spots on fly wings

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When a phenotype evolves twice in independent lineages, are the underlying molecular mechanisms similar? In the case of similar pigmentation patterns that have arisen independently in two fruit fly species, Drosophila tristis and Drosophila biarmipes, the question, becomes: is there a unique genetic path to gain a pigmentation spot on the wing? Each pigmentation pattern is prefigured by the developmental expression of yellow, a gene necessary for the production of black pigments. In each case, yellow expression results from a novel enhancer, both enhancers sharing no homology. To understand how these new regulatory activities have independently emerged, we are performing an RNAi screen to identify transcription factors controlling each enhancer. We will then characterize the candidate transcription factors identified, and we will evaluate the degree of convergence in the control of the activity of the two enhancers by closely comparing the relationship between their structure and their function. Preliminary results suggest that the transcription factor Distal-less is involved in the regulation of the enhancers of these two species.

P-068 The sequencing and manual curation of the first water strider genome (Gerris buenoi)

Armisén, David (Institut de Génomique Fonctionnelle de Lyon, FRA); The water strider genome consortium)

Although Gerromorpha's unique natural history of water surface invasion made them established models for ecology and evolution, little is known about the developmental genetic mechanisms underlying such adaptations. Recent efforts to establish water striders as new models for evolutionary developmental genetics allowed understanding some of the genetic changes responsible for phenotypic adaptations to water surface life. However, the severe lack of sequence resources, including a reference genome, hampers our ability to identify the genes and the genetic changes associated with their phenotypic adaptations. Here we report the first genome of a Gerromorphan species, the water strider Gerris buenoi, using NGS technology as well as collaborative manual annotation of genes involved in a number of phenotypic adaptations to live on water surface. Results of these studies provide some hints into the genomic basis of water surface invasion, such as expansions of the Tweedle cuticle gene family, probably associated with specific body sha-

pe. Other expanded gene families include chemosensory genes, possibly linked with prey detection, as well as large tandem duplication of genes involved in detoxification of hydrophobic compounds. Altogether, Gerris buenoi genome sequencing and analysis provide a great opportunity for integrating ecology, evolution, and developmental genetics.

P-069 Genome-wide screening of early patterning genes in spider Parasteatoda tepidariorum

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The common house spider Parasteatoda tepidariorum has emerged as a valuable non-insect model organism for studying comparative embryology. Embryos of this spider, unlike Drosophila embryos, adopt regulative development. At earliest stages, the spider embryo is spherical in shape with no morphological sign of the future body axis. Following blastoderm formation, the surface cells shift to a hemisphere of the egg to form the germ disc (stage 3), in which the first embryonic axis becomes evident. The molecular mechanisms of germ-disc formation and primary axis formation, however, are little known. Here, we conducted RNA sequencing (RNA-Seq) analysis using small portions of single spider embryos to identify the genes that show region-specific expression and that play important roles in early embryogenesis. RNA-Seq libraries were prepared from a small number of cells that were isolated from the central, peripheral or middle portion of a single embryo at stage 3 using a glass capillary. About 10-20 millions of reads per library were obtained using an Illumina MiSeq sequencer. The read data were mapped to the reference genome by a BLAT algorithm, and gene expression levels were counted by a HTSeq program. For data normalization and detection of differentially expressed genes (DEGs), the iDEGES/edgeR pipeline was used. These analyses enabled us to list dozens of genes showing significant differences in expression levels between the above three portions. Functional screening of the listed genes using parental RNAi techniques is underway.

P-070 Comparative tissue-specific transcriptomics of priapulids allows the characterization of blood and nephridia cell types and provides insights into their evolution

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Multicellular animals require complex regulatory mechanisms to create hundreds of distinct tissue types from a single genome in order to form specialised organs. Most of these organs (e.g. blood and nephridia) are shared among animals but their evolutionary origin is still under debate. Molecular studies in vertebrates, flies and flatworms have shown that conserved transcriptional programmes are involved in blood and neph-

ridia formation. However, due to the low taxon sampling, we still have a limited view of the developmental and transcriptional regulation of these tissues. We have generated tissue-specific transcriptomes from two priapulid species (Ecdysozoa, Scalidophora), in order to understand similarities and differences in the gene complement of blood and nephridial cells among animals. By using publicly available and newly generated transcriptome data from Halycriptus spinulosus and Priapulus caudatus, we have created species-specific reference transcriptomes. Following assembly and removal of redundant sequences, we have predicted and annotated putative protein-coding sequences using GO, PFAM and KEGG databases. To identify tissue-specific and differentially expressed genes between tissues at intra- and inter-species level, we have aligned high quality-filtered reads from each tissue against these reference transcriptomes. From this analysis, we classified genes as similarly expressed between tissues, preferably expressed in blood or preferably expressed in nephridia. Orthologous analysis revealed a number of conserved but also novel transcription factors and signalling molecules with potential roles in tissue-specific regulation. Further characterization of these genes accompanied by a comparative transcriptomic approach in a much broader taxon sampling will provide insights into the evolution of tissue and cell type formation in animals.

P-071 The role of FoxQ2 in insect brain development

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The central complex (CX) is a higher order structure in the insect brain that is involved in sky compass orientation, flight control, locomotor behavior, courtship and memory. It consists of neuropils including protocerebral bridge (PB), central body (CB) with upper (CBU) and lower unit (CBL), also called fan-shaped body (FB) and ellipsoid body (EB). Both CX function and development are highly studied in Drosophila melanogaster. However, in Drosophila, the CX develops during late larval stages which prohibits to study its embryonic development. As consequence, the genetic signals specifying the identity of the neuroblasts arising in the anterior region remain poorly studied. Therefore, we use Tribolium castaneum to study CX development. In Tribolium it is partially formed during embryogenesis and this model system offers a number of experimental possibilities. (Efficient systemic RNAi, transgenic approaches, tools for gene misexpression). The aim of this project is to identify the neuroblasts and their lineages that contribute to central complex development and understand the genes that are required for their spatial specification. Ultimately, we would like to understand the cellular and molecular differences that lead to the different timing of CX development in Tribolium versus Drosophila. We have shown by RNAi

that Tc-FoxQ2 is required forCX development . We are developing tools for analyzing neural development in Tribolium (e.g. generation of an antibody against FoxQ2 and of an enhancer trap line with CRISPR/Cas9 strategy to mark FoxQ2 expression in vivo) with which we will study the phenotype.

P-072 Whole Transcriptome Profiling during embryogenesis of the echiuran worm Urechis unicinctus

Cho, Sung-Jin (ChungBuk National University, KOR); Han, Yong-Hee (National University, KOR)

U. unicinctus is well adapted for a study of complete embryological and larval development. In early cleavage stages U. unicinctus desplays a isolecithal egg and holoblastic cleavage planes, but mid-late cleavage stage has a spiral cleavage pattern. The goal of this research was to enhance our understanding of gene expression during embryogenic development. Here we report the transcriptome profiling analysis of U. unicinctus early developing embryos using RNA-Seq as an attempt to gain insight into the molecular and cellular events associated with radial cleavage and spiral cleavage stage. This transcriptome dataset will be a valuable resource for molecular analyses of radial and spiral cleavage pattern in U. unicinctus and will serve as a starting point for comparisons radial species with spiral species. Futhermore, we have used immunostaining for beta-tubulin to follow spindle dynamics during cleavage stage of U. unicinctus.

P-073 Unusual rodent homeobox genes in preimplantation development

Royall, Amy (University of Oxford, GBR)

Homeobox genes are present throughout the eukaryotes. All homeobox genes encode proteins with a DNA-binding domain, the homeodomain, and most are deployed in embryogenesis. The evolution of genes encoding transcription factors is interesting due to the implications of changing vast gene-regulatory networks, particularly if there have been gains and losses of genes as seen in homeobox gene evolution. Here, we investigate the evolution and function of two groups of homeobox genes that have lineage specific expansions in rodents: CrxOS and Obox. Previous studies have demonstrated roles for CrxOS and Obox members in early mouse embryonic development, however the full repertoire of their functions remains unknown. We have investigated the evolution and function of these genes and are beginning to understand how newly evolved homeobox genes acquire function after expansions.

P-074 The extra-ocular muscles of the lamprey and their evolutionary implication

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The ancestral configuration of the vertebrate head has long been an intriguing topic in comparative morphology and evolutionary biology.

One peculiar component of the vertebrate head is the presence of extraocular muscles (EOMs), the developmental mechanism and evolution of which remain to be determined. The head mesoderm of elasmobranchs undergoes local epithelialization into three head cavities, precursors of the EOMs. In contrast, in avians, these muscles appear to develop mainly from the mesenchymal head mesoderm. Importantly, in the basal vertebrate lamprey, the head mesoderm does not show overt head cavities or signs of segmental boundaries, and the development of the EOMs is not well described. Furthermore, the disposition of the lamprey EOMs differs from those the rest of vertebrates, in which the morphological pattern of EOMs is strongly conserved. To better understand the evolution and developmental origins of the vertebrate EOMs, we explored the development of the head mesoderm and EOMs of the lamprey in detail. We found that the disposition of lamprey EOM primordia differed from that in gnathostomes, even during the earliest period of development. We also found that three components of the paraxial head mesoderm could be distinguished genetically (premandibular mesoderm; mandibular mesoderm; hyoid mesoderm), indicating that the genetic mechanisms of EOMs are conserved in all vertebrates. We conclude that the tripartite developmental origin of the EOMs is likely to have been possessed by the latest common ancestor of the vertebrates. This ancestor's EOM developmental pattern was also suggested to have resembled more that of the lamprey, and the gnathostome's disposition is likely to have been established by a secondary modification that took place in the common ancestor of crown gnathostomes.

P-075 Genetic interactions regulating leg length in water striders

Amélie Decaras (Institute of Functional Genomics of Lyon, FRA); Toubiana, William (Institute of Functional Genomics of Lyon, FRA); Khila, Abderrahman (Institute of Functional Genomics of Lyon, FRA)

Understanding the origin of species diversity is a major challenge for biologists. The semi-aquatic bugs (Heteroptera, Gerromorpha) colonized water surfaces and diversified to occupy many ecological niches ranging from small ponds to open oceans. Here we investigate the developmental genetic mechanisms modulating leg allometry; a key trait that is important for life on the water surface. These insects have generally longer legs allowing them to generate efficient movement on the fluid surface and in addition to this elongation some derived lineages such as the Gerridae, evolved a new leg ground plan allowing them to evolve a new mode of locomotion through rowing. We hypothesize that the differences in leg length between these species are encoded by differences in the activity of the genes controlling leg development. In order to study the emergence of this new leg ground plan we used the transcriptome of a derived species to establish a list of candidate genes. From this list of candidates we identified the gene shavenbaby, known for its

role in trichrome formation in Drosophila, as a regulator of leg elongation in derived species. Furthermore we show that a network involving pri (polished rice peptides), UBR3 (ubiquitin protein ligase E3), and Ubx (Ultrabithorax) that interact together for the formation of trichomes in Drosophila is required for leg elongation in Gerridea. These results suggest that the pathway required for trichome formation in Drosphila has been co-opted for the leg elongation in the Gerridae, but we still don't know exactly how these genes interact together in water striders

P-076 Ontogeny of the basicranium in lizards

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The neurocranium of vertebrates is mainly derived from early cartilaginous anlagen, the so-called chondrocranium. In general, two initial bar-shaped and paired chondrifications flank the notochord, the more rostral trabecles and the more caudal parachordals. In most reptiles, there is an additional component, the transverse acrochordal cartilage, which is placed between trabecles and parachordals. All these elements compose the base of the future chondrocranium. There are several theories concerning the development and interrelationship of these elements; i.e., the development of the basal plate, the formation of the basicranial fenestra, and the role of the acrochordal cartilage in the formation of crista sellaris. In the present study, we reexamined the basicranial development in one of the previously well-described skink species Chalcides ocellatus and compare it with that of Lacerta agilis. We found that C. ocellatus shows very similar conditions of early chondrocranial development when compared to L. agilis. The anterior most part of the notochord is not embedded into the basal plate as it was previously reported. It remains free. The medial edges of the parachordals form the lateral walls of the basicranial fenestra. Only the posterior portions of the parachordals fuse and form the basal plate. The space in-between the parachordals is fulfilled with a thin layer of cells, which, however, never chondrifies. The anterior most tips of the parachordals later fuse with the posterior edge of the acrochordal cartilage, which finally delimitates the basicranial fenestra anteriorly. Thus, crista sellaris does not form from the most anterior part of the basal plate, as it was previously thought, but from the acrochordal cartilage. We consider the observed processes a common development at least in lizards and discuss a variety of methodological approaches and differences in data interpretation as reasons for the anatomical differences reported in the literature.

P-077 Evolutionary & developmental analysis of the Alx homeobox gene family in chordates

Wang, Huijia (University of Manchester, GBR)

Members of the Alx homeobox gene family are considered to be

directly linked to craniofacial development in mammals. Comparison of Alx homeobox genes can potentially provide insights into how they contribute to the craniofacial development from a common ancestor of chordates. Our previous phylogenetic and comparative genomics studies showed there are three Alx genes (Alx1, Alx3 and Alx4) in common ancestors of Gnathostomata, derived from one ancestral Alx gene, which is probably due to two-round duplication of genome. Recently, we have identified two lineage-specific duplications of Alx1 in both Amphioxus Branchiostoma floridae and Branchiostoma lanceolatum genome. The Alx1 protein is essential for the formation of the head and face during embryonic development. Mutations in the Alx1 gene can lead to frontonasal malformation in humans and mice, and most recently, in cats. A latest study across Darwinâ€™s finch species indicated Alx1 gene also has a strong impact on the diversity of beak shape. Previous morpholino studies in our lab have demonstrated a novel role of Alx1 gene in mediating the migration of cranial neural crest (CNC) cells in zebrafish. Whole-mount in situ hybridization was performed to compare Alx1 expression domains in different model animals. Expression of Alx1 was mainly observed in the most anterior somite of amphioxus embryos. Zebrafish Alx1 was first expressed in the rostral mesoderm and then in cranial neural crest cells with the extension to the frontonasal and maxillary regions. Later, the expression was found in the pectoral fin promidia. Similar to zebrafish, the expression of Alx1 in medaka was also found in migrating neural crest cells alongside the embryo bodies. Taken together, our data suggest an essential function of Alx1 in regulating the migration of CNC cells across species and possibly contribute to the evolution of vertebrate head. .

P-078 **High variation in the onset of ossification and conserved regions of bone contact in the bony skull development of marsupial mammals**

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Development in marsupials is specialized towards an extremely short gestation and highly altricial newborns. As a result, marsupial neonates display morphological adaptations at birth related to functional constraints. However, little is known about the variability of marsupial skull development and its relation to adult skull anatomy. We studied bony skull development in five marsupial species. The relative timing of the onset of ossification was compared to literature data and the cranial ossification sequence of the marsupial ancestor was reconstructed using squared-change parsimony. The onset of ossification shows a high range of variation with little biological implications. However, for the first time, this study presents observations on the timing of the initial developmental contacts of cranial bones and their evolutionary and ecological

implications. Although certain bone contacts display high levels of variation, other connections are quite conserved. Bones that surround the oral cavity are generally the first to connect and the bones of the occipital region are among the last. The sequence of bone connections can be related to the size of the respective bones in adulthood. We discuss methodological aspects of heterochrony and skeletogenesis and conclude that bone contact is preferable over onset of ossification for studying cranial bone diversity.

P-079 A history of polydactyly in development and evolution

Lange, Axel (University of Vienna, AUT); Müller, Gerd B. (University of Vienna, AUT)

Polydactyly, the occurrence of supernumerary digits or toes, is a frequent variation in humans and other tetrapods. The earliest references of polydactyly come from the Middle Assyrian Empire, and the developmental origins of polydactyly were addressed in ancient Greece and Rome. We revisit several classical works, such as the perceptive writings on the inheritance of polydactyly by Pierre-Louis Maureau de Maupertuis in the 18th century and the forgotten treatise of Francesco Marzolo in the mid 19th century. Furthermore, we analyze how the scientific concepts concerning the processes of development and evolution were influenced by the findings of polydactyly. Polydactyly was a topic in many of the classical disputes on the nature of development, including the preformation-versus-epigenesis and the genetic-versus-epigenetic debates, but extra digit formation also plays a role in the molecular and genetic concepts of development valid today. In the evolutionary domain, polydactyly was used in the criticism of the gradualist account of variation underlying Darwin's theory, whereas contrasting views on discontinuous variation receive support from recent findings in experimental biology and the modeling of limb development.

P-080 Epigenetic mechanisms of phenotypic plasticity in response to changing environments in cockroaches

Villalba, Mariana (University of Manchester, GBR)

Phenotypic plasticity plays a major role in evolution as it enables the expression of cryptic variation, facilitates rapid adaptation to changing environments and can be a precursor to evolutionary novelties. However, to date little is known about the molecular mechanisms of plasticity, although epigenetic mechanisms have been implicated to play role in developmental and phenotypic variation seen in insects. In this project we aim to describe the developmental consequences of changing environments in the live-bearing cockroach Diploptera punctata and relate them to differences in global methylation patterns. Modern cockroaches are considered one of the more ancient groups of terrestrial arthropods. They arose around 200 Mya, and have since shown a great ability to ea-

sily adapt to widely differing environments, making them a good model to study phenotypic plasticity. In a first step, using ELISA-like assays, we quantified global-genome cytosine methylation and hydroxymethylation levels in different tissues and stages of D. punctata. We then manipulated the nutritional quality of the diet to represent good and poor conditions. Subsequently, the cytosine global â€"methylation levels were compared among individuals that were raised under different dietary conditions to establish any association between global methylation differences and variation in development and the adult phenotype.

P-081 Outside-in: studying the invagination process during embryogenesis of the milkweed bug Oncopeltus fasciatus

Novikova, Asya (Hebrew University of Jerusalem, ISR)

Most work on insect embryogenesis focuses on a small number of model species. This ignores the diversity of insect developmental mechanisms and patterns. We work on the hemipteran Oncopeltus fasciatus, which maintains many plesiomorphic characteristics in its development, and forms a useful outgroup to the well-studied holometabolous insects. Our main focus up to now has been the genes that regulate early patterning and the interactions between them in Oncopeltus. In order to broaden our perspective we have recently incorporated cell and tissue dynamics into our research program. Early embryogenesis in Oncopeltus can be clearly divided into two distinct stages: the blastoderm stage, in which a yolk mass is surrounded by single layer of cells, and the germband stage, in which a segmenting embryo is embedded within the yolk. The transition between these two stages is through a process of invagination. This is a fascinating process in terms of cell dynamics, and it is still unclear what forces dictate the migration of the cells from the surface into the yolk. To untangle this mystery, we established a protocol for fluorescent labelling of alpha-tubulin in Oncopeltus embryos. This method gives us a high-resolution view into the cellular dynamics of the process and allows us to characterize and compare cell shape and density throughout the embryo and over the entire invagination. These results provide a basis for future comparisons of cell and tissue dynamics between wild type embryos and embryos silenced for genes known to be essential for proper invagination. This will connect different levels of biological organization and improve our understanding of the mechanics of embryogenesis."

P-082 Characterization of gene regulatory network for adult skeletogenesis in a starfish Patiria pectinifera: Implications for innovation of larval skeletons in echinoderm

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The larval skeleton of echinoderms is thought to have been acquired by co-option of the adult skeletogenic system. The skeletal tissues in adults are shared by all five groups of echinoderm (sea lily, starfish, brittle star, sea cucumber, and sea urchin), whereas larval skeletons are formed in only brittle star, sea cucumber, and sea urchin embryos. Therefore, it has been believed that larval skeletons were innovated by heterochronic transfer of the adult skeletogenic mechanism into embryos of their ancestor. In fact, previous study showed that a part of regulatory genes responsible for larval skeletogenesis of sea urchins are also expressed in the adult skeletogenic regions of the sea urchin and/or starfish. Since the comprehensive gene regulatory network model in the larval skeletogenic cell lineage of a sea urchin Strongylocentrotus purpuratus is available, studies on the innovation of larval skeletons in echinoderm provide valuable information to understand the process for generation of novel characters at the gene regulatory network level. To explore how the larval skeletogenic system was established, we are currently trying to build the gene regulatory network model for adult skeletogenesis in echinoderm, which would contribute for elucidation of the "origin" of the larval skeletogenic system. In the present study, we choose a starfish Patiria pectinifera as an experimental model, and performed expression analysis of 92 regulatory genes during larval stages when adult skeletons are formed. Based on these data, we discuss the adult skeletogenic mechanism and the co-option event for innovation of larval skeletons in echinoderms.

P-083 Effect of ANO5 on osteoblast differentiation

Hu, Ying (Capital Medical University School of Medicine, Beijing, CHN)

Gnathodiaphyseal dysplasia (GDD; MIM#166260) is a rare skeletal disorder with autosomal dominant pattern and characterized by cemento-osseous swellings of jawbones and fragile long bones with diaphyseal sclerosis. The mutations in ANO5/TMEM16E gene which encodes a member of the calcium-activated chloride channel family, has been identified to be associated with GDD. In this study, we utilized the MC3T3-E1 pre-osteoblast cell lines (clone 14) to study effects of ANO5 on osteoblast differentiation. Knocking down the ANO5 gene with specific shRNA in MC3T3-E1 cell lines (clone 14) resulted insignificantly increased expression of osteoblast markers osteocalcin(20-fold),ï ¡1-collagen 1(up to 1.4-fold), Runx2(up to 2-fold)and osterix(up to 2-fold) messages in a stage-specific manner over a 21-day period compared to untransfected and scrambled controls. Alizarin red staining at culture days 14 and 21 indicated increased mineral nodule formation in Ano5 knock-down cultures. The expression of endogenous ANO5 protein in MC3T3-E1 cells increased consistently during a 21-day MC3T3 culture period. These evidences suggest that ANO5 play an important role in osteoblastogenesis as a negative regulator and we conclude that functional defect of ANO5

protein enhance osteoblast differentiation and possibly regulate bone matrix deposition. The effect of mutant ANO5 in osteoblasts may in part explain the diaphyseal hyperostosis, the severe bone resorption in the jaws and the replacement by soft fibro-osseous tissue with characteristic psammamatoid inclusions. In future, knockout mouse model should be taken into account to reveal the precise mechanism on how the mutant ANO5 results in the GDD phenotypes.

P-084 Comparative transcriptomics of eye and head development in three closely related Drosophila species

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The development of an organism and its organs is controlled by the action of gene regulatory networks (GRNs). These networks need to be tightly controlled. However in an evolutionary context, some nodes of the GRNs need to be flexible to allow morphological differences in the adults to occur. To determine the molecular changes that lead to variation in adult morphology, we study head development in the three closely related Drosophila species, D. melanogaster, D. simulans and D. mauritiana. Although these species show clear natural variation in size and shape of their compound eyes and the adjacent head cuticle, it is expected that the GRNs governing eye and head development are similar enough to compare them. We generated and analysed a comparative developmental transcriptome obtained from eye-antennal imaginal discs of the three species at three important developmental stages. We clustered genes by their expression levels to identify potentially co-expressed genes. Since all genes that exhibit a similar expression profile are likely to be regulated by similar transcription factors, we can find out more about the putative regulators of genes that are differentially expressed between the three species. This analysis revealed that the GATA factor Pannier (Pnr) is one of these putative regulators. The generation of a high confidence list of putative Pnr target genes allows us to get a better insight into the mode of function of Pnr during eye development. With this systematic analysis of our transcriptome dataset we provide an excellent basis for future studies aiming at identifying the molecular basis of differences in head morphology between Drosophila species."

P-085 The role of SFRP2 in multi-differentiation potentials of stem cells from apical papilla

Xia, Dengsheng (Capital Medical University School of Medicine, Beijing, CHN)

Objectives: Dental tissue derived mesenchymal stem cells (MSCs) are easily obtained and are considered as a favorable cell source for tissue engineering. It is unclear how much the regulation of direct differentiati-

on restricts their application. SFRP2, a WNT signaling modulator, competes with the frizzled receptor and regulates the WNT signaling pathway. The objective of the present study is to investigate the effect of SFRP2 on MSC differentiation. Methods: Here we used stem cells from apical papilla (SCAPs) to study SFRP2 functions. The gain and loss of function experiment of SFRP2 were performed by lentivirus infecting to overexpress or silence SFRP2. SCAPs were cultured in the specific inducing medium for adipogenic, neurogenic, or chondrogenic differentiation. The Oil Red O staining, Alcian Blue staining and real time RT-PCR were performed to examine the differentiation potentials. Results: We found that overexpression of SFRP2 enhanced adipogenic and neurogenic differentiation in SCAPs. In addition, overexpression of SFRP2 up-regulated the expressions of stemness-related genes, SOX2 and OCT4. SOX2 and OCT4 were significantly inhibited after silence of SFRP2 in SCAPs. Conclusions: our results suggested that SFRP2 could enhance the adipogenic and neurogenic differentiation potentials of SCAPs by up-regulating SOX2 and OCT4, and provided useful information for the molecular mechanism underlying directed differentiation in dental tissue derived MSCs.

P-086 IGFBP5 enhanced osteogenic differentiation potentials of mesenchymal stem cells via JNK and MEK/Erk signaling pathways

Shan, Zhaochen (Capital Medical University School of Medicine, Beijing, CHN)

Objectives: Mesenchymal stem cells (MSCs) mediated tissue regeneration represents a promising strategy for tissue defects, but their molecular mechanisms remain unclear; this has restricted use of MSCs. Our previous study indicated IGFBP5 exerted a valuable effect on osteogenic differentiation of MSCs, but its molecular mechanism underlying directed differentiation remains unclear. Here, we investigated how IGFBP5 could regulate the osteogenic differentiation potential in MSCs. Materials and methods: PDLSCs were isolated from periodontal ligament in the middle one-third of the root. WJCMSCs were obtained from ScienCell Research Laboratories. Lentiviral IGFBP5 shRNA was used to silence IGFBP5 gene expression in PDLSCs. Retroviruses expressing Wild type IGFBP5 with Flag tag was used to overexpression IGFBP5 in WJCMSCs. The MAPK pathway involvement was subsequently investigated in vitro. Alkaline phosphatase (ALP) activity and Alizarin Red staining were used to assess differentiation capacity as well as MAPK pathway involvement. Results: Phosphorylated c-Jun N-terminal kinase (p-JNK) and phosphorylated extracellular regulated protein kinases (p-Erk1/2) in IGFBP5 overexpressed WJCMSCs increased remarkably; consistently, silence IGFBP5 could effectively inhibited the expressions of p-JNK, p-Erk1/2 and p-MEK1/2 in PDLSCs. Furthermore, inhibition of JNK by its inhibitor, SP600125, or MEK/Erk signaling by its inhibitor, PD98059, dramatically blocked IGFBP5-enhanced osteogenesis. Conclusions: Our results showed that

IGFBP5 prompted osteogenic differentiation potentials of MSCs via JNK and MEK/Erk signaling pathways.

P-087 Analysis of senescence-related differentiation potential and gene expression profiles in human dental pulp stem cells

Fan, Zhipeng (Capital Medical University School of Medicine, Beijing, CHN)

Introduction: Dental pulp stem cells (DPSCs)-mediated dental pulp regeneration is considered as a promising method for treatment of deep caries with pulpitis, enabling conservation and restoration of teeth. However, mesenchymal stem cells (MSCs) senescence is an adverse factor for the perspective of cell-based therapies. In this study, we investigated the characteristics and expression profiles of DPSCs from young and old donors. Methods: DPSCs from young and old donors were cultured in differentiation medium and then detected their differentiation potential. Long noncoding RNA (LncRNA) microarray assays and bioinformatic analysis was performed to investigated the differences in lncRNA and mRNA expression profiles between DPSCs from young and old donors. Results: We found that DPSCs from young donors exhibited more powerful proliferation ability, osteogenic and adipogenic differentiation potentials compared with DPSCs from old donors. In DPSCs from young donors, numerous lncRNAs were significantly up-regulated (n=389) or down-regulated (n=172) compared to DPSCs from old donors. Furthermore, 304 mRNAs were differentially expressed including 247 up-regulated genes and 57 down-regulated genes in DPSCs from young donors. Bioinformatic analysis identified that several pathways may be associated with DPSCs characteristics, such as Cell cycle, RNA transport, etc, and revealed that NFYB, GTF2B and NR3C1 were identified as core regulatory factors and FR249114, FR299091 and ENST00000450004 were identified as core lncRNAs. Conclusions: Our results indicated that senescence impaired the proliferation and differentiation potentials of DPSCs. We also provided insight into the mechanisms responsible for the senescence in DPSCs.

P-088 Embryonic expression patterns of Sox9-related genes in the hagfish: implication for the evolution of the vertebrate axial skeleton

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Segmentally arranged vertebral elements comprising cartilaginous or body nodules associated with the notochord are one of the representative morphological characteristics that define the vertebrates. The status of this morphology has been a central issue in the evolutionary origin

of the vertebrates. The hagfishes, one of two groups of extant jawless vertebrates, had been believed to lack vertebral elements. However, from our previous studies in the inshore Japanese hagfish (Eptatretus burgeri), it was revealed that this animal also has cartilaginous vertebral elements at the caudal region; the hagfishes and gnathostomes conserved common gene expression patterns in Twist and Pax1/9 (sclerotome markers) as well as Biglycan/Decorin (an extracellular matrix gene). To investigate how molecular mechanisms to form vertebral elements more in details, we investigated embryonic expression patterns of two hagfish Sox9 related genes (designated as EbSox9 and EbSoxE); their homologous are known as chondorogenesis marker in the other vertebrates. Mesenchymal cells at the ventral side of caudal region, neural tube at the pharyngular stage embryo and chondrocytes in the fin ray primordia at the pre-hatching stage embryo express both EbSox9 and EbSoxE genes; their expression patterns are overlapped in these regions. On the other hand, myotomal region and inside of notochordal sheath express EbSox9, but these region do not show evident signals of EbSoxE. From distantly related molecular sequences of these genes, it is hypothesized that their diverged expression patterns might be reflect their long evolutionary course.

P-089 Ranunculacean flower terata: morpho-anatomical characterization and clues about floral developmental genetics and evolution

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Teratological organisms originate from developmental anomalies, and exhibit structures and/or a body organization that deviate from the species standard. In plants, teratological forms are often of horticultural interest. However, besides their aesthetic value, these monsters give essential clues about the formation of the wild-type groundplan. We focus on flower terata, which can be affected in their sterile and/or fertile organs, with special emphasis on the Ranunculaceae. The diversity of perianth shapes and organizations in flowers of this family is huge, and is even increased when anomalies occur during organo-and/or morphogenesis. Research on Ranunculacean flower terata has been overlooked since the middle of the 20th century, and our aim is to reactivate studies in this field. We (I) review records of flower terata in the buttercup family, (II) explore the developmental and morpho-anatomical features of flowers from horticultural varieties of Delphinium and Aquilegia, especially in the scope of actinomorphy, zygomorphy, or asymmetry exhibited at different levels and degrees, and (III) provide hypotheses relative to the genetic determinism of these deviant phenotypes and address the

issue of their evolutionary potential. We expect Ranunculaceae species to become model organisms in flower teratology studies, focusing on morpho-anatomy as well as on evo-devo or evolutionary ecology.

P-090 Flower development schedule and BC gene expression patterns in two morphs of Nigella damascena (Ranunculaceae) differing in floral architecture

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„Nigella damascena is an annual species of Ranunculaceae native to the Mediterranean Basin. The two floral morphs of N. damascena differ in the identity and number of perianth organs and in the position of the perianth-androecium boundary on the meristem. They both occur in the wild. We described a precise comparative schedule of floral development in the two morphs. We related the developmental events to the height of the elongating stem and to the time elapsed after the beginning of stem elongation. In addition, we characterized the expression pattern of B- and C-class genes in floral organs of both morphs in an attempt to better characterize the differences between the two floral groundplans. The morpho-temporal framework we have defined will allow us to compare various gene expression profiles at targeted developmental stages in both morphs, providing further insight into the molecular control of the floral dimorphism in N. damascena and into the processes underlying the transition from a differentiated (bipartite) to an undifferentiated (unipartite) perianth.

P-091 Characterization of cellular mechanisms involved in regeneration and remodeling processes in the cnidarian Clytia hemisphaerica

Peron, Sophie (Sorbonne Université, Paris, FRA; Laboratoire de Biologie du Développement de Villefranche-sur-mer, FRA)

Regeneration is a widely shared but variable property of metazoans. Classical model organisms, such as Drosophila, mouse and nematodes, have rather limited regeneration capabilities. On the contrary, cnidarians have huge morphological plasticity, which combined with their phylogenetic position as the closest relative to bilaterians, make them interesting alternative models to study regeneration. The cnidarian hydrozoan Clytia hemisphaerica has recently emerged as a promising model to study developmental biology. Its complex life cycle, alternating between a planula larva, a benthic colonial polyp stage and a pelagic medusa stage, can be completed in the lab, and tools for functional analyses, as well as assembled genome and transcriptome, are available. Compared to other

cnidarian regeneration models, Clytia has a greater complexity due to the presence of the medusae form, harboring well-defined organs, striated muscle, and an organized neurosensory system. Despite its relative complexity, the medusa of Clytia has extensive regeneration capabilities. Indeed, we show that after ablation, all the main organs (the feeding organ manubrium, gonads, and tentacle bulbs) are able to regenerate. Moreover, after bisection, the original medusa shape is restored through a fast and stereotypical remodeling process. We demonstrate that regeneration and remodeling in Clytia rely upon different mechanisms. Whereas cell proliferation is required for organ regeneration, it is not required for the restoration of the medusa shape. Indeed, manubrium regeneration seems to involve the formation of a ‚blastema-like' structure formed by cell proliferation and migration. On the contrary cell proliferation is not necessary for the medusae shape restoration which seems to rely instead on tissue and extracellular matrix reorganization. Characterization of the Clytia medusae self-repair mechanisms, in particular the comparison between regeneration and remodeling processes, provides a new perspective on regeneration in Metazoa.

P-092 Germ line dynamics in bivalve molluscs: a comparative analysis

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The life cycle of many organism features an early moment in which cells split between two lineages, the somatic line and the germ line. These represent, respectively, the beginning of body architecture in the present generation, and the beginning of body architecture in the following generation. The separation of germ cells is a key point for the development of an organism and occurs by specification. This process has two main modes of action, the ancestral one, called epigenesis, and the derived one, called preformation. In this work we investigated bivalves (Mollusca Bivalvia), a clade in which preformation has evolved. Despite the relevance of these animals in marine ecosystems, their mechanism of germ line specification and seasonal gonad reconstitution lacks a detailed study. We thus analyzed bivalve germ line development by tracking the expression of VASA, a protein often used as germ line marker. We used specific antisera produced against the VASA homolog of Ruditapes philippinarum (Subclass Heterodonta, Family Veneridae). We compared the known developmental pattern of R. philippinarum to that of two species of the Subclass Pteriomorphia, Anadara kagoshimensis (Family Arcidae) and Crassostrea gigas (Family Ostreidae), and another species of the Subclass Heterodonta, Mya arenaria (Family Myidae).

The immunohistological data obtained support for the two Subclasses a similar mechanism of primordial germ cells proliferation among the columnar epithelium of the gut. Indeed, given the taxonomic separation of the analyzed species, pertaining to two highly divergent clades, we suggest that the observed seasonal migration to the reconstituting gonad, associated with the timing of gonad maturation, could be a shared feature of bivalve molluscs. The comparative study of bivalve reproductive biology using the germ line determinant VASA can add details on the preformation mechanism and help to depict a more comprehensive picture of the role that this protein plays during cell specification.

P-093 Sex chromosome evolution in organisms with haploid-diploid life cycles

Coelho, Susana (CNRS; Roscoff, FRA)

The life cycle of sexual eukaryotes involves invariably an alternation between diploid and haploid stages. Although sex determination in many systems occurs in the diploid stage, dimorphic sexes can also be determined by genetic factors in the haploid stage. In this type of sexual system (termed UV), very common among algae and bryophytes, sex is not determined at fertilization, as in animals or angiosperms, but, instead, the U and V chromosomes pair in diploids at meiosis, and the sex of the haploid offspring is determined by whether it inherits a female (U) or male (V) chromosome. My poster will focus on how our lab is exploiting the remarkable richness of life cycle and sexual characteristics of the brown algae to gain novel insights into the functional and evolutionary interactions between the sex chromosomes and key reproductive and life cycle traits.

P-094 From sticklebacks to humans: Evolving skeletal traits by cis-regulatory changes in bone morphogenetic proteins

Indjeian, Vahan (Imperial College, London, GBR)

Changes in bone size and shape are defining features of many vertebrates, and underlie many of the traits that distinguish humans from other primates. To uncover the major loci and genomic sequence changes that regulate skeletal traits, we did high-resolution mapping experiments in sticklebacks. We identified the gene for a secreted bone morphogenetic protein, Growth/Differentiation Factor 6 (GDF6), as a major locus controlling flat dermal bone size in wild populations. Freshwater fish have a cis-acting regulatory change that increases GDF6 expression, and transgenic overexpression phenocopies evolutionary changes in dermal bone size. Comparative genomics revealed that the human GDF6 locus also has undergone distinctive regulatory evolution, including complete loss of an enhancer that is highly conserved in other mammals. Functional tests show that the ancestral enhancer drives expression in hindlimbs but not forelimbs, in anatomic domains that have been specifically modified

during the human transition to bipedalism. These results add to growing evidence that cis-regulatory modifications of BMP genes represent a common mechanism for evolving specific skeletal changes in humans and other vertebrates.

P-095 Evolution of the panarthropod ventral nerve cord: a palaeobiological perspective

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Understanding the evolution of the central nervous system (CNS) is fundamental for resolving the phylogenetic relationships within Panarthropoda (Euarthropoda, Tardigrada, Onychophora). The ground-pattern of the panarthropod CNS remains elusive, however, as there is uncertainty on which neurological characters can be regarded as ancestral among extant phyla. Fortunately, the fossil record offers a unique opportunity to reconstruct the early character evolution of the nervous system via exceptional preservation of extinct representatives. Here, we describe the ventral nerve cord (VNC) in Chengjiangocaris kunmingensis, an early Cambrian euarthropod from South China. The VNC comprises a homonymous series of condensed ganglia that extend throughout the body, each associated with a pair of biramous limbs. Submillimetric preservation reveals numerous intersegmental nerve roots that emerge from both sides of the VNC, which correspond topologically to the peripheral nerves of Priapulida and Onychophora. The VNC of C. kunmingensis evinces a unique neurological organization, demonstrates the persistence of ancestral neurological features of Ecdysozoa in derived stem-group euarthropods, and illuminates the VNC ground-pattern in Panarthropoda.

P-096 Origins and regulation of an eutherian novelty: The BGW cluster

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liferation and differentiation, while others promote apoptosis in a p75-dependent manner, but most of them remain poorly studied. The ARMCX family and HNRNPH2 are derived from retrocopies of the ARMC10 and HNRNPH1 genes respectively -conserved across bilateria, and located in autosomal chromosomes-, whereas no orthologs have been found for the BEX/TCEAL family outside of Eutheria. However, all these genes share an intriguing feature: a sequence motif in their proximal promoter region that appears to be crucial for their expression, the BGW motif. To further understand the evolution of this gene cluster, we investigated the origin of the BEX/TCEAL genes and traced it to an atypical formation in the ancestor of eutherians. Furthermore, novel features associated with BEX/TCEAL suggest a more complete scenario for the origin of the cluster: the BGW motif was already present at the HNRNPH2 locus in the ancestor of therian mammals, being subsequently duplicated and coopted in the eutherian lineage by the BEX/TCEAL ancestor and, posteriorly, by the ARMCX ancestral gene. Finally, we also studied the expression of the BEX/TCEAL genes during mouse development using in situ hybridization. We found that they are highly expressed in the brain and placenta, which are structures that require a well-tuned control of cell cycle during their development in eutherian mammals. Here we propose a scenario for the origin of the BEX/TCEAL family and for the formation of the BGW cluster where they belong. Their uncommon origin, their pattern of expression, and their putative biological function during development makes these genes an interesting subject of study to understand how lineage-specific genes could contribute to mammalian evolution."

P-097 Tbx5 genes role in retina development in zebrafish

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A key step during eye development is the establishment of the dorsoventral and proximodistal retinal polarities. This process begins immediately after the evagination of the retinal precursors, evidenced by the expression of specific genes in discrete domains; e.g. tbx5 expression in the dorsal retina. Although some signalling cascades and pathways required for the maintenance of dorsal retina identity have been identified, how tbx5 expression is regulated and its function remain unclear. We isolated a conserved non-coding element (CNE) close to tbx5a in the zebrafish genome by phylogenetic analysis. CNE injection at 1-cell stage embryos showed that it is sufficient to drive EGFP expression in the retina recapitulating endogenous tbx5a expression. In silico analysis of the CNE highlights 2 putative motifs, and several binding sites for putative dorsal retina identity activators were found in motif#1 and inhibidors in motif#2. Injection of the motifs separately revealed that motif#1 drives EGFP expression to the eye field, although it was not confined in the dorsal

retina, whereas after motif#2 injection EGFP expression was not detected in the retina, pointing towards a dorsal positive/ventral negative regulation model for dorsal-restricted tbx5a expression. Regarding tbx5 genes function, interference with tbx5a and tbx5b function caused a significant reduction of the expression of the dorsal marker efnb2a in double morphants, suggesting these two genes act together to guarantee dorsal retina identity. Further, the optic nerves of double-morphants appeared thinner than those of control siblings. The CNE identified reproduces the endogenous tbx5a expression during early retina development. In addition, a dorsal positive/ventral negative regulation model seems to be regulating tbx5a expression. Once dorsally restricted, tbx5 genes act together to ensure dorsal retina patterning in zebrafish."

P-098 Globins and hematopoiesis in the annelid Platynereis

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The Globin superfamily is prevalent across living organisms. Members of this family have been identified in animals but also in plants, fungi and bacteria. First discovered for its ability to store and transport oxygen in Vertebrates (Hemoglobin and Myoglobin), this family proved to be broader and to display a variety of functions that remain for a large part to be investigated. Phylogenetic analysis is required to determine which of these functions are ancestral and which represent lineage-specific novelties. In many Annelids, oxygen transport relies on giant soluble respiratory proteins called erythrocruorins which are assemblies of extracellular globins and linkers. We screened through the available genome and transcriptomes to get an exhaustive list of globin proteins in Platynereis. We unravel their phylogenetic relationships by proposing a phylogenetic tree of animal globins with high resolution in the Lophotrochozoan superclade. Platynereis dumerilii shares with Chordates a closed blood vascular system, along with part of the developmental toolkit for the pulsatile structure of this system, such as the tinman gene, but has no blood circulating cells. We looked for the hematopoietic, i.e. globin producing, tissues in Platynereis, intuitively expecting them to be located around the main blood vessels. Surprisingly, globin gene in situ hybridizations show that at least two of the extracellular globins (among the 7 identified) are expressed in the parapodia in well delimitated cells forming islands near the capillary network where the oxygen exchange take place in analogy with gills function."

P-099 Neuropeptides control larval specific behavior in nemerteans and brachiopods

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Animal nervous systems utilize a wide array of neuropeptides for signal transmission. Contrary to classical neurotransmitters, which only transfer action potentials, neuropeptides act in diverse ways and are often involved in triggering or altering physiological and behavioral responses. Since most studies in marine protostomes have been so far focused on annelids or molluscs, nothing is known about neuropeptides in brachiopods and nemerteans. Using an integrative approach that combines comparative transcriptomics, phylogenetic analysis, motif searches, mass spectrometry and in situ hybridization, we identified and localized a set of neuropeptides and neuropeptide receptors in the larvae of two brachiopod species (Novocrania anomala and Terebratalia transversa) and two nemertean species (Lineus longissimus and Lineus ruber). Behavioral assays and molecular analyses show the specific involvement of the FMRFamide-like peptide (FLP) FLRFamide in the defense behavior of T. transversa larvae that are triggered by muscular contraction. This mirrors the role of FLPs in the myoactivity of other metazoans. We also examined the trochozoan specific „excitatory peptide" that was formerly known to be connected with muscular activity in annelids and molluscs, and demonstrate that it specifically influences ciliary beating of L. longissimus larvae. Both peptides signal via specific G protein-coupled receptors. By receptor deorphanization, we confirm the trochozoan-specific „excitatory peptide" receptor group and a group of FLP receptors that is different from those of insect FLP receptors. These two examples demonstrate that neuropeptides show a high variation regarding their utilization during evolution. Although broadly conserved functions can be found throughout metazoans, we also demonstrate that lineage specific neuropeptides can be recruited for different functions, which indicates rapid evolution of these essential molecules

P-100 ## The bulbus organ of Parasteatoda tepidariorum - precise maneuvers with a numb structure? Revisited

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Male spiders evolved a unique structure for sperm transfer: the bulbus, a pipette like organ to take up, store and transfer sperm under terrestrial conditions. The bulbus organ is situated on the last segment of the second appendage pair of the spider, the pedipalp. During the last instar before the adult moult it develops within the tarsus segment, but many aspects of its ontogenesis are unclear. The morphology of the bulbus or-

gan ranges from a simple pear-shaped protrusion to extremely complex, sclerite equipped structures, and there is no known reversal to plesiomorphic sperm transfer modes. Despite its complexity and disparity, the bulbus organ is apparently not equipped with any nervous tissue and thus is believed to be entirely numb. However, a recent study identifies a single bulbus nerve in a single spider species. Thus, it is currently unclear whether bulbus innervation exists in other species as well. In our lab we investigate the development and morphology of the common house spider Parasteatoda tepidariorum. We study the structure of the bulbus in adult stages and its formation during postembryonic stages, using high resolution imaging techniques. Therefore, we use a multi method approach with three dimensional imaging through micro CT with high brilliance bench and synchrotron radiation sources, immunohistochemistry combined with CLSM and ultra-structure analysis with TEM. We focus on the development of the primordium of the bulbus and its transformation during moulting with a special focus on a possible presence of innervation. This work will provide an in-depth view of the structure and possible innervation of a bulbus of the complex, sclerite equipped type.

P-101 The cost of evolving the life cycle: development of Trachylina

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Complex life cycles that present in a wide range of metazoans possess high level of evolutionary plasticity. There are multiple examples of evolutionary changes in the set of the phylum-specific life cycle stages, and the most impressive of them are known from the phylum Cnidaria. Among all cnidarians, the class Hydrozoa is the most diverse group, and some of the most interesting and enigmatic cnidarians belong to the hydrozoan subclass Trachylina. In the „"typical""hydrozoan life cycle, a juvenile stage (polyp) asexually produces an adult stage (medusa); the medusa produces gametes, which fuse and the resulting embryo develops into a planula larva; the planula metamorphoses into a polyp (solitary or colonial). The main evolutionary trend of trachylinians is a reduction/loss of the polyp stage and acquiring the holopelagic life cycle. What do they ‚pay' for such drastic evolutionary changes in their life cycles? Our data on the development of the trachymedusa Aglantha digitale, as well as analysis of old papers (e.g. Metschnikoff,1886) demonstrate that trachylinians possess developmental traits, which are not only very unusual to hydrozoans, but also very peculiar to metazoans. We identified several traits of Trachylina development, which can be considered as side effects of life cycle evolution: the trachylinian larval development drastically differs from the ‚typical' hydrozoan one, as their planula directly transforms

into a medusa. Some features of the medusa stage appear very early during embryonic development; in several species, the embryo/larva has a very low number of cells resembling early embryos of ascidians and nematodes, which indicate very specific changes of developmental trajectories coupled with very severe developmental constraints. We consider the Trachylina as a crucial group for our ability to correctly interpret data regarding the early development and life cycle evolution. We are working on introduction of several Trachylina species as exciting novel models for comparative studies in evolutionary developmental biology.

P-102 Polyp-to-medusa transition as a model for studying the life cycle evolution

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A complex life cycle with metamorphosis is widespread among metazoans. Comparing life cycles of evolutionarily distant organisms, we reveal the general patterns and rules of life cycle evolution. Cnidaria, as basal metazoans, are particularly valuable for such a comparison. Recently, the molecular machinery of the polyp-to-medusa transition termed strobilation has been unraveled for the scyphozoan cnidarian Aurelia (Fuchs et al.,2014). However, comparative analysis of metazoan life cycles requires complete set of data on the cnidarian's life-cycle transitions obtained for various representatives of this phylum. Unfortunately, there is an obvious lack of knowledge on the morphogenetic basis of medusa formation. To elucidate the developmental patterns of the polyp-to-medusa transition in scyphozoans, we studied and compared the strobilation of Aurelia(Semaeostomeae) and Cassiopea(Rhizostomeae). We characterized stages and morphogenetic mechanisms of the ephyra(medusa-larva) formation during strobilation at the levels of gross-morphology and histology. We created timetables of the ephyra formation for both species. The polydisc strobilation, typical for Aurelia,leads to formation of multiple star-shaped ephyrae, while the monodisc strobilation, typical for Cassiopea,leads to formation of one ephyra with the circular bell. The main stages and the key morphogenetic processes of the ephyra formation are similar in both species. However, we detected some heterochronic changes in the development of Cassiopea. The newly detached Cassiopea ephyra seems to be more developed than the Aurelia one: it possesses manubrium and gastric system with the complex type of branching. The shape, structure and behavior of the Cassiopea ephyra make it more alike a juvenile jellyfish than a typical ephyra. We suppose that Cassiopea actually skips the stage of ephyra larva: the juvenile jellyfish is formed during strobilation. To summarize, our results demonstrate that strobilation is a promising model system for studying the conserved and evolvable patterns of the life cycle transitions."

P-103 TCF/β-catenin mediated transcriptional repression in ascidians

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TCF/β-catenin, the key effectors of Wnt signaling, normally activate transcription on cis-regulatory elements containing TCF binding sites. However, concomitant repression of separate target genes was observed but the mechanism behind such opposite regulation remained poorly understood. In the ascidian Ciona intestinalis, we previously showed that Î²-catenin dependent repression of GATAa transcription factor activity mediates germ layer segregation into ectoderm and mesendoderm[1]. Moreover, β-catenin accumulation in the vegetal region tightly correlated with GATA activity repression suggesting a direct mechanism for GATAa target gene repression. Interestingly, a GATA site multimer was similarly repressed but lacked canonical TCF binding sites. Indeed, atypical TCF sites were linked to β-catenin/TCF mediated repression in Drosophila[2] and we recently showed a direct repressive TCF/β-catenin mechanism in C. elegans on other transcription factor binding sites[3]. Direct repression of β-catenin/TCF at GATA transcription factor binding sites was therefore postulated and analysed in ascidians. We first functionally compared atypical TCF sites proposed in Drosophila with GATA sites by generating activity reporter constructs with different binding site signatures and tested the repression by β-catenin. Interestingly, we found that the animal GATA activity did not perfectly correlate with the repressability by Î²-catenin/TCF in the vegetal region. This suggests that the activation of GATA sites may depend on a different signature than the repression. Biochemical analysis followed to test the interaction of GATAa/TCF/β-catenin on 'repressive' GATA sites for atypical transcriptional switching in Ciona[4]. We will present an entirely novel mode of transcriptional repression through TCF/β-catenin important for binary cell fate decisions.

[1] Rothbächer, et al. Development (2007)

[2] Blauwkamp, et al. EMBOJ (2008)

[3] Murgan, Kari, Rothbächer, Iché-Torres, Mélénec, Hobert, Bertrand. Dev Cell (2015)

[4] Oda-Ishii, Kubo, Kari, Suzuki, RothbÃ¤cher, Satou. PLOS Genetics, in press."

P-104 Extraembryonic membranes in insects: how an evolutionary novelty can provide a model for epithelial remodeling

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The vast majority of insect species possess protective extraembryonic (EE) tissues -the amnion and serosa- around the developing embryo, which are an evolutionary novelty for this group of arthropods. Active rupture and proper withdrawal of these membranes is crucial in late embryogenesis, as EE tissue defects can fatally impair embryonic anatomy. Interestingly, this phenotype shows parallels with a human condition, in which early rupture of the amnion leads to damaging entrapment and constriction of limbs. Despite the importance of the EE membranes for the development of many insect species however, the morphology and dynamic behavior of these tissues have been poorly characterized. This gap in our knowledge is largely due to the derived morphology of the amnioserosa in Drosophila, and we therefore turned to the beetle Tribolium castaneum, an insect model with a full complement of EE tissues that more closely resembles the ancestral state. Here, we use new fluorescent enhancer trap lines for live imaging, and in particular demonstrate the use of light sheet microscopy to visualize rupture of both EE membranes, with unprecedented temporal resolution. Using these new resources, we show that the amnion and serosa stay intact as a basal-basal epithelial bilayer, contradicting the previous hypothesis of intercalation of both epithelia, and find that the EE tissues repeatedly detach and reattach throughout development. Furthermore, we show that EE rupture is initiated in a specialized anterior-ventral cap, and further characterize this cap region using 3D reconstruction of multi-view light sheet data, both in wild-type and RNAi manipulated embryos. Finally, we discuss the potential of the EE membranes of T. castaneum to serve as a more general model for studying epithelial tissue interactions during animal development.

P-105 Neuropeptide atlas of the marine annelid Platynereis dumerilii

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Neuropeptides are neuronal signaling molecules present in almost all animal taxa. They are important modulators of many different behaviors and physiological processes, including sensorimotor integration, central pattern generation, circadian rhythms, feeding and metabolism, and reproductive behaviors. Neuropeptidergic signaling is very widespread in the nervous system, and most animals possess numerous proneuropeptide genes. To better understand the complexity of neuropeptide signaling in the context of an entire organism, we are making a full body cellular resolution gene expression atlas for 98 neuropeptides identified in the marine annelid Platyneris dumerilii. We obtained expression patterns by whole mount in situ hybridization of two distinct develop-

mental stages. This enables us to visualize differences in neuropeptide signaling during a major developmental transition in the life of a marine annelid. In addition to neuropeptides, we also generated expression patterns for marker genes for some of the classical neurotransmitters (e.g. acetylcholine, glutamate) for coexpression analyses. Furthermore, we plan to combine the neuropeptide expression atlas with a full body serial sectioned electron microscopy dataset generated in our lab to reconstruct neuropeptidergic neurons and their neural circuitry. Finally, understanding neuropeptidergic connectivity, combined with the knowledge of the evolutionary histories of neuropeptides and organs, can provide valuable insight into the evolution of behavior.

P-106 Geometric morphometrics of fly wings

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Insect wings facilitate a great evolutionary success and occupation of various ecological niches. Besides flying, wings perform additional tasks during mating, allow insects to escape predators, catch prey or search for food. To maintain these functions, a great variety of differently sized and shaped wings has been evolved and distributed among species. By example of Drosophila melanogaster, it was shown that these two wing parameters, size and shape, are often regulated by the same processes during development. However, recent advances in mathematical approaches allowed us to disentangle them by using geometric morphometrics. For this study, we chose three commonly used dipteran species: Drosophila melanogaster, Ceratitis capitata and Musca domestica. We subjected them to different temperature and density and applied geometric morphometrics to determine and to compare inter- and intraspecific differences. We found that all three species exhibited sexual dimorphism in wing shape, while it could be less pronounced or absent in size. We showed that for some species wing centroid size obtained from landmarks could not be directly used as a measure of the overall wing size due to the possible shape variation among subgroups, e.g. males and females. Separation of size and shape revealed that allometry accounted only for a small percentage of the total shape variation. To define the shape variation occurring in response to different environment, we performed size correction using the multivariate regression, which identified and removed allometric components. This revealed two most changing regions, the anterior and posterior cross veins, which are likely to be wing compartments that are developmentally less robust. We also determined main trends in shape difference between the three species and showed growth trajectories. These data add to our understanding of wing size and shape interactions in the evolutionary prospect as well as their alteration in response to environmental conditions.

P-107 Taste, Teeth, and Trinity: RNA-Seq reveals shared and unique gene expression profiles between tooth and taste bud progenitors in the shark, Scyliorhinus canicula

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Sharks and other polyphyodont vertebrates retain the crown gnathostome character of continuous successional regeneration of oral teeth. How capacity for successional regeneration is maintained in some lineages but lost from others (e.g. mammals) is currently unknown. We show that a compound and dynamic Sox2+ stem cell population resident in the shark dentition connects the superficial taste-competent oral epithelium at the taste/tooth-junction (T/T-J) with the deep tooth-forming successional lamina (SL) via cells migrating through the lingual margin of the middle dental epithelium during successional regeneration of teeth. We show that both taste buds and teeth emerge from the odontogustatory band (OGB), a field of embryonic oral epithelium equivalent to the odontogenic band (OB) of mammals, and that the Sox2+ stem niches of the T/T-J and SL are derived from the OGB. We suggest that a novel collaboration between the generalized odontode gene regulatory network (GRN) - and the taste bud GRN specifically in the oropharynx was key to the evolutionary transformation between dermal odontodes (i.e. placoid scales) and oropharyngeal odontodes (i.e. teeth). Differential gene expression analyses performed with microdissected sub-regions of the shark dentition, including the T/T-J and SL stem niches in addition to developing teeth and posterior pharyngeal taste bud epithelium offer novel insights into the molecular distinction between taste, tooth, and shared fields of epithelial competence.

„The emergence of muscles was an important step in the evolution of animals. In Bilateria, muscles are a main derivative of the mesoderm. As a sister group of Bilateria, Cnidaria (e.g. corals, sea anemones, jellyfish) take a strategic position for studying the evolution of key bilaterian traits, like muscles. Cnidaria are diploblastic i.e. they lack a mesoderm, yet they possess smooth muscles and - in jellyfish - also mononuclear striated muscles.

P-108 Transcriptomic profiling of cnidarian muscle cells provides insights into the evolution of muscles

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To date myogenesis is very poorly understood outside of bilaterian animals. Classical bilaterian myogenic regulatory factors like MyoD are absent in cnidarian genomes, while other important transcription factors

(e.g. Mef2) seem to play a different role during cnidarian development. In order to get more insights into the molecular regulation of myogenesis in Cnidaria, we hence used an unbiased approach by generating muscle cell-specific/enriched transcriptomes in two cnidarian species, Aurelia aurita (Scyphozoa) and Nematostella vectensis (Anthozoa) by either microdissection of muscular tissue, or dissociation and subsequent fluorescent-activated cell sorting (FACS) of muscle cells in transgenic animals. We found that genes associated with myogenesis in Bilateria are likewise expressed in muscle cells. Moreover, we found genes that have not been described to be involved in bilaterian myogenesis to be upregulated in cnidarian muscle cells. Interestingly, also genes known to have neurogenic properties are expressed in cnidarian muscles, reviving the discussion about a common evolutionary origin of muscle cells and neurons. Currently candidate genes that were validated by in-situ hybridization are tested functionally by CRISPR-Cas9 mediated gene knockout.

P-109 Genomic changes of symbiont for the multi-algae retaining protists

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Protists often retain symbionts such as algae. This phenomenon is key to understand the reason why photosynthetic organisms appear in different kinds of phyla. There are three stages of becoming a „plant“ via endosymbiosis: 1. temporary symbiosis in which host need new algae from outside, 2. persistent symbiosis in which host do not need to incorporate new algae, 3. nucleomorph stage. The third stage is well studied so far. However, there are few lights on earlier stages. The symbiosis between chlorella and ciliate is found to be in the early stages. Moreover, we found that the chlorella that can be symbiont in the ciliates could be incorporated to another protist as new symbiosis. Therefore, we sequenced genomes of symbiont chlorella and free-living chlorella, and compared their genomic structures. From this analysis, we found „switch“ in genomic changes for chlorella to be hosted in different kinds of protist.

P-110 Quantifying gene expression dynamics of developmentally important genes

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Critical functional evidence for the roles of developmental genes comes from experiments in which the activity of a gene is „“knocked out““. In cases where development of an organ or organism is arrested alto-

gether, the specific gene is considered to be absolutely required for development. In the same time, there appears to be a large number of genes that, despite being expressed during individual organ development, have no detectable phenotypic effect when null mutated. We asked whether the expression of these absolutely required genes differs from the dispensable genes in measures such as expression level and dynamics during early organ development. We address this question using the mammalian tooth. Especially mouse molar tooth development is well characterized, with dozens of genes known to be absolutely required for normal development. We focused on a critical step in tooth development, namely the transition from bud stage to cap stage. At this developmental time point the tooth crown patterning begins, and experimental modification of several signaling pathways causes phenotypic effects. To obtain a robust readout of the relatively subtle expression dynamics of normal organ development, we performed both microarray and RNA sequencing analyses on mouse E13 and E14 molars. Combining global expression profiles with experimental evidence on dispensability of individual genes, allows us to test whether expression profiles themselves might be informative about critical genes for each organ and the evolutionary conservation of development.

P-111 DISTAG/EsTBCCd1 orchestrates apical-basal axis formation and organ initiation in Ectocarpus

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Although plants and animals independently evolved multicellularity from unicellular ancestors, developmental programs in these two groups share several fundamental features. For example, in both lineages asymmetric division of the zygote immediately establishes the main body axis of the early embryo and this represents the first major patterning event during embryogenesis. The first cell division also plays a critical role during the development of a third group of complex multicellular eukaryotes, the brown algae. However, whilst the molecular processes that regulate multicellular development have been studied in considerable detail in the plant and animal lineages, to date no developmental regulatory genes have been identified in the brown algae. With the emergence of Ectocarpus as a genetically tractable model for the brown algae it is now possible to analyse developmental patterning processes in this important, but underexplored, lineage. We report here the identification of DISTAG (DIS), a key gene required for the establishment of the root-like system of Ectocarpus. In dis mutants, division of the initial cell is abnormal and both the gametophyte and sporophyte generations of the life cycle are devoid of rooting structures. The DISTAG gene, which encodes a tubulin binding cofactor C family member, lead to disruption of Golgi function in the initial cell and subsequent loss of the basal system

in this organism. We discuss how distag mutants link subcellular events within the initial cell with early axis formation and the acquisition of apical/basal cell identities, and how our study highlights the fundamental importance of the first cell division in specifying later developmental patterning across the Eukaryotes.

P-112 A genomic perspective on the evolution of development in Xenoturbella and implications for its position on the bilaterian tree

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The enigmatic Xenoturbella is key to our understanding of early bilaterian evolution. However, the phylogenetic position of Xenoturbella is hotly debated. While recent studies place them as an outgroup to all Nephrozoa, there is good evidence to place them as an ingroup of Deuterostomes within Xenambulacraria. We use an EvoDevo approach to improve our understanding of its genetic and developmental toolkit. Specifically, we complement data from a preliminary X. bocki genome with a several transcriptomic data sets. Additionally, we are using a novel approach of RNA-Seq of tomographic slices to analyse differential expression along the body axis. From these data we will compare the X. bocki gene set with the core genome of Bilateria and Deuterostomes. Using the RNA-Seq we can analyse the differential expression of body patterning genes. We are thus able to address two important questions: (i) if the morphological uniformity of X. bocki is reflected on the genetic level, or if distinct body regions can be described by different expression patterns;(ii) if expression of key developmental regulators (e.g. HOX genes) is similar or different to other Bilateria? Especially, the second point will hopefully aid our understanding of the phylogenetic affinities of this enigmatic taxon, but can also reveal developmental system drift.At the same time, we are interested in describing genomic idiosyncrasies of the Xenoturbella lineage. Annotating genes and finding gene families important for these animals will enhance our knowledge about their biology. This again allows us to address the question whether the genome of Xenoturbella is similarly conserved as its morphology, or if it is highly evolved from the Bilaterian ground state. Our data thus give insights into the genomic adaptation of this evolutionary old lineage and potentially the time and speed of its divergence from the last common bilaterian ancestor.

P-113 Phototactic navigation in marine larvae with ciliary eyes

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Light serves as an important environmental cue in marine habitats and is already exploited by early developmental stages to control physiological processes and to navigate in their three dimensional habitat. A

phototactic mechanism requires the ability to sense the direction of incoming light, neural integration of the stimuli and the execution of the appropriate response with the locomotion apparatus. Even though phototaxis can be observed in a vast number of marine invertebrate larvae it is unclear if underlying mechanisms evolved independently in certain lineages or share a common origin. The coronated larvae of the Bryozoan Tricellaria inopinata exhibit a strong positive phototactic behavior after hatching. While a lot of protostome larvae utilize microvillar photoreceptors to achieve a phototactic response, only ciliary type photoreceptors are known in Bryozoans. Electron microscopic investigations confirmed the ciliary nature of the photoreceptors present in the eyespots of T.inopinata. Consistently, the photoreceptors express an opsin that falls into an opsin group similar to ciliary opsins. Like many other marine invertebrate larvae the larvae of T. inopinata propel themselves through the water with the help of cilia and exhibit a helical swimming pattern while phototactic. In polychaetes it could be shown that the photoreceptor acts as a sensor-motor neuron and innervates adjacent ciliated cells to change the ciliary beating pattern using ACh signaling. Likewise the T. inopinata photoreceptor cells express vAChT and behavioral assays with a variety of neuronal blocking agents identified nAChr antagonists"capability to inhibit phototaxis. This study aims to provide a comprehensive analysis of the phototactic response in larvae of T. inopinata by close characterization of the photoreceptors involved, reconstruction of neural circuitry and steering mechanism to shed light on the evolution of phototaxis in marine invertebrate larvae.

P-114 Arthropod sesquiterpenoid hormonal system and microRNAs

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The phylum Arthropoda contains the largest number of described living animal species, and their successful radiations have long been linked to their rigid exoskeleton in conjunction with their specialized endocrine systems. In evo-devo, we usually focus on understanding how developmental genes contribute to evolution, especially during early embryogenesis. In order to understand how hormones can contribute to the evolution of these animals, here, we first categorized the sesquiterpenoid and ecdysteroid pathway genes in the non-insect arthropod genomes, which are known to play important roles in the regulation of moulting and metamorphosis in insects. Further, we also revealed how microRNAs involve in the regulation of sesquiterpenoid hormones in different arthropods, to understand how microRNAs may contribute to the evolution of the most diverse animal phylum on the earth.

P-115 Regulatory evolution leading to morphological innovations: the case of the mesmerizing turtle carapace

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The turtle shell is a morphological trait not observed in other animal group, and thus a genuine morphological innovation within tetrapods. Requiring a complete transformation of the tetrapod body plan, the turtle shell results from an open, fan-like ribcage formed by plate-like ribs enclosing the shoulder girdle (which otherwise remains outside in the rest of amniotes). The carapacial ridge (CR) is an embryonic structure, consisting of an ectodermal ridge underlained by a condensed mesenchyme, that during development is thought to control the development of the carapace side of the shell. In the past, we have shown the specific expression of few developmental genes in the CR, not expressed in equivalent areas of other amniotes, but otherwise likely co-opted from other developmental modules (such as the limbs, as first proposed by Anne Burke in 1989). However, can these few candidates explain the probably complicated origin of such a structure? And what is more, how did these genes become expressed in this unique turtle wonder? In this study, using the Chinese soft-shell turtle, Pelodiscus sinensis, embryos we have performed a comparative transcriptomics (RNA-seq) and regulatory (histone modification ChIP-seq) analyses of the CR and equivalent and unrelated structures (limbs and body walls) from turtles as well as different amniotes. We have been able to identify hundreds of genes that are specifically expressed in the CR of P. sinensis that might be involved in the turtle shell development, as well as around 500 hundred unique turtle CR-specific enhancers. These regulatory innovations, linked to a specific expression, are probably key to explain how the CR-specific genes were co-opted in the turtle lineage from previously unrelated developmental modules.

P-116 Xenoturbella bocki - A revised perspective

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Xenoturbella bocki is a marine worm found at the bottom of a Swedish fjord. It is a representative of the Xenacoelomorpha (Xenoturbellida and Acoelomorpha). Where it fits in the animal kingdom is highly controversial and has been argued about since its discovery in 1915. Its evolution remains a mystery - ranging from ancient ancestor to simplified close relative of chordates. Until recently, X. bocki and X. westbladi have been the only two nominal species described within the Xenoturbellida but the recent discovery of four new Xenoturbella species from the deep waters of the eastern Pacific Ocean has brought up the potential for new investigations. Taking into account that most of our knowledge is based on studies from the 70's to late 90's it is about time for a revised view of X. bocki. We are comparing its morphology in close detail using many techniques - ranging from traditional histology over scanning electron

microscopy (SEM) to more recent techniques like Micro Computed Tomography (ÂµCT) - to better understand the evolution of this controversial animal.

P-117 Molecular characterisation of skeletal regeneration in the brittle star

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Echinoderms are a deuterostome phylum of marine invertebrates, which are well known for their extensive regenerative capabilities. We use the brittle star Amphiura filiformis to understand the cellular and molecular aspects of skeletogenesis during adult arm regeneration and the potential role of the FGF signalling pathway in this process. Newly compiled transcriptomic data, spatio-temporal expression analysis and pharmacological treatments were used to characterise genes involved in adult arm regeneration in A. filiformis. We find that FGF signalling perturbation using the SU5402 inhibitor interferes with skeleton formation during both embryonic development and adult regeneration of the brittle star. A differential analysis screen using RNAseq data on treated and untreated embryonic samples yielded a transcriptome-wide overview of the downstream targets of FGF signalling. We find several skeletogenic genes specifically affected by SU5402 also in the adult regenerating arm. A large-scale analysis of candidate genes (identified in the transcriptome-wide embryonic screen) in adult arm regeneration revealed a conservation of network components downstream of FGF signalling between those two developmental modes.

P-118 Comparative transcriptomics reveals extensive developmental system drift in serial appendages morphogenesis

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Gene pleiotropy imposes constraints on phenotypic evolution. This should be especially true for serial appendages, which develop with similar sets of genes, expressed in similar conditions. Despite this, they often display moderate to large morphological differences within the same body (like fore/hindlimb in horse/bat). How do developmental systems cope with such pleiotropy, to maintain marked capacity for uncorrelated morphological evolution? Working towards an answer implies comparing the developmental systems of two serial organs with different morphologies (here: lower/upper molars), in two species, with a case of drastic morphological change (mouse upper but not lower molar) and a control (hamster). Among these 4 molars, is there a correlation between differences in developmental systems and differences in final morphologies? We compared molar crown formation with a standard

approach, and with a tight transcriptome timeseries to get a quantitative molecular profiling of developmental states. Our data identify common trends in the development of all molars. Upper and lower molars have their specificities since the early steps of morphogenesis, at the levels of the pattern of cusp formation, cellular composition and biased gene expression. The extent of difference in lower vs. upper molar development within one species does correlate with the extent of difference in final morphology. However, the specificity of lower vs. upper molar development is drowned among the rapid evolution of development, which is highly species-specific in term of expression levels and temporal profiles. Divergence in developmental systems is as high for lower as it is for upper molar, despite much lesser morphological changes in lower molar crown. Hence, this points to an extensive drift in this developmental system. We propose that differential morphological evolution of serial appendages is facilitated by developmental system drift (which enable one appendage to cope with extensive changes in the other), which itself is likely facilitated by their morphodynamic mode of development.

P-119 Evolution-Development congruence in pattern formation dynamics: bifurcations in gene expression and regulation of networks structures

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Search for possible relationships between phylogeny and ontogeny is one of the most important issues in the field of evolutionary developmental biology. By representing developmental dynamics of spatially located cells with gene expression dynamics with cell-to-cell interaction under external morphogen gradient, evolved are gene regulation networks under mutation and selection with the fitness to approach a prescribed spatial pattern of expressed genes. For most of thousands of numerical evolution experiments, evolution of pattern over generations and development of pattern by an evolved network exhibit remarkable congruence. Here, both the pattern dynamics consist of several epochs to form successive stripe formations between quasi-stationary regimes. In evolution, the regimes are generations needed to hit relevant mutations, while in development, they are due to the emergence of slowly varying expression that controls the pattern change. Successive pattern changes are thus generated, which are regulated by successive combinations of feedback or feedforward regulations under the upstream feedforward network that reads the morphogen gradient. By using a pattern generated by the upstream feedforward network as a boundary condition, downstream networks form later stripe patterns. These epochal changes in development and evolution are represented as same bifurcations in dynamical-systems theory, and this agreement of bifurcations lead to the evolution-development congruences. Violation of the evolution-development congruence, observed exceptionally, is

shown to be originated in alteration of the boundary due to mutation at the upstream feedforward network. Our results provide a new look on developmental stages, punctuated equilibrium, developmental bottlenecks, and evolutionary acquisition of novelty in morphogenesis.

P-120 MicroCT Imaging for EvoDevo: 3D embryos, digital beasties, and virtual museums

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3D imaging has become a familiar player in developmental and comparative biology, offering ever more realistic views of the native structures of organisms and materials. For morphology-based studies of development and evolution, X-ray microtomography (microCT) is the most suitable method to visualize 3D micromorphology in whole embryos and other intact samples. Contrast-enhanced microCT can produce images with microscopic detail and high contrast among various non-mineralized tissues - histology without sectioning. The accuracy of any analysis based on 3D images depends first on the quality of the sample, and second on the fidelity of the imaging process. Thus we are refining our methods for fixation, tissue stabilization, and contrast staining of whole samples for microCT imaging. The images generated by microCT are size-calibrated and suitable for quantitative 3D analyses of developmental morphology. We are currently establishing datasets and workflows to measure and model intraspecific variation, asymmetry, and growth during development. Continuing work on dual-energy (spectrally-sensitive, „“two-color““ microCT will demonstrate simultaneous imaging of different tissues or materials, e.g. skeletal hydroxyapatite amid counterstained soft tissues, and 3D localization and quantification of molecular probes in counterstained whole embryos. Further collaborative work is aimed at imaging cultured and regenerating tissues within artificial scaffolds and incorporating novel biomarkers such as nanoparticles. Digital volume images are inherently shareable, and we have recently published the first new (millipede) species description to be based partly on its cybertype - a set of virtual specimens made from microCT images of the physical type material for the species. We have also made a developmental atlas of the squid Euprymna scolopes available online, and we are currently creating a high-resolution 3D atlas of Sprague-Dawley rat development as a basis for analyzing mutations, experimental perturbations, and for quantitative comparisons with other species.

P-121 Evolution and development of the nervous system in Sepia officinalis

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The neurogenesis process during development and growth gives organisms the capacity to increase their abilities and/or to renew old cells. Well described in vertebrates, this process remains to be explored in non-vertebrates animals. Here we have chosen to study dynamics of neurogenesis in a cephalopod, Sepia officinalis, because of its continuous growth throughout adult life and its highly centralized and hierarchical brain allowing rich behavioral repertoires comparable to those of several mammals. We aim to test the hypothesis of a relationship between the dynamics of brain neurogenesis and the cognitive abilities acquisition at different steps of the biological cycle. Dynamics of neurogenesis has been studied on optic lobes (OL) and brain (BR) from the central nervous system (CNS) and stellate ganglia (SG) from the peripheral nervous system (PNS) between embryonic stages (starting at stage 24) and adulthood. We have 1) estimated by isotropic fractionator and immunocytochemistry the number of neurons (with anti-NeuN antibody) and non-neuronal cells and 2) examined the functional differentiation of neurons focusing on the dopaminergic system (with anti-Nurr1 receptor probe), known to play a key role on learning and memory processes. Tissue expressions of these markers have also been explored by in situ hybridization in order to establish the cartography of their expressions on CNS and PNS. First results indicate that these 3 nervous structures (OL, BR and SG) gain mass faster than they gain cells. The increase in neuron number is higher during the embryonic stages than the adult and the OLs and SG thus gain neurons faster than the BR suggesting that neurogenesis dynamics is higher in the brain after hatching. A significant increase of the dopaminergic neurons has been also found between stage 24 and adult developmental stage, which are localized mainly in the olfactory organs, statocysts, optic lobes and the sensory motor lobes of the brain confirming a precocious set up of the sensory system control.

P-122 Germ-disc formation in the common house-spider Parasteatoda tepidariorum

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Determination of the embryonic body axes is a crucial developmental process of bilaterally symmetric animals. The establishment of the embryonic axes of spiders has been best studied in the common house-spider Parasteatoda tepidariorum. It has been shown that a group of migratory cells, called the cumulus, are needed to establish the dorsoventral (DV) body axis. In addition, transplantation of the cumulus is able induce a secondary axis in other spider embryos. However, the establishment of the anteroposterior (AP) body axis occurs first and is linked to the formation of the germ-disc. Neither of these processes are well understood. The formation of the germ-disc is one of the most important processes during early spider embryogenesis, as the centre of the germ-disc marks

the posterior of the spider embryo, while the rim of the disc will give rise to the anterior. Furthermore, the cumulus also develops from the centre of the germ-disc. Until now, the process of germ-disc formation has not been fully analysed at the cellular and molecular level. To get a better understanding of how the germ-disc is established, I will present new labelling approaches to mark different cellular components in live and fixed spider embryos. In addition, I have carried out RNA sequencing to find new genes that are involved in axial patterning and in the formation of the germ-disc.

P-123 Skeletal development in ophiuroids provides insights into evolution of gene regulatory networks

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A mesodermally derived skeleton formed by several calcified elements originated at the base of the Echinodermata phylum and characterizes all adult forms. However, only two of the five extant classes of echinoderms develop extended skeleton in the larva: the echinoids (sea urchins) and the ophiuroids (brittle stars). This provides an excellent system to study mechanisms of cooption and evolution of gene regulatory networks (GRN) underlying developmental processes. In this study we analyze the development of skeleton in ophuroid embryos and adult arm regenerates to identify general features of skeletogenesis and specific embryonic developmental genes. High-resolution spatio-temporal gene expression data are coupled with disruption of signaling pathways (i.e. Fgf and Notch signaling) and transcriptomic data. The resulting data are then compared side-by-side to the well-characterized sea urchin mesoderm regulatory network. Our study identifies a high degree of rewiring between larval skeleton formation in ophiuroids and echinoids. For instance, some nodes are absent in ophiuroids (i.e. foxb and dri), while other have heterochronic expression (e.g. nk7) or are not functionally similar in the two species (e.g. pmar1 and pplx). Finally, at the level of differentiation, class specific genes are identified. Our results together with recent studies done in pencil sea urchins (cidaroids) shed light into the evolution of echinoderm GRN governing larval skeleton development.

P-124 Regulation of gene expression divergence in three closely related Drosophila species

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Developmental gene regulatory networks (GRNs) must be tightly controlled to give rise to functioning body parts. But they also have to be

flexible enough to allow the evolution of different adult morphologies. The function of key developmental regulators is known to be conserved across distant animal phyla („toolkit" genes). Therefore, divergence in the expression of these factors could play an important role in establishing morphological differences. The three closely related Drosophila species D. mauritiana, D. simulans and D. melanogaster are excellent models to study the molecular basis of morphological evolution, as they exhibit clear morphological differences in eye size and head shape and their short divergence time allows the application of quantitative genetics and interbreeding approaches. Using these species, we aim at answering two key questions: 1) Are genes with many or few connections within a developmental GRN more prone to be differentially expressed between species? 2) Are the observed interspecific expression differences due to changes in the regulatory region of the gene itself (cis) or due to changes in upstream regulators (trans)? We have sequenced the transcriptomes of the eye-antennal imaginal discs of the three Drosophila species at key developmental time points to identify genes differentially expressed throughout eye and head development. For well-established genetic networks, we tested the connectivity of differentially expressed genes and could see that highly connected genes are often differentially expressed. We also sequenced imaginal discs of F1 hybrids to study the relative expression of the alleles in these animals compared to their parents. Our results indicate that most differences are due to changes in trans, and this is also the case in other developing tissues (wing imaginal discs). These results differ from previous studies on adult Drosophila tissues, suggesting that different developmental stages might be subject to different evolutionary mechanisms influencing gene expression divergence.

P-125 Biting into the Genome to Phenome map: developmental genetic modularity of cichlid fish dentitions

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Teleost fishes provide an especially rich evolutionary context for studying the mechanisms of dental divergence because of the numerous axes along which their teeth have diverged phenotypically and presumably developmentally. Using both a review of in situ hybridization in teleosts and de novo transcriptome sequencing in a cichlid fish, we examine whether over 300 genes thought to play a role in developing mice teeth are expressed in the tooth-bearing jaws of teleosts. The similarities and putative differences in gene expression documented between the two most commonly used teleost tooth models, zebrafish and cichlids, highlight what can be learned from comparisons of teleost model systems in studies of tooth development. Both types of gene expression analysis also provide substantial evidence for conservation of tooth gene expres-

sion from teleosts to mammals as well as between initial and replacement teeth. Additionally, we found that the cichlid oral and pharyngeal jaws share expression in a substantial percentage of genes that influence tooth development indicating that the dentitions on these two jaws are not highly modular at the level of gene expression. Our transcriptome analyses also suggest sub-functionalization between gene paralogs expressed in teeth and paralogs expressed in other body structures is likely a common pattern across teleost diversity.

P-126 Seasonal plasticity of thermal reaction norms for development within and between generations in insects

Lopatina, Elena B. (St Petersburg State University, RUS)

The rate of insect growth and development is usually regulated by direct influence of temperature but may also be modified by other seasonal cues (photoperiod, food etc). We suppose that the variation in developmental time, which is observed in insects reared under different photoperiods, is generally due to modification of the thermal reaction norms for development. Assuming a linear relationship between developmental rate and temperature we have shown that photoperiod affects the temperature-sensitivity of development in some insects, that is, alters the slope of the regression line and the thermal threshold for development. In northern temperate (Russian) populations of P. apterus, a short-day photoperiod of 12 h accelerates larval development as compared to long-day conditions (20 - 22 h) at lower temperatures, but the reverse is true at higher temperatures. As a result, the slope of the regression line is shallower and the thermal threshold is lower (larval development is less temperature-dependent) under short-day conditions. It means that the bugs from early-summer and late-summer generations demonstrate different thermal sensitivity of development. In a southern population of P. apterus from Israel, a long-day photoperiod of 16 h accelerates larval development under all temperature regimes, which is consistent with its native dry subtropical climate. The thermal sensitivities of development under long- and short-day (10 h) conditions are similar, but the thermal threshold is lower under the former photoperiod. Adult bug body mass increases with temperature in all populations and under all photoperiodic conditions. The adaptive significance of seasonal and geographical changes in the thermal sensitivity of development will be discussed.

P-127 Origin and evolution of caste differentiation genes in ants

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The emergence of morphologically differentiated castes in colonial insects represents a major transition in evolution that evolved independently in ants, bees and wasps. Female siblings have very similar geno-

mes, but some develop into gynes (prospective queens) and most others into workers, a reproductive division of labor based on irreversible bifurcation of larval developmental pathways. To understand the evolution of gene expression networks associated with reproductive division of labor in ants, we investigated the genes with caste-biased expression in six ant lineages for which sequenced genomes were available and mapped their times of origin on the insect phylogeny, using the genomes of 35 insect species covering all major insect lineages. We found that both ancestral and younger, lineage-specific genes contribute to caste differentiation in a clearly stratified pattern. For example, in the attine fungus-growing ants, most genes with expression bias towards gynes originate from ancestral non-social Hymenoptera, whereas the majority of genes highly expressed in large workers originated after the emergence of the family Formicidae, consistent with sterile workers being an ant-specific and thus evolutionarily derived innovation. In addition, caste-biased genes originating from the common ancestor of all insects were found to be enriched for TCA cycle functions, while caste-biased genes that originated in the common ancestor of the Hymenoptera were enriched for G protein signalling pathways. We further examined dn/ds ratios and were able to confirm that caste-biased genes evolved faster than non-biased genes.

P-128 Endoderm out of the mouth: pre-oral gut in non-teleost fishes reveals an ancient mode of foregut development

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In all vertebrates, oro-pharyngeal development is considered rather uniform. From anterior to posterior, it comprises progressive formation of mouth and pharyngeal arches, where ectoderm generally outlines the outer, whereas endoderm the inner surfaces and structures. Here we present evidence that in all non-teleost fishes, development of the mouth is preceded by considerable foregut evagination that forms a distinct „pre-oral gut" along the roof of their prospective mouth. MicroCT imaging of complete embryonic series of African bichirs, American gars, and European sturgeons detailed an early pouching of their anterior-most archenteron with subsequent formation of prominent diverticula in the premandibular domain. Further in vivo lineage tracing mapped a contribution of this pre-oral endoderm to orofacial epidermis, including lips, sensory barbels, attachment organs, or teeth. This presents the first direct evidence of external surfaces and structures of vertebrate head to be thoroughly derived from the endoderm. Embryonic formation of the pre-oral gut is prominent in all three basal (non-teleost) fish lineages and

thus seems arguably ancestral for ray-finned fishes (Actinopterygii). In teleosts, such a foregut morphogenesis has been suppressed probably due to radical transformation of their early embryonic development and foregut compression. On the other hand, pre-oral gut formation seems to be at least rudimentarily present in many other vertebrates and the early foregut expansion that forms diverticula with a central lumen continuous with buccal cavity appears in many Deuterostomes. Hatschek's diverticulum of embryonic Amphioxus (Cephalochordates), oral (buccal) glands of appendicularian tunicates, or stomochord (buccal diverticulum) of hemichordate acorn worms are all examples of this kind of foregut morphogenesis. The above-described peculiar formation of the prominent pre-oral gut in non-teleost fishes thus reveals rather an ancient blueprint of foregut morphogenesis than a clade-specific curiosity.

P-129 A role for the dorsal surface selector gene apterous in generating morphological diversification of wing patterns in butterflies

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Butterflies are brightly colored insects that show extensive variations in wing patterns between the dorsal and ventral surfaces. These surface-specific patterns often serve different signalling functions and are shaped by natural and, sexual selection. However, the molecular and developmental basis of these surface-specific modifications has not been studied. A potential candidate gene mediating morphological diversity between wing surfaces in butterflies is apterous, a known dorsal surface selector in the fruit fly, Drosophila melanogaster. In D.melanogaster, the dorsal specific expression of apterous leads to wing imaginal disc folding and sac-like wing formation. In order to check for a potential role of apterous in mediating dorsal-specific wing patterning in butterflies, we used CRISPR/Cas9 targeted gene editing to disrupt the apterous sequence in the African squinting bush brown, Bicyclus anynana. Apterous mutant individuals showed ventral wing patterns, as well as ventral pheromone producing and dispersing organs of males, the androconia, appearing on the dorsal surface. In addition, dorsal androconia were reduced in these mutants. These results highlight a dorsal surface selector role for apterous in butterfly wing patterns - modifying ventral wing patterns into a dorsal-specific identity. In addition, apterous appears to have a dual role in androconial development, both as a repressor and an activator of this male-specific secondary sexual trait, underlining the complexity in how this gene regulates similar traits when they occur on opposite sides of a wing.

P-130 Retinoic acid patterns the oral skeleton of vertebrates along the dorso-ventral axis

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Retinoic acid (RA) is the active metabolite of vitamin A. In vertebrate and some invertebrate embryos it acts as a strong morphogen necessary for normal development. Disruptions of RA signaling lead to malformations, particularly in the neural tube and pharynx. Two main enzymes control the levels of RA in the tissue - Raldh2 catalyzing the oxidation of Retinaldehyde to the active form and Cyp26 actively degrading RA. We compared the expression patterns of the genes for these two enzymes in representatives of both jawless and jawed vertebrates - lamprey (Petromyzon marinus) and frog (Xenopus laevis). In both models, they are expressed in ectoderm overlying premaxillary and first arch neural-crest-derived mesenchyme, creating a dorso-ventral gradient of RA. Treatments with ectopic RA after the neural crest cells (NCCs) have already migrated result into morphological changes of the premaxillary and first arch skeleton. The dorsal elements shift ventrally and often fuse with the ventral skeletal elements. These changes in morphology are associated with changes in expression of several patterning genes - Alx4 in frog and its lamprey ortholog expand ventrally in the first arch, while the ventral shifts in the expression of Msx1b, Prrx2, Tbx3a, and their lamprey orthologs result into the loss of the dorsal domains. Surprisingly we did not observe alteration in Dlx expression in the first arch nor an AP shift of Hox expression in the pharynx, the latter being in strong contrast to the effects of ectopic RA on central nervous system. Lack of the expression of both Raldh2 and Cyp26 orthologs in the oral region of the basal chordate relative of vertebrates amphioxus, suggests that the patterning role of RA in the anterior mesenchyme represents a vertebrate evolutionary novelty presumably coinciding with the evolution of neural crest.

P-131 Genome-wide identification of Hedgehog signaling targets in axial patterning of the early embryo of the spider Parasteatoda tepidariorum

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Hedgehog (Hh) signaling regulates formation of the anterior-posterior (AP) body axis in the early embryo of the spider Parasteatoda tepidariorum. Since the early embryo provides a simple and static cellular field, this is becoming a good model for the study of Hh-mediated pattern formation. The involvement of Hh signaling in the early process of axial patterning raises at least two evolutionary questions; one is about the difference in the key players of AP patterning between Drosophila and the spider. What changes intervene between Bicoid- and Hh-mediated

patterning systems? Another is about the ancestral developmental role of Hh signaling; it functions in patterning various tissues, such as the Drosophila segments and imaginal disc and vertebrate neural tube and limb. What ancestral role existed? To address these questions, we started genome-wide identification of Hedgehog targets in the spider. Taking advantage of genome information that recently became available, we conducted RNA sequencing combining with parental RNA interference (pRNAi) against hh and patched, which encodes a negative regulator of Hh signaling. We identified approximately 100 genes whose expression levels changed both in hh and ptc pRNAi. Half of the genes showed localized expression in the early embryo. These identified genes represented an enrichment of spider homologs of Drosophila and vertebrate genes involved in imaginal disc, limb, and neural tube patterning. Among the identified genes we further focused on the msh (msx) related transcription factor gene that is involved in vertebrate limb and neural tube development to find that msh is required to initiate oscillatory gene expression for the posterior segmentation in the spider embryo. Our results show dynamic aspects of early embryonic patterning and shared features of Hh-mediated patterning in the early spider embryo with other systems.

P-132 Evolving Eusociality: Using Drosophila to understand how queen pheromone inhibits reproduction in worker honeybees

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This work aims to understand the evolution of eusociality (the social structure where a dominant caste reproduces, and the repressed caste rears the offspring) in honeybees, particularly how queen mandibular pheromone (QMP) induces reproductive constraint in the worker. We are using the easily manipulatable Drosophila melanogaster to investigate this process. Newly emerged virgin female Drosophila were exposed to synthetic QMP for 48 hours, their ovaries removed and mature oocytes counted as a measure of fecundity. QMP exposure caused a significant reduction in the number of mature oocytes in a dose responsive way. Drosophila were exposed for various periods QMP, to generate a time-course across ovary development. This showed that the number of mature oocytes was reduced significantly from 24 hours onwards. We have demonstrated that this response is plastic and reversible by removing Drosophila from QMP and allowing ovarian development to proceed, leading to a significant recovery of phenotype. RNA-seq is currently being carried out on ovaries from QMP exposed Drosophila across these time points, as well as those with recovered phenotypes. This allows investigation into which genes are showing altered expression during this process. The non-social and highly-diverged Drosophila responding to QMP from the eusocial honeybee gives insights into the evolution of

this social structure. It raises the possibility of a conserved mechanism of responding reproductively to environmental cues, which may have been co-opted into a novel role in this eusocial species. Drosophila provide an excellent genetic tool to further understand this process.

P-133 Commissureless regulation of Slit-Robo signalling in insects

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Slit-Robo signaling is a key mediator of axon guidance decisions in divergent organisms ranging from planaria to vertebrates. Not surprisingly, Slit and Robo homologues can be identified in all of the sequenced insect genomes. In contrast to this conservation of ligand and receptor, organisms have evolved various mechanisms to regulate Slit-Robo signaling. In Drosophila, Commissureless is a key post-translational regulator of the Robo receptor that functions to prevent cell surface accumulation of Robo. Two additional Comm-family members are found in Drosophila and they vary in their ability to regulate Robo receptors. We are investigating the evolution and function of Comm-like genes in insects. Bioinformatic studies indicate that Comm-like genes are present in most Dipteran genomes, although the number of Comm-family members varies. Divergent Comm-like genes can be identified in representatives of Trichoptera, Coleoptera, Hymenoptera, Phthiraptera, Hemiptera, Blattaria, Ephemeroptera, and Odonata, but not outside of insects. The presence of a Comm-like gene in many diverse insect orders suggests it was present early in insect evolution. There is evidence supporting three independent losses of this Comm-like gene: 1) the absence from sequenced Lepidopteran genomes, 2) the absence from Tribolium but presence in more basal Coleopteran genomes, and 3) the presence in basal Hymenoptera, like the sawfly, and absence in more derived Hymenoptera including ants, bees, and most wasps. We are investigating the functional properties of divergent Comm-family members from a variety of insects using several approaches, including RNAi and a Drosophila cell culture assay for Robo regulation."

P-134 Assembly of a novel gene network in a conserved developmental field yields an evolutionary novelty

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How novel morphological traits arise in organisms has long been a major question in evolutionary biology. Most of the studies about the evolutionary novelty, for instance, the beetles""sclerotized forewing (elytra), beetles""horn and water strider's antennae, are based on candidate genes known from Drosophila melanogaster, leading to a bias against towards conserved genes. Gin-traps are physical defensive organs found at the lateral margin of the abdomen of pupae among many Coleoptera

and some Lepidoptera species. Gin-traps are considered as an evolutionary novelty for the following reasons. Firstly, they are only present in some holometabolous insect taxa. Secondly, they are only present in the pupal stage which emerged during the evolution of holometablous insects. Therefore, gin traps are an excellent study case in order to answer the question on how evolutionary novelties arise. Gin-traps were reported to be wing serial homolog because they required the function of two wing selector genes, vestigial and scalloped. We wanted to know to which extent they share the common gene regulatory network. Therefore, we used the candidate approach to detect the involvement of Tribolium castaneum wing genes in the gin-trap development. Among the 22 wing genes, 10 were involved in both wing and gin-trap formation while 7 were wing-specific. In order to identify novel genes integrated to the network, we selected all the gin-trap phenotypes from the iBeetle-Base which contains phenotypic data of 4480 genes knocked down at larval stages. Three signaling pathways, EGFR, Notch and Bursicon, were involved in the gin-trap development. We also found several gin-trap specific genes, empty spiracles, highwire, Abdominal-A and caspar. Taken together we found that the evolution of gin-traps was based on the re-deployment of a large part of the wing patterning network at the same segmental position. However, some genes were lost from the network while a similar number of other factors were newly integrated into the network."

P-135 Shaping the embryo from outside: The role of Dorsocross in extraembryonic morphogenesis

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Epithelial morphogenesis is one of the first processes in embryogenesis, remodeling the blastoderm to create the form of the embryo. In insects it is not only the embryonic tissue that establishes the three-dimensional shape, but also the extraembryonic membranes, simple epithelia, have a large influence on embryonic morphogenesis. The extraembryonic membranes of the red flour beetle Tribolium castaneum, the amnion and the serosa, perform a variety of movements including intra- and inter-tissue fusions, inter-tissue detachment and controlled rupture. As external protective covers, they are easily accessible for live imaging and therefore a good model to study epithelial rearrangements in vivo. Here, we describe how the T-box transcription factor Dorsocross (Doc) controls all major events in Tribolium extraembryonic morphogenesis. This is in contrast to Drosophila, where Doc's only extraembryonic role is the maintenance of the single extraembryonic membrane, the amnioserosa. We show that this transition in function is accompanied by changes in upstream and downstream gene regulation. In particular, Tc-Doc is not only downstream of BMP signaling, as known from Drosophila, but also locally upstream in particular domains important for Tc-Doc mediated

epithelial reorganization. Tc-Doc is also phenotypically linked to its fellow U-shaped group member Tc-hindsight. We suggest that Doc's ancestral role was to control extraembryonic morphogenetic movements and that this role has been lost in the lineage leading to Drosophila. On the other hand, Dorsocross also has a number of embryonic functions in Drosophila that do not seem to be conserved in Tribolium, providing an excellent case study of how a transcription factor can gain new functions during evolution, including a switch from extraembryonic to novel embryonic roles

P-136 Toll genes have an ancestral role in axis elongation

Benton, Matthew A. (University of Cologne, DEU)

One of the key morphogenetic processes used during development is the controlled intercalation of cells between their neighbours. This process has been co-opted into a range of developmental events, and also underlies an event that occurs in each major group of bilaterians: elongation of the embryo along the anterior-posterior axis. In Drosophila, a novel component of this process was recently discovered, where it was shown that three Toll genes function together to drive cell intercalation during germband extension. Embryo elongation is conserved across the arthropods, and cell intercalation has been shown to be involved in some species. It is therefore possible that the Toll gene function observed in Drosophila is widely conserved. Alternatively, since Drosophila embryogenesis is highly modified compared with other insects, the cell intercalation function of Toll genes could be an evolutionary novelty. I will present our results from a large comparative study in which we found that the Toll gene function in embryo elongation is, in fact, widely conserved amongst arthropods. In our project, we combined expression analysis techniques with gene knockdown and high-resolution fluorescence live imaging to definitively show that two Toll genes are required for cell intercalation in the beetle, Tribolium castaneum. We then found that these genes belong to a previously undescribed Toll subfamily, and that members of this subfamily exhibit striped expression (as seen in Tribolium and previously reported in Drosophila) in embryos of six other arthropod species spanning the entire phylum. Last, we found that two of these Toll genes are required for normal morphogenesis during embryo elongation in the spider, Parasteatoda tepidariorum, a member of the most basally branching arthropod lineage. From our findings we hypothesise that Toll genes had a morphogenetic function in embryo elongation in the last common ancestor of all arthropods, which existed over 550 million years ago.

P-137 Super-sizing teeth - from mice to elephants

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The sizes of the majority of organs scale with body size - larger bodies require larger organs. The question of how organs follow the growth of the body as a whole is intriguing as is, but also brings new challenges such as adjusting the regulation of organ shape. The molar tooth is an example of an organ the size of which scales with overall body size. Several experimental attempts to change molar size have led to changes in shape as well. However, the evolutionary history of mammals shows that the size and shape of molars can be regulated independently. We aim to reveal the developmental adjustments behind shape regulation in differently sized animals, and to find out how size affects the patterning events. We have analysed the similarities and differences in tooth development between the rat (Rattus norvegicus) and the mouse (Mus musculus). The antero-posterior and bucco-lingual length of the first molar of the rat is roughly double that of the mouse, but the shape has remained similar. Preliminary results suggest that this kind of „"super-sizing""involves adjustments to three parameters; the antero-posterior dimension of the tooth bud, the distance between the secondary enamel knots, and the period of growth after patterning events. To gain insight on how shape is regulated in the upper size extreme, we have analysed rare embryonic specimens of the African elephant (Loxodonta africana), the largest extant terrestrial mammal. We combine our comparative analysis with experimental work and computational simulation to describe how teeth are made in different sizes, and how the largest molars of today are built."

P-138 **How ancient is the vertebrate kidney: did the simple Xenacoelomorph worms lose or never have kidney-like structures?**

Robertson, Helen (University College London, GBR)

Structures specialised for the role of ultrafiltration and excretion are thought to be found exclusively within members of the Bilateria, where they are necessary for the elimination of waste end-products of metabolism, and to carry out osmoregulation. Despite this common function, the morphology of these structures varies widely between different taxa, leading to the historic suggestion that ultrafiltratory structures are not all homologous. More recent evidence for the homology of filtratory structures has been provided by the morphological similarity between the sites of ultrafiltration in the vertebrate kidney and the Drosophila melanogaster nephrocyte. Furthermore, the critical structural proteins necessary for carrying out ultrafiltration are conserved between vertebrates and Drosophila. One group of bilaterally symmetrical animals, the Xenacoelomorpha (Xenoturbella + Acoelomorpha) have a very simple body plan, and are commonly believed to lack any defined ultrafiltratory organs. The phylogenetic position of the Xenacoelomorpha is debated: previous work has suggested they are a member of the deuterostomes, whilst alternative publications suggest they are outside of the main

group of Bilaterians (protostomes + deuterostomes), which have been named Nephrozoa implying the nephrocytes are an innovation of this clade. We have found orthologs of these structural proteins in the transcriptomes of members of the Xenacoelomorpha, which could be indicative of an ultrafiltratory capacity. Using molecular approaches we aim to characterise the expression patterns and possible filtratory function of these genes in Xenoturbella and different Acoelomorpha species. Given their intriguing phylogenetic position, understanding the role of these genes in members of the Xenacoelomorpha could shed light on the origin and homology of filtratory structures within the Bilateria. Furthermore, identifying structures specialised for ultrafiltration in these animals would contribute to our wider understanding of their evolutionary history.

P-139 Endoderm on the face: fate-mapping the pre-oral gut in sturgeon

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During early head development, pharyngeal endoderm undergoes a series of morphogenetic changes that provide important clues for the patterning of some key vertebrate structures, such as pharyngeal arches, jaws, or brain. The standard vertebrate scheme, well-defined on Xenopus model, comprises a sequential formation of mouth and pharyngeal pouches, whose opening involves a tight interaction between the directly juxtaposed ectoderm and endoderm germ layers. Mouth opening occurs within the so-called stomodeal or buccopharyngeal membrane, which represents the anteriormost limit of endoderm expansion. Consequently, endoderm-derived epithelia are restricted to the inner lining of the oral cavity and do not contribute to the external facial structures as a rule. Our MicroCT analysis of early sturgeon pharyngogenesis has revealed that the anteriormost foregut gives rise to a wide shovel-like projection, which expands anteriorly along the roof of the prospective mouth to cover the developing rostrum of sturgeon larvae. As a result, this anteriormost endoderm is found well in front of the presumptive mouth area and therefore in a pre-oral position. We have adopted an experimental fate-mapping technique previously used in bichirs and confirmed the endodermal origin of this pre-oral gut domain. Furthermore, it allowed us to follow its fate during late embryonic and larval development. In free-swimming embryos, the pre-oral endoderm emerges on the ventral surface of developing face, where it later contributes not only to the epithelial lining of the mouth cavity including lips and teeth, but also the external epithelia at the base of sturgeon rostrum, including sensory barbels. We thus conclude that, unlike in Xenopus, the anterior expansion of the sturgeon foregut endoderm is not limited by the presumptive

mouth. As a result, the endoderm both significantly exceeds anterior from the mouth and, most surprisingly, it contributes to external orofacial structures, which in other vertebrates are derived exclusively from the ectoderm."

P-140 An evolutionary novelty in insect eggs

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Insects are extraordinarily successful and comprise more than three quarters of all described animal species. In an eco-evo-devo approach, we have shown that an evolutionary novelty in insect eggs, the serosa, protects the developing embryo of the holometabolous beetle Tribolium castaneum against desiccation and infection (1,2). The serosa is an extraembryonic epithelium of zygotic origin that folds over the embryo and yolk during early development. Only the insects possess this membrane; it is absent in their sister group, the crustaceans. To investigate if the serosa has a protective role in other insects too, we expanded our research to the hemimetabolous milkweed bug Oncopeltus fasciatus. RNAsequencing and qPCR data upon bacterial challenge show that the Oncopeltus egg becomes highly immune responsive when the serosa is present, and remains so when the serosa retracts and the ectoderm of the late embryo is exposed at the surface of the yolk. This suggests that, in hemimetabolous insects, the serosa temporarily provides the egg with an innate immune response until the embryo proper becomes immune competent. In situ hybridizations on antimicrobial peptide mRNAs are currently carried out to confirm this. We propose that the evolutionary origin of the serosa facilitated the spectacular radiation of the insects.

(1) Jacobs CG, Spaink HP, van der Zee M.(2014) The extraembryonic serosa is a frontier epithelium providing the insect egg with a full-range innate immune response. Elife. 2014; 3. e04111

(2) Jacobs, C.G.C., Rezende, G.L., Lamers, G.E.M. and van der Zee, M. (2013) The extraembryonic serosa protects the insect egg against desiccation. Proceedings of the Royal Society B 280(1764):20131082.

P-141 Using sponges as a model to study the evolution of the Wnt/beta-catenin signaling pathwayi

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The discovery of conserved homologs of the Wnt/beta-catenin pathway in sponges (one of the earliest branching metazoan lineages) raised questions about whether a functional Wnt/beta-catenin pathway is present in sponges and what its role may be in organisms of such relative

simplicity. To gain more insight in the role of beta-catenin in sponges, we identified tissue-specific and subcellular localization patterns of beta-catenin by performing immunostaining using a polyclonal antibody against beta-catenin of the freshwater sponge Ephydatia muelleri. Our immunostaining data show that beta-catenin is detected in the nuclei of archeaocytes (i.e. mesenchymal cells) and pinacoderm cells (i.e. epithelial cells), suggesting a conserved role as a transcription factor, possibly part of the Wnt pathway. We also observed staining at cell boundaries of the pinacoderm, which is consistent with a role in cell-cell adhesion. Staining was not detected in cell boundaries of the choanoderm (composed of choanoflagellate-like cells, that pumps water through a water canal system used for feeding and respiration), which could indicate this tissue does not use cadherin/catenin adhesion mechanisms. To further test the role of beta- catenin in sponges, we performed a Co-IP and are in the process of identifying binding partners of beta-catenin. In addition, we are studying the function of the Wnt/beta-catenin pathway in vivo by exposing sponges to drugs that should inhibit GSK3beta. Our preliminary results showed that sponges treated with the drugs are depleted from phosphorylated beta-catenin, indicating that the drugs are able to inhibit GSK3beta and thus preventing phosphorylation of beta-catenin. We are in the process of further validating these results and comparing them to the phenotypic effects.

P-142 Gut-like ectodermal tissue in a sea anemone challenges germ layer homology

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The homology of germ layers, and their evolutionary origin are debated since their discovery. Cnidarians (e.g. sea anemones, jellyfish) develop from two germ layers, the outer ectoderm and the inner endoderm, while bilaterian animals (e.g. flies, worms or vertebrates) possess in addition the intermediate mesoderm. Currently, it is assumed that the cnidarian endoderm (or „endomesoderm') shares a common evolutionary origin with both the bilaterian endoderm and mesoderm. Here, we test this hypothesis by studying the fate of germ layers, the localisation of gut-like cell types, and the expression of a large number of „endodermal"and „mesodermal"transcription factors in the sea anemone Nematostella vectensis (Anthozoa). By following the fate of transgenic, fluorescently labelled cell patches transplanted onto non-fluorescent embryos, we have revealed an ectodermal origin of the pharynx and the septal filament, an integral part of the inner gastrodermis. Strikingly, we find that this ectodermal tissue displays a developmental transcription factor expression profile (foxA, hhex, islet, soxB1, hlxB9, tbx2/3, nkx6) and a cell type complement (digestive exocrine, and insulinergic) reminiscent of the

developing bilaterian midgut, and especially the vertebrate pancreas. Endodermal derivatives of N. vectensis, instead, display cell functions and transcription factor profiles, which are similar to bilaterian mesoderm-derived tissues, in particular to the somatic gonad and cardiogenic tissue. Our data thus supports a new hypothesis of germ layer evolution where bilaterian and cnidarian endoderm are not homologous.

P-143 The evolution of collagen and SPARC secretion during tooth development in vertebrates

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Vertebrate skeletal tissues develop from the activity of specific cells, all able to secrete a collagenous extra-cellular matrix which may or may not calcify. In this work, we describe the expression patterns of the major fibrillary collagen genes and genes of the Secreted Protein, Acidic, Cysteine-Rich (SPARC) family in two chondrichthyan species and one tetrapod where the SPARC family has poorly expanded into Secretory Calcium-binding PhosphoProtein (SCPP) duplicates. We show expression of all these genes in the mesenchymal compartment (odontoblasts) of teeth and the placoid scales of the catshark, except for the expression of SPARC-Like in the inner epithelium of chondrichthyan teeth and transient faint expression of SPARC in the xenopus inner dental epithelium. Our results involve a restrained SPARC-Like expression in the epithelial layer of calcifying teeth (maturation stage) in chondrichthyans and no expression of collagen genes by ameloblasts. This result questions the cellular origin of chondrichthyan enameloid and its homology to enamel/enameloid found in osteichthyans. In contrast, a strongly conserved feature of odontoblasts in jawed vertebrate is therefore the co-expression of major fibrillar collagen genes and the SPARC gene. This observation calls for a putative gene regulatory network involved in extracellular matrix calcification which could also be shared between odontoblasts and osteoblasts of osteichthyans. These results therefore lead to various scenarios for the evolution of SPARC/SCPP genes in the gene regulatory networks involved in ameloblast and odontoblast function.

P-144 Analysing dynamics of spiral cleavage and the cell lineage of the flatworm Maritigrella crozieri by home-built SPIM microscopy

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To better understand the evolution of marine invertebrate body plans we focus on the comparative developmental biology of the tiger flatworm Maritigrella crozieri. This polyclad flatworm undergoes stereotypical spiral cleavage pattern and has a planktotrophic larval stage,

which shares some morphological similarities to spiralian's trochophore larvae such as are found in marine annelids and molluscs. Despite these observed similarities, the question whether these larvae represent an ancient feature or whether they are a case of convergent evolution is still unresolved. We are particularly interested in the spiral cleavage pattern and also in complex larval structures such as ciliary bands and apical organ with putative homology to similar structures in canonical annelid and mollusc trochophores. We study early cleavage and the elaboration of these larval structures during embryogenesis of Maritigrella with an emphasis on discovering their origins amongst the early blastomeres using cell lineage tracing. To achieve this we have built a Selective Plane Illumination Microscope (SPIM) and are using injected fluorescent markers to follow cell division and study spiral cleavage pattern in vivo.

P-145 Amphioxus witnessed the dorso-ventral inversion

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The hypothesis of D-V inversion suggests that this inversion occurred either in a vertebrate ancestor or more deeply in a chordate ancestor. This hypothesis has been revived based mainly on the expression pattern of bmp and chordin (chn) genes. Our studies on developmental mechanisms for dorsal determination and mouth formation in amphioxus support that the D-V inversion occurred in the last common chordate ancestor. We show multiple lines of similarity in early development between amphioxus and sea urchins. The sperm entry point is not restricted to the animal hemisphere and does not affect embryonic axis determination. Establishment of the D-V axis is initiated by an asymmetrical expression of nodal and lefty genes in a simple spherical coeloblastula. Genes such as gsc, chn, not, and bra are downstream target genes of Nodal signaling in the asymmetrical nodal-lefty expression domain. bmp2/4 and chn are co-expressed, and bmp2/4 and pSmad1/5/8 show counter distributions along the D-V axis. One important difference is that the asymmetrical Nodal signaling initiates oral ectoderm specification in sea urchin embryos, but leads to dorsal axis formation in amphioxus embryos. These observations suggest homology between sea urchin oral formation and chordate dorsal formation, which is consistent with the D-V inversion hypothesis. As chordates utilized the mechanism of the ancestral oral formation for their dorsal formation, they were needed to create a new mouth. Amphioxus has a mouth derived from left first somitocoelom like the coelomic pore found in ambulacrarians, and vertebrates have acquired a new stomodeum via the anterior pan-placode. Thus amphioxus developmental pattern displays multiple traits that implicate that the D-V inversion occurred in a chordate ancestor.

P-146 Identification of a novel gene required for maintaining differentiation

states in telotrophic Tribolium castaneum oogenesis

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The beetle Tribolium represents telotrophic ovaries, which differ fundamentally from the polytrophic ovary of Drosophila. In Drosophila, the tight spatial and temporal association of germline stem cells and somatic stem cells makes it very difficult to analyse the somatic stem cell lineage. In Tribolium, however, systemic RNAi in pupal and adult stages allows the functional analysis of cell fates independently of potential effects on the germ line stem cells. To identify genes that affect the follicle stem cell lineage, we participated in the iBeetle screen, a genome-wide RNAi screen, aimed at the functional analysis of all genes in Tribolium. Of the 8465 genes screened, 1744 (21%) resulted in the cessation of egg-production. Depletion of TC003132 - a putative casein kinase II substrate - results in severe phenotypes. Upon adult RNAi, encapsulation and alignment of egg-chambers is disturbed and ovarioles are depleted of follicle cells, including central pre-follicular cells. In addition, the so-called somatic-plug - a group of small somatic cells located at the posterior end of the tropharium - is dispersed. As monitored by Eya expression, central pre-follicular cells become disorganized and cease mitosis, which may eventually result in the loss of the somatic linage. These results indicate a function of TC003132 in proliferation and differentiation of early somatic follicle cell lineages. Interestingly, TC003132 RNAi also affects the differentiation of germ-line derived cells, as we observed „nurse-cell-like" behaviour of otherwise arrested pro-oocytes. While it remains to be elucidated as to whether these cells still have pro-oocyte fates, it is tempting to speculate that in the absence of TC003132 pro-oocyte fate is omitted and germ-line cells trans-differentiate into nurse-cells. Taken together, our results indicate a key function for TC003132 in maintaining the differentiation state of the germ-line and of somatic cell-lineages in telotrophic Tribolium oogenesis.

P-147 ### Spiralian specific TALE homeobox genes and evolution of spiralian development

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Spiralia, including mollusks, annelids and platyhelminths, is one of three major groups of Bilateria. Spiralia show the unique development called „spiralian development", characterized by the geometry of early cleavage patterns and conserved fate map of the blastomeres. In the course of spiralian development, blastomere-specific property is established along A-V axis, but molecular basis for this is largely unclear. Here, we performed a genome-wide survey of TALE homeobox genes in spiralian

genomes and performed a phylogenetic analysis. We found that there are spiralia-specific novel TALE family genes, which arose at the spiralian common ancestor. Most species have three or more genes in this family, which are probably gained by gene duplications. First, we isolated these genes from mollusk (gastropod and bivalve) and annelid (polychaete), and examined expression patterns in their early development. In summary, (1) expression was detected at early cleavage stage (egg - 32 cell stage), (2) expression was biased along A-V axis, and (3) the expression patterns were different from each other among novel TALE genes. Second, we tested their function in gastropod by overexpression and MO analysis. We observed that inhibition/overexpression induced the elimination /expansion of the specific region corresponding to expression site of each TALE genes. In addition, perturbation of certain novel TALE gene often leads to the change of expression pattern of other novel TALE genes. These result suggest that concerted expression of novel TALE genes conduct establishing lineage specific property of blastomere along A-V axis in spiralia. We propose that gain, duplications and diversification of novel spiralian specific TALE genes contributed to evolution of spiralian development, as with the case of Hox and other toolkit genes to the evolution of metazoan body plan."

P-148 No new head without a new heart: FoxN3is involved in the development of the interatrial septum in the African clawed frog, Xenopus laevis (Anura, Pipidae)

Naumann, Benjamin (Friedrich Schiller University, Jena, DEU); Schmidt, Jennifer (Friedrich Schiller University, Jena, DEU); Olsson, Lennart (Friedrich Schiller University, Jena, DEU)

In 1983, Gans and Northcutt proposed that vertebrates evolved from chordate-like ancestors primarily by innovations and remodeling in the head region. The „new head" was associated with a shift from a passive filter-feeding to an active predatory life style. For this, a higher metabolic rate and an increase in blood supply was needed. Thus, a strongly muscularized and multi-chambered heart was a key feature indispensible for this evolutionary transition. During vertebrate evolution, the primarily two-chambered heart (atrium and ventricle) becomes further subdivided by the emergence of an interatrial septum in the tetrapod lineage. This newly formed three-chambered heart with separate pulmonary and systemic blood flows might have been an important prerequisite for the evolution of the early terrestrial vertebrates and is still present in extant amphibians. Unfortunately little is known about the genetic control of the formation of the interatrial septum. A morpholino-mediated knock down of the FoxN3 gene in the African clawed frog, Xenopus laevis, causes loss of the interatrial septum, resulting in a two-chambered heart with a single undivided atrium. FoxN3, a member of the forkhead/winged helix family of transcription factors, has been shown to be essential

for normal cranio-facial development in X. laevis and mouse. Expressed in the neural crest cells, FoxN3 seems to be a major player in the development of the rostral cartilages, the filigreed gill basket and the particular head muscle arrangement in Xenopus tadpoles. These structures are evolutionary novelties present only in frog tadpoles. In addition to our data concerning the interatrial septum, FoxN3 is also important for the formation of specific craniofacial and cardiac structures, which can be regarded as evolutionary novelties. This dual function in cranial and cardiac development tightens the embryonic connection between the head and the heart and promotes a more integrated view of their evolutionary and developmental history.

P-149 The evolutionary origin of bilaterian smooth and striated muscles: insights from annelids

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Vertebrate musculature is marked by a duality between smooth and striated muscles. These muscles differ in position (predominantly visceral versus somatic, respectively), function (digestion versus locomotion), contraction speed, and reliance on nervous inputs. They derive from different mesodermal populations, and express distinct complements of transcription factors and effector genes. Though this duality is deep and pervasive, its evolutionary origin remains unknown, with smooth muscles having often been assumed to represent a vertebrate innovation. This view has been apparently supported by the absence of visceral smooth muscles in the two best-characterized protostome model species, Caenorhabditis elegans and Drosophila melanogaster. However, an ancestral state reconstruction based on a broad sampling of morphological data across the bilaterian tree of life reveals that the presence of both gut smooth muscles and somatic striated muscles in many phyla, suggesting that those two types of myocytes might have been already present in the last common ancestor of protostomes and deuterostomes. We tested this hypothesis by an in-depth molecular, developmental, structural and functional description of musculature in the protostome Platynereis dumerilii, and found populations of somatic striated myocytes and gut smooth myocytes that closely match their vertebrate counterparts in location, structure, contractile properties, reliance on the nervous system, and molecular profile. Together, these data indicate that the smooth/striated duality likely predated the last common protostome/deuterostome ancestor, and that both muscle complements evolved from fast versus slow-contracting cells in pre-bilaterian animals.

P-150 Cephalopod and scaphopod mollusks share a similar BMP signaling gene expression profile during dorsal-ventral body axis formation

with chordates

Wollesen, Tim (University of Vienna, AUT); Wanninger, Andreas (University of Vienna, AUT)

Bone morphogenetic proteins (BMPs) play a crucial role in dorsal-ventral (DV) body axis formation in bilaterian animals. While BMP signaling genes are predominantly expressed on the dorsal side in protostomes, their antagonists such as Chordin are predominantly expressed on the ventral side. These expression domains are inverted in chordates, with the BMPs localized on the ventral side and their antagonists on the dorsal side. The latter condition has been interpreted as a consequence of DV axis inversion that occurred during early chordate evolution. The vast majority of protostomes exhibits a pronounced anterior-posterior axis, while scaphopod and cephalopod mollusks are exceptional in having an elongated DV body axis. To date the molecular basis of DV axis formation is still poorly studied in the Mollusca, however, it is known that Bmp2/4 is expressed in the region of the dorsal shell field of various gastropods and a bivalve. We investigated the expression of selected BMP signaling genes and their antagonists in representatives of three additional molluscan clades: the conchiferans Antalis entalis (a scaphopod) and Idiosepius notoides (a cephalopod), as well as the aculiferan Acanthochitona crinita (a polyplacophoran). We show that these genes are expressed in a typical protostome-like manner in the polyplacophoran, while they are expressed in a chordate-like fashion in the scaphopod and the cephalopod. This indicates that respective BMP signaling genes and their antagonists have been recruited into the formation of the DV axis in an inverted fashion in scaphopods and cephalopods. This condition has so far not been reported for any other protostome and might be the explanation for the extremely pronounced DV body axes of scaphopods and cephalopods.

P-151 Evolution of eye size and head morphology between Drosophila americana and D. novamexicana

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The morphology of animal organs is usually conserved, since it is under intense selection both within and between species. Thus, changes in the relative size and shape of organs likely represent functional adaptations to an ever changing environment. Nevertheless, the molecular basis of such changes is not always the same. For instance, differences in eye size between species of the melanogaster group were found to be caused mainly by facet size, while intraspecific variation is mainly due to changes in ommatidia number. Therefore, it is imperative to study divergent

groups of species to determine if changes in size and morphology are governed by general or specific mechanisms across the entire Drosophila genus.Preliminary data shows major differences in eye size between species of the D. virilis group which are largest between D. novamexicana (smallest eyes) and D. americana from the south of the distribution (biggest eyes). These species are diverging from D. melanogaster for at least 40 million years, representing an excellent model to understand if natural variation in eye size and head morphology is due to changes in the same underlying gene regulatory network in divergent Drosophila lineages. In order to reveal the major genomic regions responsible for the observed differences we used a combination of geometrics morphometrics and genotype-phenotype association studies involving backcross progeny of crosses between F1 hybrids and D. novamexicana. In these analyses we find clear differences in normalized eye size and head shapes, which are mainly caused by genes located on the 2nd, 3rd and 4th chromosomes. The developmental stage at which these differences arise is being identified using immunohistological experiments in larval eye-antennal imaginal discs. Moreover, a Genome-Wide Association Study (GWAS) of pools of individuals showing extreme values of normalized eye size after 17 generations of recombination between hybrids is revealing candidate SNPs.

P-152 Non-canonical gene expression during axolotl limb development

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Since its evolution during the Devonian period the tetrapod limb has evolved a large number of forms for a variety of functions, such as swimming, flying, and jumping. Despite the many functions, the order of development of skeletal elements is conserved in tetrapods. Two of these patterns are: (i) ossification occurs in a posterior-anterior direction, beginning with the posterior elements (ulna/ fibula), followed by anterior zeugopodial elements (radius/tibia). The formation of the digital arch begins with condensation of digits IV and finishes with digit I; (ii) autopod development begins with a paddle stage, in which digits are formed together and are subsequently separated. The only exception to these patterns occurs in salamanders, where the ossification occurs in an anterior-posterior direction, in other words, the anterior zeugopodial elements are formed before the posterior elements and digit formation begins with digits I and II and ends with digit V. Moreover, in free-swimming aquatic salamanders (such as the axolotl - Ambystoma mexicanum), digits bud one by one, first the preaxial digits followed by the postaxial ones. The genetic mechanisms underlying this unique limb development pattern are unknown and could involve expression changes to important genes for limb patterning. Here, we analyzed Etv4, Pat-

ched1, Alx4 and Irx3 gene expression in axolotls and tested the activity in vivo of the ultra-conserved Shh enhancer called ZRS. We found that the transcription factor Etv4 shows a non-canonical pattern expression in axolotls and although axolotls do not present a paddle stage, Irx3 gene expression is found in an equivalent interdigital membrane. The axolotl ZRS sequence containing the Ets1 transcription factor binding site, which drives Shh expression in mouse limb, was not capable of driving reporter gene expression in transgenic assay. These findings can help us to elucidate the unique salamander limb development pattern.

P-153 Length matters: practical considerations for interspecific RNA-seq approaches

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The advent of next generation sequencing technologies has facilitated a robust genome-wide quantification of gene expression. In the evo-devo field, the comparison of gene expression across species and developmental time-points has become an excellent tool to generate and test new hypotheses. For model systems, genomic references and bioinformatics analyses pipelines are well-established. However, for evolutionary developmental studies in emerging model systems key steps of the RNA-seq data analysis remain uncertain. Here we use a comparative developmental RNA-seq dataset of three Drosophila species to: 1) evaluate the quality of existing genomes, 2) compare the performance of current statistical methods and 3) propose a re-annotation pipeline that can easily be adapted for other species. First, we show that the published genomes and annotations of the three species D. melanogaster, D. simulans and D. mauritiana have limitations for interspecific gene expression studies. This is due to missing gene models in at least one of the genome annotations, unclear orthology assignments and significant gene length differences in the different species. A comprehensive evaluation of four statistical frameworks shows that none of these methods sufficiently accounts for interspecific gene length differences, what inevitably results in false positive candidate genes. In order to solve this problem, we present a straight-forward reciprocal re-annotation pipeline that allows to reliably compare the expression for nearly all genes annotated in D. melanogaster. Eventually, we validate our pipeline applying qPCR for randomly chosen genes. We conclude that published reference genomes and transcriptomes should be re-annotated before using them as references for RNA-seq experiments. This will allow to include as many genes as possible and to account for a potential length bias among gene models. In the end, we propose that our established re-annotation pipeline can easily be adopted for genomic references of other animals and

plants to improve comparative expression analyses.

P-154 Key losses in hox coding and regulatory elements in the Gulf Pipefish

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The remarkable level of morphological diversity in the family Syngnathidae (pipefish, pipehorses, seahorses, and seadragons) makes this clade of fish an excellent resource to explore the developmental genetic basis of extreme morphological evolution. Syngnathid fish have novel morphologies such as highly derived skulls and the presence of male pregnancy. The elongated syngnathid body plan is a striking novelty, particularly in the pipefish. Highly conserved hox cluster genes are responsible for positional information in many early developmental processes. Despite the significant amount of hox gene DNA sequence conservation, clustering in the genome, and patterns of expression throughout metazoa, changes in hox genes may underlie a significant amount of animal body plan diversity. We hypothesized that changes in hox genes content or regulation in the syngnathid lineage may have contributed to the evolution of their elongated body plan. To test this hypothesis, we sequenced, annotated and confirmed the orthology of 45 hox genes in the Gulf pipefish genome - the first syngnathid reference genome. Additionally, we searched for cis-regulatory elements and miRNAs co-localized near hox genes. Our results indicate that Gulf pipefish have the typical number of hox genes and hox intergenic noncoding elements for teleost fish, with a few key losses potentially related to axial elongation. The hox 7 genes, which have been hypothesized to be associated with rib loss, appear to have deteriorated independently in the tetraodontid pufferfish lineage and the pipefish lineage. A rhombomere 4 enhancer element for hoxA2b appears to have been lost as well. Therefore a subset of pipefish hox genes may be associated with body plan diversification via differential regulation and gene loss.

P-155 Dissecting the genetic basis of head morphology and evolution in Nasonia

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The evolution of the head was a major step in life's history for the ability to perceive and interact with our environments. The complexities of cranial development bring up numerous questions on the matter of how specific morphology is inscribed in the genome. Several developmental challenges are encountered as many major sensory organs all arise from a common primordium. Proper morphological development of the head depends on complex interactions among several genes acting within multiple tissues. Multifaceted gene interactions rapidly become geneti-

cally intractable in diploid organisms as the number of genes involved increases. This difficulty is significantly reduced using a haploid model system, like Nasonia wasps. The Nasonia genus is fitting for studies in developmental genetics and molecular evolution due to their haplodiploid genetics and the ability for interspecies crosses that result in fertile hybrid offspring. Crosses between two closely related species reveal novel hybrid phenotypes, likely due to negative epistatic interactions. We have begun to unravel these gene interactions and characterize their roles in development by combining the high-throughput techniques of multiplexed shotgun genotyping (MSG) with our method of 3D imaging for phenotyping. MSG software allows for whole genome genotyping of hundreds of individuals simultaneously. We can use this massive genotyping dataset to identify genomic regions that contribute to head shape differences and development incompatibilities between the species, and identify the nature of epistatic interactions among involved loci. Our preliminary results confirm that Nasonia is a uniquely powerful system with which to probe the role of complex gene interactions in the evolution of form.

P-156 Breakdown of Meckel's cartilage provides clues to the evolution of mammals

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The separation of the middle ear ossicles from the mandible by the breakdown of the Meckel's cartilage is a key anatomical change during the evolution of mammals. Recently, fossil mammal-like reptiles have been described with persistent Meckel's cartilage, evidenced by either an ossified Meckel's rod or by a groove in the dentary bone interpreted to be the result of a maintained Meckel's cartilage. These fossils are believed to be transitory forms, since extant non-mammalian gnathostomes maintain Meckel's cartilage, although it does not undergo ossification. We present here evidence to suggest that the biological mechanism underlying the breakdown of Meckel's cartilage is the recruitment of osteoclast-like chondroclast cells to the cartilage. We demonstrate that these clast cells are associated with the Meckel's cartilage of mice and opossums, but not that of non-mammalian species. We then demonstrate that the absence of clast cells in mice due to a null mutation of cFos results in the persistence Meckel's cartilage. Furthermore, we demonstrate that in osteoblast marker osteocalcin is observed with the Meckel's of cFos mutant mice, suggesting that the mammalian Meckel's cartilage is able to undergo ossification in the absence of breakdown. Taken together, these data identify a possible cellular mechanism at the heart of the evolution of mammals.

P-157 FRUITFULL: Interplay between conservation and divergence to shape Cardamine hursuta fruit

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Adaptations for dispersal are ubiquitous in nature and fruits play an important role in the seed dispersal of flowering plants. To identify the genetic basis for different seed dispersal strategies, we employ comparative studies between Cardamine hirsuta and its close relative Arabidopsis thaliana. These species have very similar dehiscent fruits, where seed dispersal occurs via pod shatter. This process in non-explosive in A. thaliana and relies on the precise patterning of fruit tissues (Liljegren et al., 2004). However, in C. hirsuta, pod shatter is explosive, resulting in ballistic seed dispersal. To identify genetic regulators of fruit patterning in C. hirsuta, we screened for mutants with indehiscent fruit. We identified the recessive valveless (val) mutant which has indehiscent and non-explosive fruit. This mutant lacks valve tissue entirely, thus preventing dehiscence. VALVELESS was identified by positional cloning and shown to encode the C. hirsuta ortholog of the well-characterized A. thaliana fruit patterning gene FRUITFULL (AtFUL). C. hirsuta and A. thaliana FRUITFUL genes are well conserved and highly similar at the sequence level. Indeed, AtFUL is sufficient to rescue the C. hirsuta val mutant, suggesting functional conservation between the two species. In the val mutant, valve tissue is homeotically converted into valve margin both in terms of cell fate and marker gene expression. This is similar to the ful mutant phenotype in A. thaliana. However, unlike A. thaliana ful, the val mutant in C. hirsuta does not exhibit ectopic lignification, indicating possible divergence in the genetic network controlling valve tissue identity in C. hirsuta.

P-158 Genetic underpinnings of leaf diversity

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High-throughput sequencing technologies have revolutionized evolutionary biology but the identification of causal genetic changes underpinning the diversity of biological forms remains a significant challenge. This is particularly relevant at the macroevolutionary scale, where classical approaches based on interspecific crosses are difficult to use to link genotypic and phenotypic variation. Leaves of seed plants offer attractive prospects to understand the molecular basis of morphological

change because they exhibit substantial heritable variation at different evolutionary scales. Comparisons between the reference plant Arabidopsis thaliana, which bears simple leaves and its complex-leaved relative Cardamine hirsuta have led to considerable insight on how leaf form develops and diversifies. To gain further insight into the mechanisms that gave rise to different leaf shapes in these two species, we compared their gene expression profiles in developing leaves. We identified several transcription factors expressed at higher levels in Cardamine than in Arabidopsis. We showed that a subset of these genes is expressed in novel expression domains that may represent previously uncharacterized morphogenetic domains of complex leaves. We expressed these genes in Arabidopsis to test whether they are sufficient to generate leaf complexity in simple leaves, and reduced their expression in Cardamine to assess whether they are necessary for compound leaf development. Our results reveal a distribution of effects, with several differentially expressed transcription factors contributing disproportionally to leaf shape. Our findings suggest that change in leaf morphology occurs via a limited number of evolutionary paths, influenced by a defined set of major-effect molecular players.

P-159 The roles of Zax and Xbap in amphibian head development

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Anuran tadpoles have several novel, unique structures which only exist in the larvae and disappear during metamorphosis. The most drastic of these novelties are the rostralia and the derived organisation of cranial muscles that goes along with these. In addition to the primary jaw joint an intramandibular joint between Meckels cartilage and infrarostralia is present. This leads to the formation of a novel feeding apparatus which might be a key to the evolutionary success of this group. Our aim is to find the molecular basis of joint formation in anuran heads and, more general, to find an explanation for how novelties evolve. We investigate the molecular basis of the formation of the anuran jaw joints using functional knock-down of the bagpipe gene Xbap and the bagpipe related homebox gene zampogna (Zax) in Xenopus laevis and Bombina orientalis. The knock-down is performed by injecting morpholino antisense oligonucleotides. Xenopus tadpoles treated with Xbap-morpholino are lacking both the intramandibular and the primary jaw joint. Knock-down of Zax in Xenopus laevis causes a fatal deformation of the anterior part of the head and leads to missing rostralia. MeckelÂ´s cartilage and the infrarostrals are fused and no intramandibular joint is present. Higher doses cause a complete loss of head structures including mouth, eyes and cartilages. Our findings indicate that both genes investigated are essential for the development of the anuran head, especially the anuran jaw. The lack of bapx1 in agnathans and its appearance in gnathostomes in combination with its joint-forming function in anurans could shed

light on how the jaw evolved. Furthermore, the co-option of the related gene Zax in anurans could explain how the rostralia as novelties evolved.

P-160 Seasonal plasticity of thermal reaction norms for development within and between generations in insects

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The rate of insect growth and development is usually regulated by direct influence of temperature but may also be modified by other seasonal cues (photoperiod, food etc). We suppose that the variation in developmental time, which is observed in insects reared under different photoperiods, is generally due to modification of the thermal reaction norms for development. Assuming a linear relationship between developmental rate and temperature we have shown that photoperiod affects the temperature-sensitivity of development in some insects, that is, alters the slope of the regression line and the thermal threshold for development. In northern temperate (Russian) populations of P. apterus, a short-day photoperiod of 12 h accelerates larval development as compared to long-day conditions (20 - 22 h) at lower temperatures, but the reverse is true at higher temperatures. As a result, the slope of the regression line is shallower and the thermal threshold is lower (larval development is less temperature-dependent) under short-day conditions. It means that the bugs from early-summer and late-summer generations demonstrate different thermal sensitivity of development. In a southern population of P. apterus from Israel, a long-day photoperiod of 16 h accelerates larval development under all temperature regimes, which is consistent with its native dry subtropical climate. The thermal sensitivities of development under long- and short-day (10 h) conditions are similar, but the thermal threshold is lower under the former photoperiod. Adult bug body mass increases with temperature in all populations and under all photoperiodic conditions. The adaptive significance of seasonal and geographical changes in the thermal sensitivity of development will be discussed.

P-161 Dynamics of Growth Zone Patterning in the Milkweed Bug Oncopeltus fasciatus

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We describe the dynamic process of abdominal segment generation in the milkweed bug Oncopeltus fasciatus. We have built a comprehensive database of morphological measurements of the growing germ band throughout segmentation. Our data show that while sequential segment addition is a reiterative process, its rate is not uniform over time. We examine the relative contribution of newly formed versus existing tissue to the formation of new segments. Furthermore, we assess the role of cell division in segmentation through the use of embryos stained for

phosphorylated histone 3 (pH3). The expression patterns of a number of key genes, most notably invected (inv) and even-skipped (eve), are used as markers for different stages of segment formation. With these markers we describe morphological and mechanistic changes in the growth zone and in nascent segments during the process of abdominal segmentation. We use this to develop a model for the dynamics of the growth zone during segmentation in Oncopeltus, demonstrating that the growth zone is functionally subdivided into two separate regions, devoted to growth and differentiation respectively, correlated with the expression of specific genes. We then generalize from Oncopeltus to the arthropod segmentation process in general.

P-162 Phosphorylation level of scute regulates evolution of bristle patterns in Diptera

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Evolution of animal morphology is the key point of evolutionary developmental biology. So far, most evo-devo studies on morphological diversification focused on changes at transcriptional level, such as on genes, transcriptional factors and enhancers, but the regulation of animal morphological evolution remains largely unexplored at post-translational level. We used dorsal central (DC) bristles on thorax of Diptera as a phenotypic marker to explore how post-translational mechanisms regulate animal morphological evolution. We analyzed Diptera proneural genes scute and found a number of serine phosphorylation sites on the 3"end of bHLH binding domain of scute Then, we uncovered that the poly-serine phosphorylation sites had a significant positive correlations with DC bristle numbers among Diptera, and these poly-serine phosphorylation sites could be phosphorylated by cdc2. To test the potential correlation between cdc2-induced serine phosphorylation sites of scute and DC bristle numbers in Diptera, we mutated all three cdc2-induced sites in D. melanogaster and two cdc2-induced sites in M. domestica. By using GAL4 system, we found that overexpression of normal Drosophila and Musca scutes in transgenic flies produced many extra bristles in notum, but overexpression of mutated Drosophila and Musca scutes failed to generate extra bristles in notum due to being unable to be phosphorylated. Our results suggest (1) the cdc2-induced phosphorylation status in 3"bHLH domain of scute is a key determinant of neuronal differentiation, (2) phosphorylational regulation at post-translational level could be responsible for animal morphological diversification, (3) this post-translational regulation of bristle development pattern might be evolutionarily conserved through ~100 Mya

P-163 Strigolactones regulate shoot branching in land plants: evolution of the signalling pathway

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Strigolactones (SLs) are phytohormones regulating various developmental processes, including shoot branching and root architecture in vascular plants. Exuded in the soil, SLs have been described as host-presence signals for parasitic weeds, inducing their seed germination. SLs also promote hyphal growth of Arbuscular Mycorrhizal fungi, beneficial to plant growth. SLs are found in the extant descendants of early land plants as the moss Physcomitrella patens (P. patens) and even in some charophytes. Great progress has been achieved in deciphering the SL synthesis and signaling pathways in vascular plants, but the evolution of SL pathway remains elusive. To investigate SL pathway evolution, we have undertaken a reverse genetics approach completed with transcriptomic analyses in the bryophyte model P. patens. Knock-Out mutants have been obtained in both CAROTENOID CLEAVAGE DEOXYGENASE 8 (PpCCD8) and MORE AXILLARY GROWTH 2 (PpMAX2) moss genes, which homologs in vascular plants are involved in SL synthesis and signalling respectively. Characterization of the Ppccd8 mutant has shown that SLs control moss filament extension, and branching of leafy shoot. The first steps of hormone synthesis seem similar in non-vascular and vascular plants. In contrast, analysis of Ppmax2 mutant suggests that SL signalling is more divergent. Furthermore, there is no true ortholog for the SL receptor gene DWARF14 (D14) in the moss genome, but as many as 13 homologs (called PpKAI2-Like genes) are present. We have obtained several multiple mutants in the PpKAI2-Like genes, through CRISPR-Cas9 strategy. These mutants are now being characterized for their response to SLs. In addition, PpKAI2-Like proteins are being expressed for binding assays. Latest results on the project will be presented."

P-164 Divergence beyond constraints: a comparative analysis of thermal reaction norms for development in leaf beetles

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The diversity of developmental periods is immense: some organisms reach the adult stage in a matter of days, whereas others take years to reach maturity. The picture is even more complicated with ectotherms whose developmental periods heavily depend on ambient temperature. This is why thermal reaction norms for development have recently become one of the leitmotifs of ecological-evolutionary research. I will begin with explaining why and how a reaction norm to temperature should be measured instead of absolute durations od developmental periods.

Then I will consider the approaches to describing the phenotypic variation of thermal reaction norms and possible patterns of this variation, as well as some generalizations and predictions made in previous studies as to what may constrain the evolution of developmental rate. For example, the „warmer is better" principle states that adaptation to colder climates necessarily results in slower development because the organism cannot fully compensate for the inhibiting effect of low temperatures. The putatively ubiquitous correlation between the slope and x-intercept of the reaction norm further suggests that faster development at low temperatures must reduce performance at high temperatures. The common-intersection hypothesis posits that developmental rate at the optimal temperature should be evolutionarily conserved. The actual importance of these constraints will be tested on a unique large dataset compiled for leaf beetles.

P-165 Role of a classical Cadherin in epithelialization and germ layer formation of Nematostella vectensis

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Differential expression of Cadherin molecules participates in cell-cell recognition and cell-cell segregation, and is crucial for the germ layer formation during embryo development of the triploblastic Bilateria. Nematostella vectensis belongs to Cnidaria, a sister group of Bilateria, is an excellent model to study the evolution of germ layer formation. Three classical cadherins have been identified in Nematostella. They are characterized by typical intracellular domains, which connect the adhesion complex to the cytoskeleton. In contrast, the extracellular parts of Nematostella classical cadherins rather resemble the non-classical cadherins. One of the cadherin genes, cadherin3 is expressed maternally and broadly throughout development. We generated an antibody to study the establishment of cell polarity, epithelialization and the emergence of the ectodermal-endodermal border in the developing embryo as well as in aggregates of dissociated embryonic cells. By the characterization of the Cadherin3 localization, we show that epithelialization and germ layer segregation occurs similarly in both embryos and aggregates. Epithelialization starts with the accumulation of Cadherin3 at the apical part of the cells. Strikingly, Cadherin3 also forms cell-cell contacts at the basal side of cells. Loss of the Cadherin3 on the basal side of the pre-endodermal plate defines the future endoderm in the embryo. Segregation of the ectoderm in the aggregates happens similarly, by the formation of the basal contacts only in the outer cell layer. To test the role of Cadherin3 during development, we knocked down Cadherin3 by morpholino injection. Cadherin3 morphant embryos fail to gastrulate, while aggregates can not form cell-cell contacts de novo and fall apart

into single cells. Thus, despite of the non-conventional extracellular domain structure of classical cadherins of Nematostella vectensis, Cadherin3 has similar functions as the bilateral classical cadherins: it plays an important role in cell adhesion and participates in germ layer segregation during development."

P-166 Olfactory metamorphosis in terrestrial hermit crabs - ontogenetic transformation of a water to a land nose

Tina, Kirchhoff (University of Greifswald, DEU); Harzsch, Steffen (University of Greifswald, DEU)

During the evolutionary history of Crustacea, several taxa independently invaded land to establish a terrestrial life style. Terrestrial crustaceans include for example members of the hermit crabs (Anomala), such as the giant robber crab Birgus latro (Linnaeus, 1767). These animals depend on the ocean for reproduction but conquer the land during late larval development. The eggs of B. latro are fertilized on land and carried by females under their pleon over several months. Shortly before hatching, they are released into the ocean, where the first larval stage (zoeal) hatch when in contact with salt water. Across four successive marine zoeal stages, the marine benthic megalopa develops. This stage enters an empty gastropod shell to finally invade the terrestrial habitat. During larval settlement and metamorphosis as well as the transition to land, the larvae undergo drastic changes in habitat, morphology, behavior and physiology.
In order to gain insights into the larval olfactory system of B. latro, we investigated the structure of the first pair of antennae and the morphology of the brain in a multi-methodological approach. For the analysis of the peripheral olfactory pathway we used scanning-electron microscopy and fluorescence microscopy, whereas the architecture of the brain was examined by using classical histology and immunhistochemical stainings as well as X-ray micro-computed tomography. First results showed that the olfactory receptor organs, known as aesthetascs, are long and slender in marine larvae, whereas those of the terrestrial stages are progressively shorter and stouter. The central olfactory pathway consists of two main processing neuropils, the olfactory lobes (OL) and the hemiellipsoid bodies. The OL consists of spherical „proto-glomerulia" which display an allatostatin-immunoreactivity already in the first larval stage and a strong FMRFamide-immunoreactivity from the second stage onwards. However, serotonin expression in the glomeruli is detectable in the terrestrial megalopa for the first time.

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P-167 Light & Salt - Thyroid hormone deiodinase paralogues and the evolution of complex life-history strategy in salmonids

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Anadromy has evolved within salmonids as a life history strategy. Juvenile, freshwater-fit («parr») detect photoperiod then salinity changes and undergo a dramatic transition called «smoltification», to become migratory «smolts» thriving in marine environments. A complex endocrine cascade involving the thyroid hormone system leads to phenotype plasticity and profound changes in metabolism and osmoregulation, and a large brain remodeling. We have recently described (Lorgen et al. 2015) a case of sub- (or neo-) functionalization following a salmonid-specific gene duplication that might have been important in the evolution of anadromy. The gene encoding the type 2 thyroid hormone deiodinase (dio2), a main activational switch for the thyroid hormone signaling, gave rise to dio2b, mostly in the brain and responsive to light, and dio2a, mostly in the gills and responsive to salinity. The upregulation of dio2b before the actual endocrine peak might correspond to a very early preparative phase, and dio2a induction by exposure to sea water at the end of smoltification correlates with the changes in ion transporters for sea water tolerance. We present here our first results on the descriptive and functional characterization of the structures, cell types and differentiation stages that express the dio2 paralogues in the brain and the gills during smoltification in the Atlantic salmon (Salmo salar). We compared two strains, a wild anadromous strain (Vosso), and a strain that has become landlocked i fresh water following the postglacial uplift in Norway (Blege). We also propose candidates for upstream regulators.

P-168 A genetic parallel between flightlessness evolution in the Galapagos Cormorant

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Changes in the morphology and size of limbs have played a key role in the adaptive evolution of species. Our own ancestors experienced such changes as they transitioned towards a bipedal, manually dexterous primate. However, despite the ubiquity and evolutionary importance of these modifications, we have a very limited idea of how these changes occur on a genetic and molecular level, especially in vertebrates. In order to fill this gap, we studied a recent case of extreme wing size reduction leading to flightlessness in the Galapagos Cormorant (Phalacrocorax harrisi). We sequenced and de novo assembled the whole genome of four cormorant species and applied a joint predictive and comparative genomics approach to identify genetic variants that severely impact protein function in the Galapagos Cormorant. Among these variants, we found a significant enrichment for genes that cause skeletal ciliopathies when mutated in humans. The primary cilium is essential for Hedhehog (Hh) signaling in vertebrates and individuals affected by ciliopathies have

small limbs and rib cages mirroring the phenotype of P. harrisi. Furthermore, we show that CUX1, a highly conserved transcription factor, has a four amino acid deletion in P. harrisi that affects its ability to promote chondrogenesis and regulate the expression of cilia related genes, many of which are impacted by function-altering variants themselves. Our results strongly suggest that the combined effect of variants affecting cilia function and Hh signaling contributed to the evolution of highly reduced wings and other skeletal adaptations associated with loss of flight in P. harrisi.

P-169 The genetic background of cranial sensory ganglia development and evolution

Papadogiannis, Vasileios (University of Oxford, GBR)

Cranial sensory ganglia are considered a vertebrate evolutionary novelty, holding great importance in the organisation of sensory neural circuits in the head. Their development is widely conserved among vertebrates, while hypotheses have been made on their origin and homologues in other chordates. The aim of this project has been the identification of marker genes expressed in the developing ganglia and the characterisation of regulatory pathways orchestrating the process in different vertebrates. A set of marker genes upregulated in specific ganglia was selected and their expression was analysed in taxa of evolutionary interest. By employing a comparative approach to uncover conserved patterns, as well as key differences, it was attempted to shed light on the genetic background that governs ganglionic development and how this evolved.
The wide diversity of eye designs present in arthropods makes them a unique group to study eye evolution. However, most of our knowledge on the development and neural architecture of the visual system comes from few model organisms. To better understand the diversity and evolution of the arthropod visual system I am studying the eye of the crustacean Parhyale hawaiensis, focusing on its development, neuroarchitecture and function. The compound eye of Parhyale is composed of few ommatidia, which facilitates the mapping of neuronal connections between the eye and the optic lobe. Furthermore, allying the transparent embryo with the possibility of transgenesis and genetic engineering, makes Parhyale a powerful tool for in vivo studies of compound eye development and axonal targeting.

P-170 Exploring the development and evolution of the crustacean eye

Ramos, A. Patricia (École Normale Supérieure de Lyon, FRA); Averof, Michalis (École Normale Supérieure de Lyon, FRA)

The wide diversity of eyes present in arthropods makes them a unique group to study eye evolution. However, most of our knowledge on the development and neural architecture of the visual system comes from just a few model organisms. To better understand the diversity and

evolution of the arthropod visual system I am studying the eye of the crustacean Parhyale hawaiensis, focusing on its development, neuroarchitecture and function. The compound eye of Parhyale is composed of few ommatidia, which facilitates the mapping of neuronal connections between the eye and the optic lobe. Furthermore, allying the transparent embryo with the possibility of transgenesis and genetic engineering, makes Parhyale a powerful tool for in vivo studies of compound eye development and axonal targeting. Parhyale has an apposition compound eye, which has a different optical arrangement from the superposition compound eye, found in Drosophila and other insects. This is followed by differences in the neural architecture of the optic lobe. I am now developing transgenic eye markers and a Brainbow-like stochastic cell labelling in Parhyale to better describe the neuroanatomy of the visual system. With these tools I hope to understand how different photoreceptor projections connect with each other and with the optic lobe, to gain insights into the processing of visual signals. On the developmental side, unlike Drosophila, the eye of Parhyale does not have a fixed number of ommatidia. Instead the eye keeps growing throughout life time, raising questions on how/where new photoreceptors are formed and how the fully developed brain copes with the addition of these new cells.

P-171 Cruziana, Rusophycus and the record of arthropod limb evolution

Kesidis, Giannis (Uppsala University, SWE)

The most iconic of all trace fossils, Cruziana and Rusophycus, have intrigued generations of ichnologists. While their stratigraphic significance and ichnospecific diversity has been thoroughly documented, their mode of formation is still far from clear. The research community is divided regarding the formation of Cruziana. Major issues are the position of the organism in relation to the benthos and the limbs or parts thereof participating in the formation of the trace. The position of the trace maker as an epi- or endo- benthic organism is a crucial aspect of understanding the formation of Cruziana and Rusophycus. Here we discuss the mode of formation of Cruziana through interpretation of material from the Ordovician Sajir formation of Saudi Arabia and the lower Paleozoic of Baltica. Furthermore we attempt to clarify if behavioural evolution can be studied through interpretation of associated trace fossils. Due to the very nature of Cruziana and Rusophycus of preserving fine details of the ventral morphology of the trace producers it is implied that even minor changes in body plan and appendage morphology and function would be documented extensively in the fossil record. Understanding the mode of formation of arthropod trace fossils is crucial in understanding patterns of limb and body plan evolution. Can we document an increasing behavioural repertoire in the Paleozoic? In this report we wish to illustrate the difficulty of working with aspects of trace fossil formation and whether the evolution of arthropod limbs could be documented by

the ornament of associated trace fossils.

P-172 Morphological variation in the upper Cambrian trilobite-like arthropod Agnostus pisiformis

Jackson, Illiam (Uppsala University, SWE)

The Cambrian explosion remains one of the most intriguing events in the history of life. Despite it being much studied, the mechanics governing the radiation remain unclear. A large part of the discussion surrounding the nature of the event regards the relative importance of environmental and/or developmental factors. While multiple theories on this issue have been put forward, very little data exists against which to test them. Separating the effects of environment and development has proved particularly difficult given the confounding interplay between them. This interplay itself has not been a popular object of study. One of the reasons for this is the difficulty of approaching it experimentally with contemporary phylogenetic approaches. My research applies a novel morphometric methodology to the problem using Agnostus pisiformis, a trilobite-like arthropod of Cambrian Series 3, as a model organism. Geographically distant assemblages recovered from ecologically different depositional environments are found to exhibit ontogenetic variation. These findings are interpreted theoretically as an example of genetically canalized morphological development increasing in variation across a gradient of environmental stress.

P-173 Brachiopod origins and the Cambrian radiation: total evidence systematics as a tool to infer deep lophophorate relationships

Butler, Aodhán D. (Uppsala University, SWE; Stanford University, USA)

A major open question in resolving metazoan relationships concerns the phylogeny of the Lophotrochozoa, in which uncertainty prevails despite a wealth of molecular data and methodological strides in analysing these large datasets. Within Lophotrochozoa, brachiopods and allied clades are among the first biomineralised metazoans to appear in the fossil record and represent a significant component of the oldest known fossil records of biomineralised animals, as disclosed by the tommotiids, enigmatic 'small shelly fossil' faunas of the early Cambrian, yet agreement about the placement and affinity of these early forms is remarkably poor despite a growing body of evidence supporting a tentative lophotrochozoan and stem-brachiopod affinity. While the brachiopod fossil record is ultimately the key to determining character homology and polarity during the evolution of the distinctive brachiopod body plan, correctly reading this record has been clouded by disagreement about relationships among the living clades. Persistent questions remain about the monophyly of brachiopods with respect to phoronids, and the relationships of the calcitic-shelled to phosphatic-shelled brachiopods. Currently, we are implementing the first extensive phylogenomic investigation of

extant brachiopods and phoronids, this will aid resolution of the pattern of these deep evolutionary relationships. This new tree, combined with the tommotiid / stem-brachiopod fossil record, will also illuminate the pattern of biomineral changes—unique among Metazoa—during the Cambrian radiation, setting the stage for developing testable mechanistic hypotheses to explain how and why these transformations occurred. Preliminary combined analyses suggest the origin of the lophophorates within Cambrian phosphatic tommotiid fossils is plausible.

P-174 Anterior-posterior patterning in the Rotifer, Brachionus plicatilis

Blommaert, Julie (University of Innsbruck, AUT); Duncan, Elizabeth (University of Leeds, GBR); Dearden, Peter (University of Otago, NZL)

During embryonic development, in many animals, one of the first and most important steps is the formation of the embryonic axes. The anterior-posterior axis determines where the head and tail regions of the animal will be but is not well-understood in rotifers or Lophotrochozonas. Previ-ous studies have indicated that the posterior of the rotifer is reduced when compared to other animals, implying that there may be a difference in the establishment of the anterior-posterior axis. Analysis of this part of devel-opment in rotifers is instrumental in increasing our understanding of de-velopment and the evolution of such processes. Two genes, orthodenticle (Otx) and caudal (Cad) are important in establishing the anterior and pos-terior regions of metazoan embryos, respectively and have been selected as markers for these regions. Here, I have examined the phylogenetic relationships of the rotifer Otx and Cad genes with their orthologs throughout the animal kingdom, and the expression patterns of these genes in B. plicatilis embryos. The Otx gene is expressed in the anterior of the embryo early in development, and later during development staining is seen in putative developing neural tis-sue. Expression of Cad was seen ubiquitously early in development, with expression in the most posterior sections of the embryo later in develop-ment. Three further homeobox containing genes, also thought to be in-volved specification along the anterior-posterior axis, were identified in B. plicatilis. We have shown that Otx and Cad can be used as markers for anterior and posterior development in B. plicatilis embryos; that their expression pat-terns are consistent with those seen in other model animals; and that fur-ther homeobox genes remain to be characterised in this species. Expres-sion patterns of these three other homeobox genes alongside functional studies will give us a greater insight into the formation of this axis in B. plicatilis.

P-175 NEPTUNE evo-devo symposium on neurobiology and marine animal models: Lisbon 9-11 November 2016

Fellows of the Marie-Curie ITN network "NEPTUNE"

P-176 Why and how genetic canalization evolves in gene regulatory networks

Rünneburger, Estelle (Université Paris-Sud); Le Rouzic, Arnaud (Université Paris-Sud, FRA)

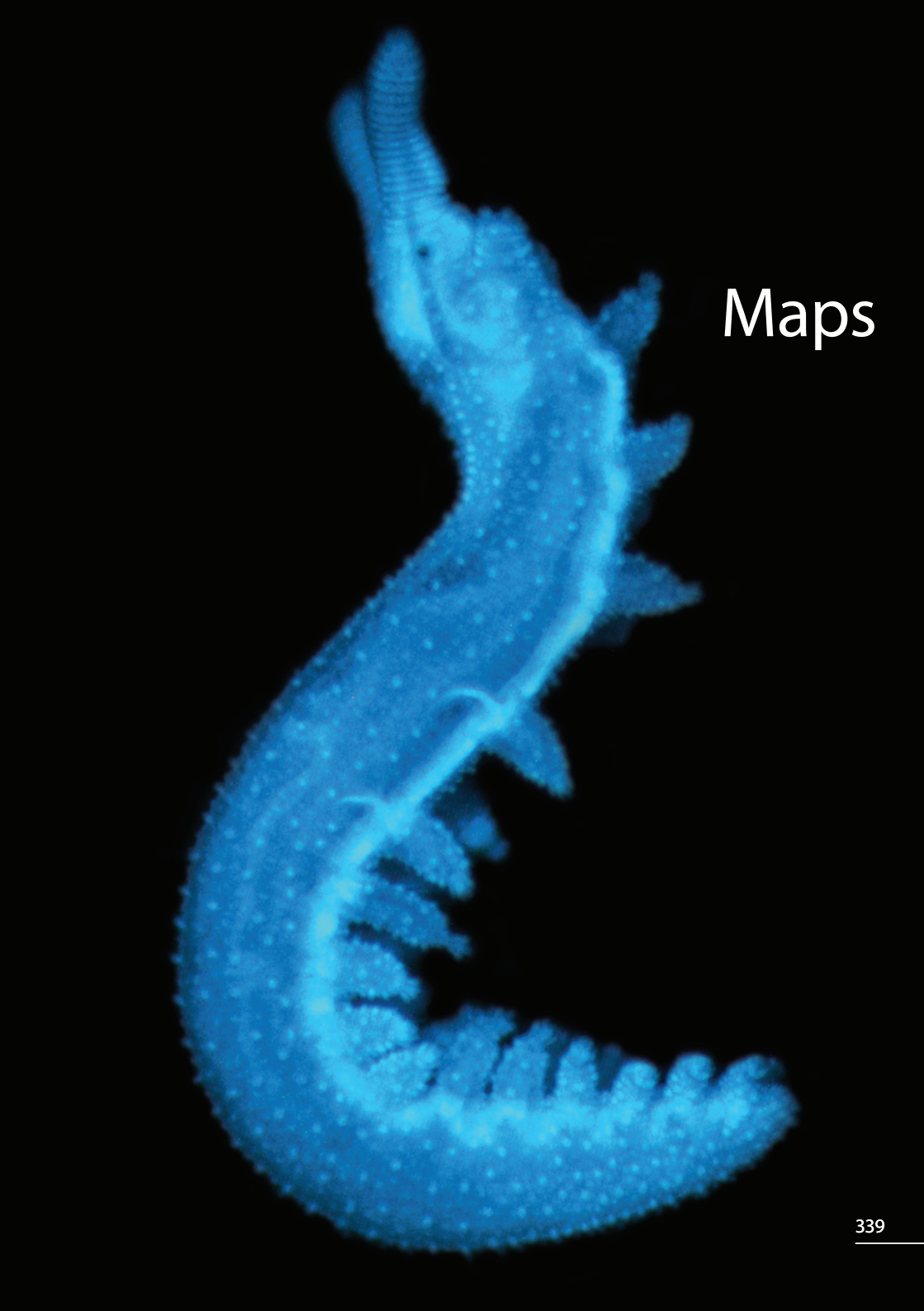
Genetic canalization is commonly described as the capacity of an organism's phenotype to remain unchanged in spite of mutations. As selection for such properties is weak and indirect, whether or not genetic canalization can reasonably evolve in complex genetic architectures is still an open question. In order to describe the conditions in which substantial canalization is expected to emerge in a stable environment, we used a quantitative model of gene regulatory network, combined with a individual-based simulation framework.We showed that most parameters associated with the network topology (complexity and size of the network) have less influence than mutational parameters (rate and size of mutations) on the evolution of genetic canalization. We also established that selecting for extreme phenotypic optima (nil or full gene expression) leads to much higher canalization than selecting for intermediate expression levels. We finally showed that constrained networks become less canalized than networks in which some genes could evolve freely (without stabilizing selection pressure on gene expression). Taken together, theses results lead us to propose a two-fold mechanism involved in the evolution of genetic canalization in gene regulatory networks: the shrinkage of mutational target (useless genes are virtually removed from the network) and redundancy in gene regulation (so that regulatory factors can be lost without affecting gene expression).

P-177 CLAVATA is an ancient pathway for shoot apical meristem function

Sang, Stephanie (University of Bristol, GBR); Aoyama, Tsuyoshi (University of Bristol, GBR); Harrison, Jill (University of Bristol, GBR)

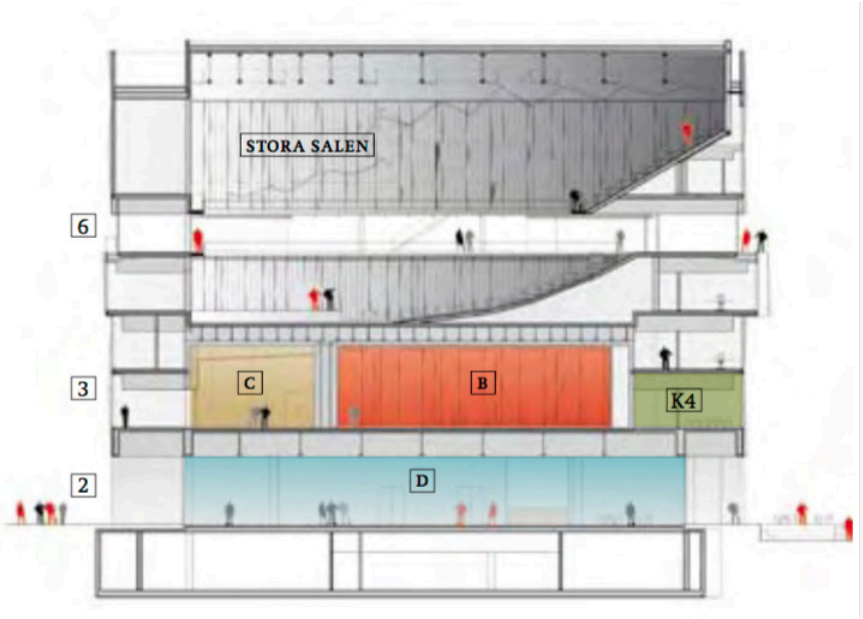
In plants, new organs and tissue form from stem cells in the shoot tips. In Arabidopsis, correctly maintaining the size of the stem cell pool is critical for normal shoot development, and this function is performed by the CLV pathway. By undertaking BLAST searches in a moss, we have found that CLV3, CLV1 and RPK2 are conserved elements of the CLV pathway. We have generated promoter: NLS-GFP-GUS fusion lines to characterize the location and timing of CLV gene activity in the moss, Physcomitrella patens. We are using a reverse genetic approach to determine CLV1a and CLV1b functions. Out results suggest that CLV is an ancient pathway that has conserved roles in meristem function in land plants.

Notes



Maps

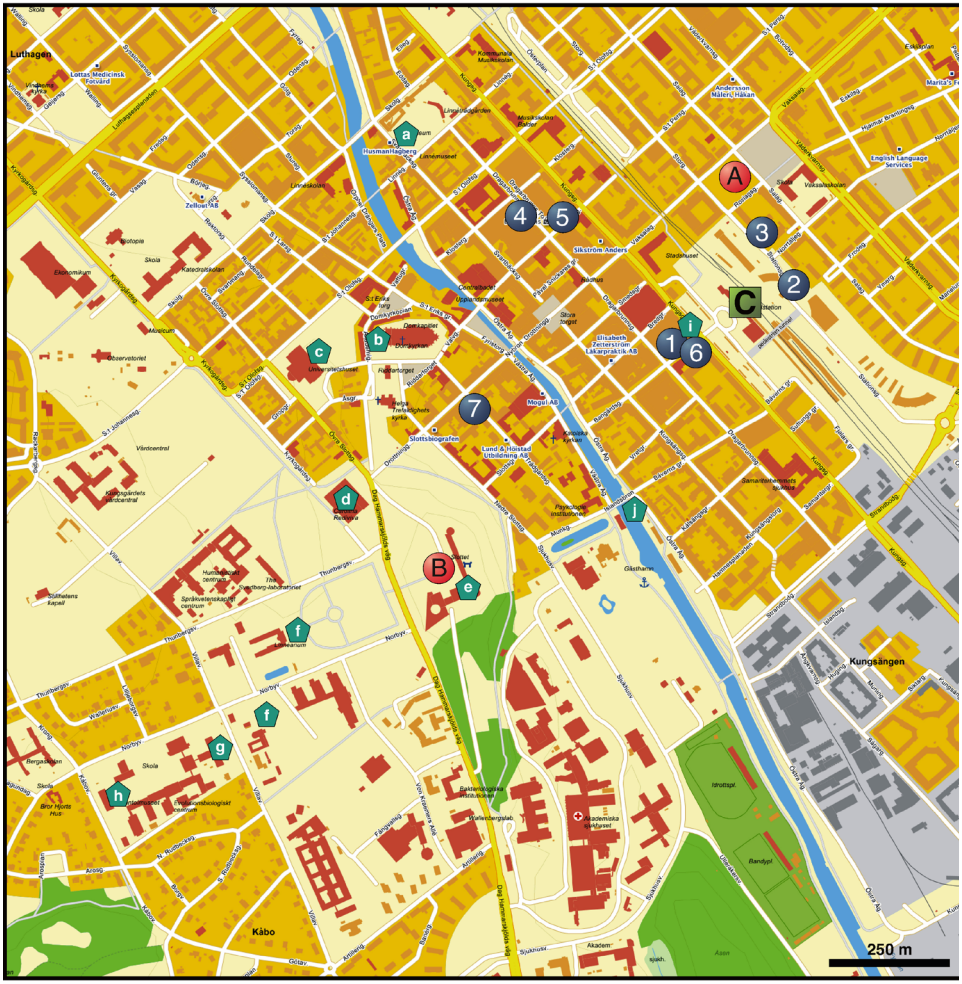
Layout of the Venue



Floor Six: Stora Salen, exhibitors, posters, breaks, help desk

Floor Three: Sal B, Sal C, K3+K4

Floor Two: entry, registration on 26th



Conference locations:

- A Uppsala Concert and Congress Hall (conference venue and ice breaker party)
- B Uppsala Castle (conference dinner)

Accommodation:

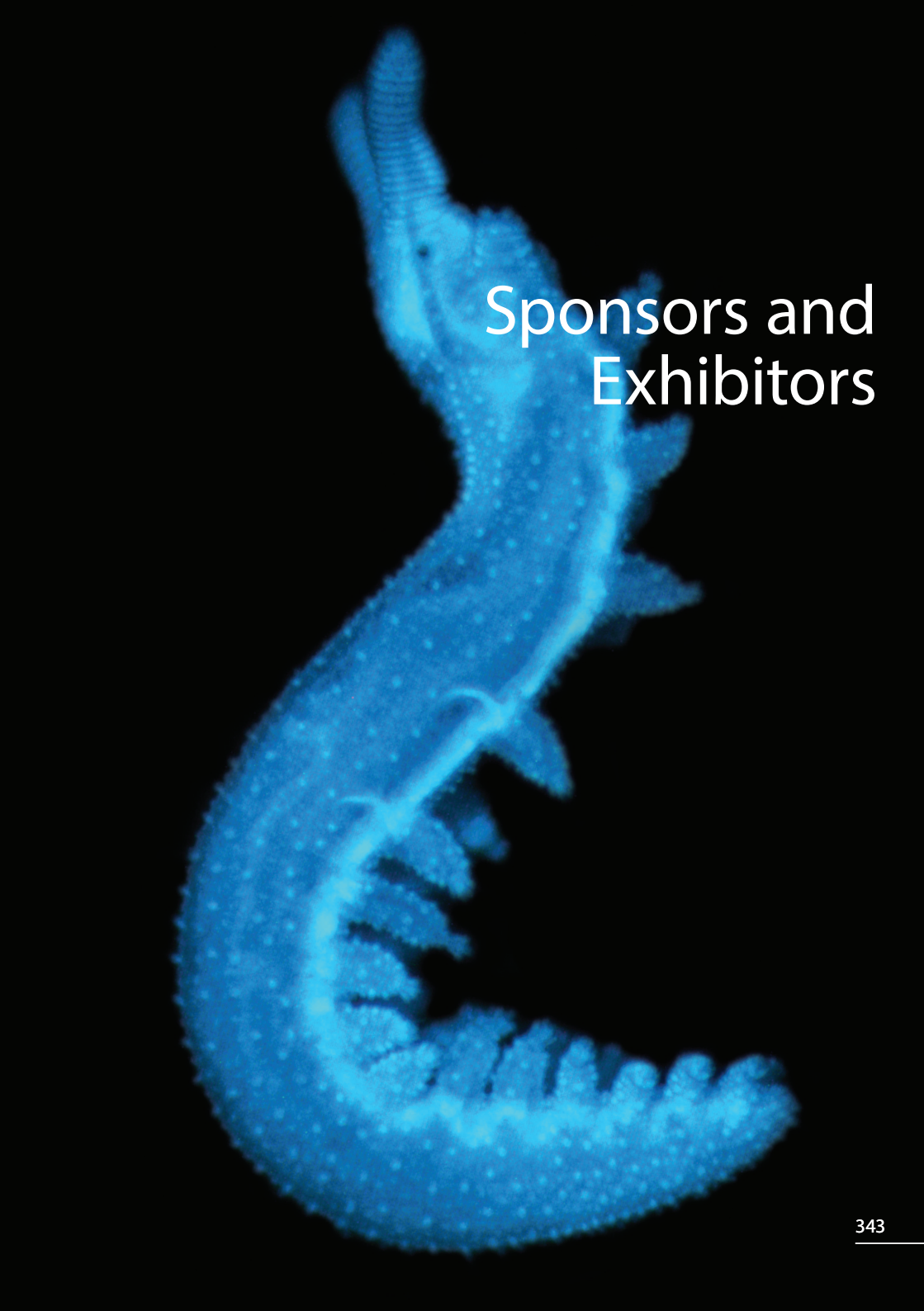
- 1 Hotell Svava
- 2 Radisson Blu
- 3 Radisson Park Inn
- 4 Clarion Hotel Gillet
- 5 Uppsala City Hostel
- 6 Hotell Centralstation
- 7 Uppsala CityStay Hotel

C ***Centralstation*** (train station)

Tourist attractions and sites of interest:

- a Linné Garden
- b Cathedral and Gustavianum
- c University Main Building
- d Carolina Rediviva Library
- e Uppsala Castle
- f Linnéanum and Botanical Garden
- g Museum of Evolution (Zoology)
- h Museum of Evolution (Palaeontology)
- i Tourist information
- j Departure boat tour

Notes



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