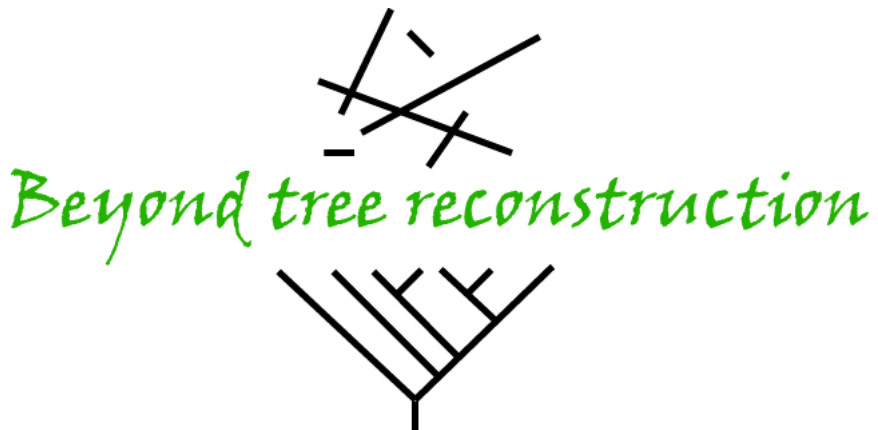


**DZG GRADUATE MEETING
ZOOLOGICAL SYSTEMATICS
LEIPZIG 2012**

March 22nd-23rd



PROGRAMME & ABSTRACTS

UNIVERSITÄT LEIPZIG



RESEARCH
ACADEMY
LEIPZIG



Organisers

Christoph Bleidorn
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General information

Arrival

The meeting will be held at the Research Academy Leipzig in the city centre of Leipzig. It can be conveniently reached by car, train, aeroplane and/or public city transport. Consult the [map](#) for further details. Please consider that parking spaces in the city centre will be limited and subject to payment.

Registration

Registration will be possible during the two days of the meeting, starting from 12am on Thursday, 22nd at the registration desk in the Research Academy.

Talks & Posters

Please make sure that your presentation is compatible with our equipment before your talk. You will have ample opportunity to do so during the meeting. In general, the following formats are supported: .ppt, .pptx, .pdf, .odp & prezzi (flash). Posters should be in portrait format and not larger than DIN A0 (841x1189mm).

Social evening

The social evening will take place at the "Zoologische Lehr- und Studiensammlung" of the University of Leipzig (see [map](#)) on Thursday, starting at 8pm. An amount of food and beverages will be provided.

Addresses & Numbers

Research Academy Leipzig

Burgstraße 21, 04109 Leipzig

☎ +49 341 97 32 350

<http://www.zv.uni-leipzig.de/forschung/ral>

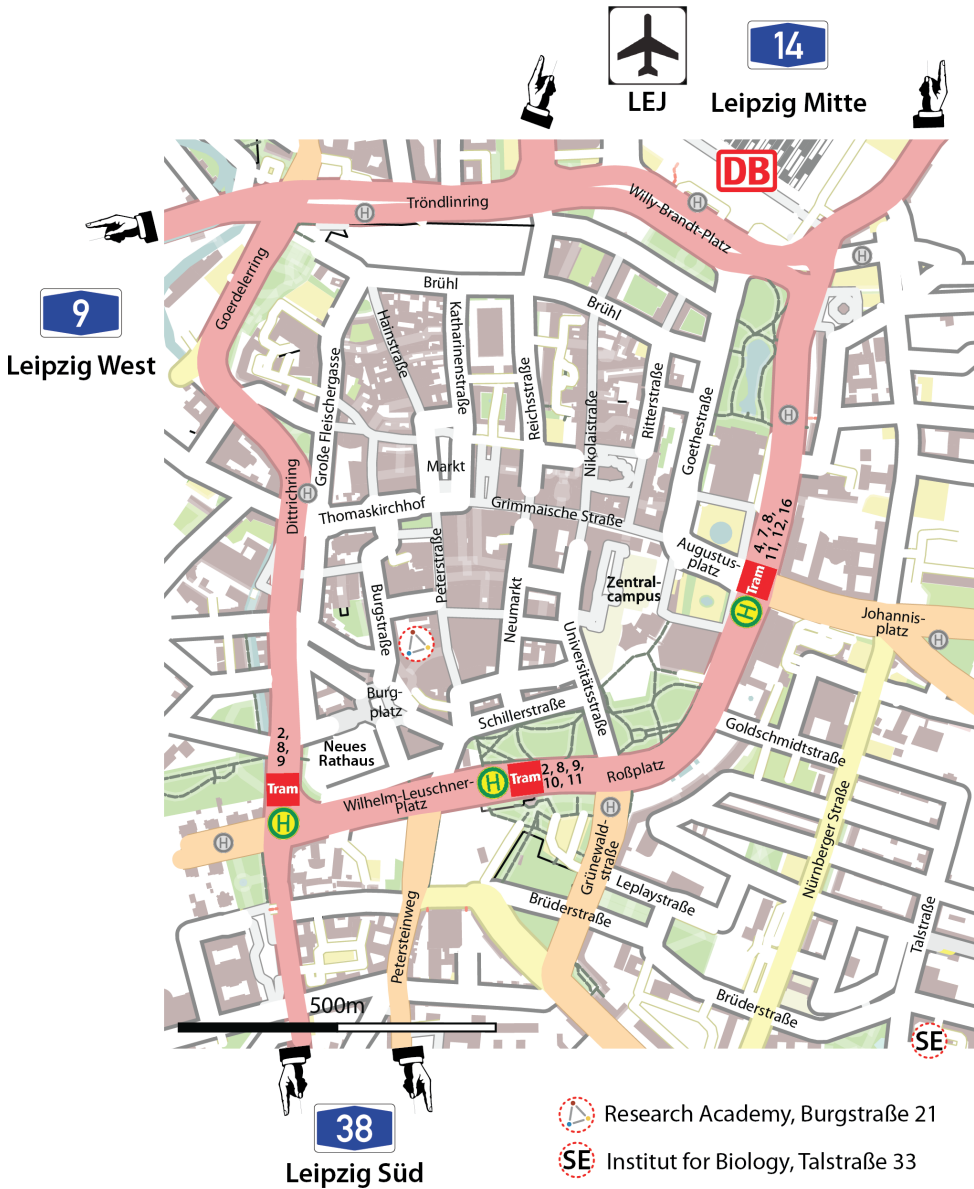
Zoologische Lehr- und Studiensammlung at the Institute for Biology

Talstraße 33, 04103 Leipzig

☎ +49 341 97 36 720

http://www.uni-leipzig.de/~agspzoo/deu/index_deu.htm

Map



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Schedule: Thursday, March 22nd

- | | |
|--------------------|--|
| 14.00-14.15 | Welcome address of the organisers
CHRISTOPH BLEIDORN & LARS PODSIADLOWSKI |
| 14.15-14.30 | Introduction to the Research Academy Leipzig
MARTIN SCHLEGEL |
| 14.30-15.10 | <i>Invited talk</i>
Why phylogeneticists should do phylogenetics and
philosophers philosophy
LARS VOGT |
| 15.10-15.50 | <i>Invited talk</i>
Making sense of mammals: why evolution matters
OLAF R.P. BININDA-EMONDS |
| 15.50-16.20 | Coffee break |
| 16.20-17.00 | <i>Invited talk</i>
Science after the tree: the challenges of bridging the
gaps between metazoan body plans
RONALD A. JENNER |
| 17.00-17.15 | <i>Contributed talk</i>
Geographic structure of intraspecific genetic diversity in
marine Gastrotricha: taxonomic consequences and
possible historic reasons
ALEXANDER KIENEKE |
| 17.15-17.30 | <i>Contributed talk</i>
Microsatellite analysis of genetic structure in urban sand
lizard populations
CLAUDIA ANDRES |
| 17.30-17.50 | Coffee break |

Schedule: Thursday, March 22nd (continued)

- 17.50-18.05** *Contributed talk*
Reconstruction of annelid phylogeny using next generation sequencing data
ANNE WEIGERT
- 18.05-18.20** *Contributed talk*
On the annelid ground pattern: implications for the evolution of body musculature in polychaetes and allies
CONRAD HELM
- 18.20-19.00** **Poster session**
- from 20.00** **Social evening at the "Zoologische Lehr- und Studiensammlung" of the University**

supported by:



Schedule: Friday, March 23rd

- | | |
|--------------------|---|
| 09.30-09.45 | <i>Contributed talk</i>
Novel and neglected morphological characters in velvet worms (Onychophora)
IVO DE SENA OLIVEIRA |
| 09.45-10.00 | <i>Contributed talk</i>
Co-phylogenetic analysis of tick-transmitted <i>Orbivirus</i>
MANJA MARZ |
| 10.00-10.15 | <i>Contributed talk</i>
Exploring horizontal transmission of <i>Wolbachia</i> among bees (Anthophila) and their kleptoparasites
MICHAEL GERTH |
| 10.15-10.30 | <i>Contributed talk</i>
Near Intron Pairs and the metazoan tree
JÖRG LEHMANN |
| 10.30-10.45 | <i>Contributed talk</i>
The phylogeny of the former archiannelidan taxa Protodrilidae and Polygordiidae based on molecular data
ANJA GOLOMBEK |
| 10.45-11.00 | <i>Contributed talk</i>
Bird phylogeny and the activity of avian SINE retroposons
ALEXANDER SUH |
| 11.00-11.20 | Coffee break |
| 11.20-12.00 | <i>Invited talk</i>
Between sensation and artefact: when do we trust a tree-based reconstruction of natural history?
SVEN BRADLER |
| 12.00-13.00 | Lunch break |

Schedule: Friday, March 23rd (continued)

- | | |
|--------------------|--|
| 13.00-13.40 | <i>Invited talk</i>
Myxozoa - evolution of cnidarian parasites
ALEXANDER GRUHL |
| 13.40-13.55 | <i>Contributed talk</i>
Comparative analyses of the evolution of metazoan chitin synthases
ANNE ZAKRZEWSKI |
| 13.55-14.10 | <i>Contributed talk</i>
The small set of arthropod collagens and collagenases
SEBASTIAN MARTIN |
| 14.10-14.40 | Coffee break |
| 14.40-14.55 | <i>Contributed talk</i>
<i>Sacculina carcini</i> - a crustacean genome masked in a fungus-like body
PETER LESNY |
| 14.55-15.10 | <i>Contributed talk</i>
Computational methods for gene order analyses
MATTHIAS BERNT |
| 15.10-16.00 | Round table
Senior researchers share their experiences on
"Scientific projects: from ideas to publications"
with graduate students |
| 16.00 | Departure |

For full author lists & affiliations,
see abstract section or click title

List of posters (alphabetically by first author)

P1

ALEXANDER DONATH

Unravelling the evolution of insects - challenges in the 1KITE project

P2

CARINA EISENHARDT

Near intron pairs (NIPs) and the phylogeny of beetles and related insects

P3

FRANZISKA ANNI FRANKE

Evolution of the Wnt family genes in Onychophora

P4

KATRIN FRIEDEMANN

Evolution of attachment structures in Acercaria

P5

JOSÉ HORACIO GRAU

Autonomous LTR retroelements in the genome of *Silurana (Xenopus) tropicalis* and the transcriptome of *Pelophylax (Rana) ridibundus*

P6

LARS HERING

Opsins in Onychophora (velvet worms) suggest a single origin and subsequent diversification of visual pigments in arthropods

P7

MARIBEL HERNANDEZ-ROSALES

Simulation of gene family histories

P8

HANS-PETER KATZMANN

The hypostome-labrum complex in euarthropods – different names for different structures!

For full author lists & affiliations,
see abstract section or click title

List of posters (continued)

P9

RENE KÖHLER

Mass fingerprints for discrimination of critical species complexes: *Miomantis* (Mantodea) as a model case

P10

SANDRA MEID

Image annotation in MorphDBase

P11

PATRICK PACHL

Convergent evolution of defense mechanisms in oribatid mites (Acari, Oribatida) shows no “ghosts of predation past”

P12

SANDY RICHTER

Analyses of the genomic structure of α -glycerotoxin

P13

HELGE VON SALTZWEDEL

Niche differentiation of the parthenogenetic oribatid mite *Oppiella nova* (Acari, Oribatida) investigated by molecular markers

P14

STEFAN SCHAFER

Phylogeny of Onychophora (velvet worms) based on mitogenomics

P15

ANNE WEIGERT

A survey of Hox gene expression in adult *Owenia* cf. *fusiformis*

For full author lists & affiliations,
see abstract section or click title

Abstracts of talks & posters (alphabetically by presenting author)

Microsatellite analysis of genetic structure in urban Sand lizard populations

CLAUDIA ANDRES (University of Leipzig), KLAUS HENLE (Helmholtz-Zentrum für Umweltforschung Leipzig), MARTIN SCHLEGEL (University of Leipzig)

Biodiversity on earth is threatened by fragmentation and loss of habitats, leading to larger distances between populations, thus impeding gene flow. These processes can result in local, regional, or even global disappearance of species. To investigate the effect of recent anthropogenic habitat fragmentation we surveyed the genetic diversity of eleven Sand Lizard (*Lacerta agilis*) populations in fragmented habitats in and around the city of Leipzig. On the basis of 12 microsatellite loci and 20 individuals per population we analysed diversity parameters like pairwise distances, allelic richness and heterozygosity, as well as the genetic population structure in correlation with GPS-coordinates of captured individuals. All of these approaches revealed a distinct population structure in the *L. agilis* populations. However, neither severe effects of fragmentation nor signs of isolation could be detected in the microsatellite data. This leaves the question open if the duration of fragmentation is yet too short to be detected already or if there are actually no effects of fragmentation.

Computational methods for gene order analyses

MATTHIAS BERNT (University of Leipzig), MARTIN MIDDENDORF (University of Leipzig)

Mitochondrial gene orders are supposed to be a good source of phylogenetic information, particularly for the analysis of deep metazoan phylogenetic relationships. One possibility to access this information is to reconstruct parsimonious rearrangement scenarios. This can for example be done for pairs of species or along the edges of a given phylogenetic tree starting from the leaves corresponding to the gene orders of contemporary species. We present computational tools for gene order analysis that considers the four different types of gene order rearrangements important for mitochondrial gene orders: inversions, transpositions, inverse transpositions, and tandem duplication random loss operations. CREx is a heuristic method for computing short pairwise rearrangement scenarios. Based on CREx the TreeREx method reconstructs the rearrangements on the edges of a given phylogenetic tree. For the analysis of gene order evolution without a given phylogenetic tree we present a novel approach to obtain a comprehensive overview of likely rearrangements.

Abstracts of talks & posters (continued)

Making sense of mammals: why evolution matters

OLAF R. P. BININDA-EMONDS (University of Oldenburg)

Evolution is the framework under which all of biology operates. Even so, it remains that many researchers fail to account for evolutionary relatedness when performing comparative biological analyses. In this talk, I show how employing an evolutionary perspective has led to numerous new insights and even a few surprises concerning mammalian biology and ecology. In particular, I focus on the role played in this regard by so-called supertrees generated from the combination of existing phylogenetic information. Because of the larger size and more comprehensive nature, supertrees have enabled us to test a wider range of hypotheses than before and with greater statistical power. I conclude with a look at the mammalian supertree, a phylogenetic estimate for nearly all living mammals species, and the surprises that this evolutionary tree has already provided us.

Between sensation and artefact: when do we trust a tree-based reconstruction of natural history?

SVEN BRADLER (University of Göttingen)

When challenging an accepted explanation of biological patterns, one should be confident to produce valid inferences based on accurate data, which regularly consist of phylogenetic trees. One central question of macroevolutionary research is whether or not evolution is biased in a particular direction. Analyses of trends and biases in trait evolution have become increasingly sophisticated in recent years, often associated with presumably causal ecological correlates. Besides this more general debate on evolutionary trends, one specific topic has gained growing attention by the scientific community – the potential irreversibility of character evolution or Dollo's Law. A nascent number of studies has been published during the past decade providing more or less convincing examples of reverse evolution or violation of Dollo's Law, ranging from life history strategies like sexual or asexual reproduction and direct or indirect development to complex anatomical characters such as eyes, legs and wings. Based on miscellaneous tree architectures, the proposed scenarios usually received different degrees of acceptance by evolutionary biologists. However, trait re-evolution may be hardest to detect under conditions when it is most likely to occur. Additional information supporting or rejecting the distinct hypotheses needs to come from various tree-independent sources such as biogeography and functionally associated character systems.

Abstracts of talks & posters (continued)

Novel and neglected morphological characters in velvet worms (Onychophora)

IVO DE SENA OLIVEIRA (University of Leipzig), GEORG MAYER (University of Leipzig)

Onychophorans or velvet worms comprise a small group of invertebrates, which play an important role for studying biodiversity, biogeography and conservation. Typically, these animals are regarded as morphologically uniform, showing few characters useful for species designation. Recent molecular studies revealed a high degree of cryptic speciation and endemism among various onychophoran subgroups whereas morphological diversity has not been explored sufficiently thus far. Here, we present new morphological data using scanning electron microscopy on moulted skins and preserved specimens of different onychophoran species (including both Peripatidae and Peripatopsidae). We detected variation occurring among a number of novel and neglected characters and character states associated with various papillae and structures, including volcano-like and bean-shaped papillae, modified sensillae, interpedal organs, embryonic foot projections, chemoreceptors, and tracheal pits. These findings show that the morphological diversity among Onychophora species has been underestimated thus far. The investigation of this diversity might help taxonomists to describing new species and performing reliable taxonomical revisions. In addition, the inclusion of the new characters in morphological data matrices will help clarify the phylogeny of Onychophora, in particular of Peripatidae, which is arguably the least studied major onychophoran subgroup.

Unravelling the evolution of insects - challenges in the 1KITE project

ALEXANDER DONATH (on behalf of the 1KITE consortium) (Zoological Research Museum Alexander König, Bonn)

1KITE (1K Insect Transcriptome Evolution) is an international research initiative that aims to study the transcriptomes of 1,000 insect species encompassing all recognized insect orders. The expected sequence data will allow inferring for the first time a robust phylogenetic backbone tree of insects, one of the most species-rich groups of metazoan organisms. Preliminary analyses of the already available sequences show that the obtained data are of yet unparalleled size and quality. Thus, 1KITE not only shows the need for but explicitly includes the development of new software for data quality assessment, phylogenetic reconstruction, and molecular dating that will allow for advanced and accelerated analyses of such large amounts of sequence data.

Abstracts of talks & posters (continued)

Near intron pairs (NIPs) and the phylogeny of beetles and related insects

CARINA EISENHARDT (University of Leipzig), JÖRG LEHMANN (University of Leipzig), PETER F. STADLER (University of Leipzig), VEIKO KRAUSS (University of Leipzig)

Today, the reconstruction of the organismal evolutionary tree is based mainly on molecular sequence data. However, the resolution is sometimes insufficient, particular in deep branches. We found a new phylogenetic marker class which we called near intron pair (NIP). This marker is derived by insertion of a novel intron located less than 50 nt from an evolutionary older intron position. Since correct splicing is impeded by very small exons, such near intron pairs (NIPs) very rarely coexist. The gain of the novel intron is nearly always associated with the loss of the old intron. In cases of intron migration both events are directly connected. Therefore, it should be possible to characterize one of the introns as ancient (plesiomorphic) and the other as novel (derived or apomorphic). The suitability of NIPs as a phylogenetic marker was demonstrated by analysis of the evolutionary positions of Hymenoptera and Coleoptera in relation to Lepidoptera and Diptera using genome project and genomic PCR data. Now the resulting phylogenetic informative intron distributions are investigated in representative species of other holometabolic insect orders in order to expand the genome-scaled studies of holometabolic insects. Additionally, we evaluate the two hypothetical pathways to NIPs (consecutive intron loss and intron gain versus intron migration) and determine the relative age of the novel intron positions. Evaluating 38 NIPs localized in 23 genes, we found one case, where the Neuropterida share a synapomorphic intron position with coleopterans exclusively. This supports a sistergroup-relationship between Neuropterida and Coleoptera (Neuropteriformia). In addition, we found one common derived intron of Strepsiptera with Polyphaga excluding the Adephaga. This suggests a position of the Strepsiptera inside the Coleoptera. Furthermore, we found that all derived intron positions are of moderate age. Some evidence point out that at least two of these novel intron positions resulted from intron migration and did not involve the insertion of novel introns.

Abstracts of talks & posters (continued)

Evolution of the Wnt family genes in Onychophora

FRANZISKA ANNI FRANKE (University of Leipzig), LARS HERING (University of Leipzig), GEORG MAYER (University of Leipzig)

Organisation of the body into serially repeated units or segments is found in several distantly related animal groups, including chordates, annelids and arthropods. The evolutionary origin of body segmentation in these groups is under debate and it is unclear whether segmentation has evolved once, twice, or several times among bilaterians. Gene expression studies in one of the closest relatives of arthropods, the Onychophora, might help to clarify this issue since the onychophoran body shows both segmental and non-segmental features. Previous studies have shown that the Wnt family genes, including wingless (Wnt1), play a crucial role in the segmentation process of the arthropod embryo. However, the function of these genes in onychophoran development remains obscure. To assess whether onychophorans and arthropods share a common segment patterning mechanism, we have identified the complete set of Wnt genes in the embryonic transcriptomes of two onychophoran species using Next Generation Sequencing methods. Our phylogenetic analysis of the obtained sequences shows that two genes, Wnt8 and Wnt3, are missing from the onychophoran transcriptomes. Ongoing expression studies of the identified Wnt orthologs will help to understand the function of these genes and clarify their involvement in the segmentation process of the onychophoran embryo.

Evolution of attachment structures in Acercaria

KATRIN FRIEDEMANN (University of Jena), ROLF G. BEUTEL (University of Jena)

The Acercaria are an extremely diverse group of insects comprising mainly plant-sucking insects like cicada, plant- and treehoppers, true bugs, aphids and other plant lice, but also parasitic taxa like the true lice. The relationships between the main groups of the Acercaria are still controversial. The efficiency as plant feeders is connected to the ability to walk on different plant surfaces. Therefore the Acercaria display an unusually broad variation of different types of attachment devices. The aim is to investigate the structure of different types of attachment pads, their evolutionary changes, and correlations with surface modifications in host plants. An evolutionary scenario for the relevant structures is developed based on solid phylogenetic hypothesis.

Abstracts of talks & posters (continued)

Exploring horizontal transmission of *Wolbachia* among bees (Anthophila) and their kleptoparasites

MICHAEL GERTH (University of Leipzig), JULIANE RÖTHE (University of Leipzig), CHRISTOPH BLEIDORN (University of Leipzig)

Wolbachia is a widespread intracellular bacterial symbiont of many arthropods. It is best known for its ability to manipulate its hosts reproduction, thereby enhancing its own vertical transmission. Some studies suggest that *Wolbachia* must also be transmitted horizontally between host species quite frequently. However, the mechanism thereof is not understood. In our study we aimed to test by multi-gene phylogenetic analyses of *Wolbachia*- strains from bee hosts whether the bacteria can be transmitted from bees to their kleptoparasites.

First results show that most bees bear quite similar *Wolbachia* strains and suggest that horizontal transfer of infections between bees and their kleptoparasites may occur. However, other pathways do not seem unlikely and need further exploration.

The phylogeny of the former archiannelidan taxa Protodrilidae and Polygordiidae based on molecular data

ANJA GOLOMBEK (Zoological Research Museum Alexander König, Bonn), TORSTEN H. STRUCK (Zoological Research Museum Alexander König, Bonn)

Marine interstitial annelid taxa are characterized by a small body size and an apparently simple body organisation. Initially, several of these interstitial taxa have been considered as primitive annelids and as part of the basal grade "Archiannelida" (e.g., Protodrilidae, Saccocirridae, or Polygordiidae). Conversely, these taxa were regarded as a polyphyletic assemblage of highly derived but secondarily simplified annelids adapted to the interstitial realm. Anatomical and ultrastructural similarities of pharyngeal organs and palps group Protodrilidae, Protodriloidae, and Saccocirridae together as Protodrilida, with an eventual paedomorphic origin within Spionida. In case of Polygordiidae, morphological similarities of cuticle, musculature, and locomotory patterns suggested a closer relationship to Opheliidae. However, these similarities could also reflect convergent adaptations to coarse gravel sediments. First molecular analyses based on 18S- and 28S-rDNA neither support a monophyletic taxon Protodrilida nor a sistergroup relationship of Polygordiidae and Opheliidae, but indicate a possible sistergroup relationship of Polygordiidae and Saccocirridae as well as these taxa being part of a basal radiation although with weak support. On the other hand, preliminary ML analyses of mitochondrial sequence data indicate a sistergroup relationship of Polygordiidae and Protodrilidae (Protodrilida), and both are not part of the basal radiation albeit with low support. Furthermore, neither Spionida nor Opheliidae are the sister of this clade.

Abstracts of talks & posters (continued)

Myxozoa - evolution of cnidarian parasites

ALEXANDER GRUHL (Natural History Museum, London)

Myxozoans are endoparasites that have complex life cycles involving aquatic invertebrates (annelids, bryozoans) as primary hosts and teleost fishes as secondary hosts. Most myxozoans are morphologically very simple and lack major metazoan features like gametes, gonads, gut, nervous system or body axes. Therefore, this taxon has long been considered phylogenetically problematic and was for example suggested to be a group of protistan eukaryotes. Recent phylogenomic data suggest a cnidarian affinity for Myxozoa. However, conflicting signals and low support values, possibly due to high rates of sequence evolution still weaken this confidence. I will give examples of morphological characters that can help to settle the position of the Myxozoa. The appreciation of myxozoans as metazoans and cnidarians implies that morphological simplicity is derived. This, together with the recognition of varying degrees of simplification within Myxozoa, allows to investigate mechanisms and possible evolutionary causes for the reduction of morphological characters.

Abstracts of talks & posters (continued)

Autonomous LTR retroelements in the genome of *Silurana (Xenopus) tropicalis* and the transcriptome of *Pelophylax (Rana) ridibundus*

JOSÉ HORACIO GRAU (Museum für Naturkunde, Berlin), Albert Poustka (Max Planck Institute for Molecular Genetics, Berlin), Martin Meixner (Services in Molecular Biology GmbH), Jörg Plötner (Museum für Naturkunde, Berlin)

Long terminal repeat retroelements (LTR-RTs) constitute a diverse group of mobile genetic elements or transposable elements widespread across eukaryote genomes. They play an important role in genome evolution because of their ability to create large scale mutations and genome rearrangements. LTR-RTs are transposed by reverse transcription of an RNA intermediate. Even though transcription of transposable elements is not sufficient to cause their transposition, transcriptional activity is a necessary first step towards the mobilization of retroelements. Since no comprehensive study on the transcription of LTR-RTs is available so far, the aim of our study was to assess the occurrence of LTR-RTs within frog transcriptomes. For this we identified and compared retroelements from the genome and EST library of *Silurana (Xenopus) tropicalis*, and two transcriptomes of brain and testis of the advanced frog species *Pelophylax (Rana) ridibundus*. In order to assess the diversity of mobile elements within frog genomes we first scanned the genome of *S. tropicalis* where we identified a total of 7474 complete LTR-RTs. The protein predictions of *S. tropicalis* EST library and *P. ridibundus* transcriptomes were scanned for the retrotranscriptase domain of the POL protein which is present in all LTR-RTs. The results yielded several hundred proteins and fragments specific of LTR-RTs. All four datasets were then combined with other known retroelements, aligned and prepared for phylogenetic analysis. The resulting trees show that retroelements from families BEL/PAO, Retroviridae, Ty3/Gypsy and TY1/Copia are well diversified in the frog genome and many of them represent new classes and clades. The results suggest that LTR retroelements are highly active within the genome with exception of the Ty1/Copia family where two novel classes have been found. Although overall transcriptional profiles differed significantly between brain and testis transcriptomes, no significant differences in transcriptional activity of retroelements between brain and testis have been identified so far.

Abstracts of talks & posters (continued)

On the annelid ground pattern: implications for the evolution of body musculature in polychaetes and allies

CONRAD HELM (University of Leipzig), CHRISTOPH BLEIDORN (University of Leipzig)

Developmental modes and body plan diversification within annelids are as diverse as the habitat types these lophotrochozoans are distributed in. Thus, it is inevitable to investigate a huge variety of taxa sampled across the annelid tree of life to understand character evolution for several organ systems. One such character complex is the muscular system. Although representing a distinct and consistent character complex, our knowledge concerning ground patterns and variability of character plasticity within annelids is still sparse. In order to extend our knowledge concerning the variability of muscular patterns within Annelida, and to reconstruct a hypothetical muscular ground pattern valid for annelids and allies, we analyzed the distribution of f-actin, a widespread element of muscle fibers, within different annelid taxa using phalloidin labeling in conjunction with confocal laser scanning microscopy (clsm). Our investigations broaden the knowledge concerning the evolution of muscular characters in lophotrochozoans and provide implications for the evolution of muscular patterns in polychaetes and allies.

Opsins in Onychophora (velvet worms) suggest a single origin and subsequent diversification of visual pigments in arthropods

LARS HERING (University of Leipzig), CHRISTOPH BLEIDORN (University of Leipzig), GEORG MAYER (University of Leipzig)

Multiple visual pigments, prerequisites for colour vision, are found in arthropods, but the evolutionary origin of their diversity has remained obscure. We explored the opsin genes in two distantly related species of Onychophora, the putative sister group of Arthropoda, using deep transcriptome sequencing techniques. Surprisingly, our data reveal the presence of only one opsin gene (onypsin) in each onychophoran species. In our phylogenetic analyses, the onypsins represent the sister group to the monophyletic clade of visual r-opsins of arthropods. These findings provide evidence for monochromatic vision in velvet worms and in the last common ancestor of Onychophora and Arthropoda, suggesting that the diversification of visual pigments and colour vision evolved in arthropods, along with the evolution of compound eyes – one of the most sophisticated visual systems known. Thus, we assume that the Early Cambrian stem-lineage arthropods without compound eyes, such as *Opabinia regalis*, displayed no colour vision.

Abstracts of talks & posters (continued)

Simulation of gene family histories

MARIBEL HERNANDEZ-ROSALES (University of Leipzig), NICOLAS WIESEKE (University of Leipzig), MARC HELLMUTH (University of Leipzig), PETER STADLER (University of Leipzig)

The reconstruction of the evolutionary history of large gene families has remained a hard and complex problem, which amounts to disentangling speciation events from gene duplication events. The evaluation of reconstruction algorithms is hampered, furthermore, by the lack of well-studied cases that could serve as a gold standard. We present here a simulation environment designed to generate large gene families with complex duplication histories on which reconstruction algorithms can be tested and software tools can be benchmarked.

Science after the tree: the challenges of bridging the gaps between metazoan body plans

RONALD A. JENNER (Natural History Museum, London)

As we draw nearer to a consensus of the phylogeny of Metazoa, we can start using the tree to understand the intricacies of animal body plan evolution. However, the major gaps between phenotypically dissimilar taxa stand in the way of achieving any detailed understanding of the divergence of the crown body plans of higher-level taxa. I will discuss the many challenges of bridging these gaps, and the difficulties of formulating testable scenarios of body plan evolution.

The hypostome-labrum complex in euarthropods – different names for different structures!

HANS PETER KATZMANN (University of Ulm), JOACHIM T. HAUG (Yale University), ANDREAS MAAS (University of Ulm), DIETER WALOSSEK (University of Ulm)

Aiming at demonstrating that hypostome and labrum are two different structures with different origins and different tasks, we will investigate a wider range of euarthropod taxa including fossil representatives, applying modern documentation methods including 3D imaging. Our aims are the homologization of the different structures around the mouth opening, a standardized terminology and the reconstruction of the evolution of the hypostome-labrum complex within the Euarthropoda.

Abstracts of talks & posters (continued)

Geographic structure of intraspecific genetic diversity in marine Gastrotricha: taxonomic consequences and possible historic reasons

ALEXANDER KIENEKE (DZMB Wilhelmshaven), PEDRO MARTÍNEZ ARBIZU (DZMB Wilhelmshaven), DIEGO FONTANETO (Imperial College London)

A substantial fraction of marine meiobenthic taxa such as Gastrotricha are known to lack active or passive dispersal stages and thus assumed to be characterized by a poor dispersal capacity. This should be displayed by low levels of gene flow between geographically separated populations and lead to a distinct spatial structure of genetic diversity. However, most traditional and phenotypically defined species are widely (globally) distributed, and this creates a paradox situation. To shed light on this apparent paradox, we test (1) whether such wide distribution may be due to misidentification and lumping of cryptic species with more restricted distributions and (2) whether spatial structures exist for the within-species genetic diversity of marine gastrotrichs at a regional spatial scale. As a model, we used a number of species of the genus *Turbanella* from different European shorelines of the NE Atlantic and adjacent shelf regions.

DNA taxonomy by means of mitochondrial plus nuclear sequence data, and statistic tests support distinctness of four traditional species (*Turbanella ambronensis*, *T. bocqueti*, *T. cornuta*, and *T. mustela*). Furthermore, we found evidence for two cryptic species within *T. hyalina* that occur sympatrically at different sites. An effect of geography on the intraspecific genetic structure of the most sampled species *T. cornuta* and *T. hyalina* is indeed present, with the potential for performing phylogeographic inference and for understanding past colonization processes of these microscopic animals. Holocene coastline transformations of the studied area much likely had an influence on the present-day distribution of distinct genetic variants. On the other hand, the discovery of a widely distributed haplotype indicates long-distance dispersal as well, despite the assumed low dispersal ability of gastrotrichs. Is this an indication for recent human-mediated dispersal?

Abstracts of talks & posters (continued)

Mass fingerprints for discrimination of critical species complexes: *Miomantis* (Mantodea) as a model case

RENÉ KÖHLER (University of Cologne), REINHARD PREDEL (University of Cologne)

Species complexes are often difficult to describe because of high intraspecific morphological variability on the one hand and a lack of distinct morphological characters on the other hand. Here we used neuropeptides which co-evolve with their respective receptors as marker to distinguish insect taxa, focusing on Praying Mantids. MALDI-TOF mass spectra of thoracic and abdominal perisymphathetic Organs in which extended FMRF amides and CAPA-periviscerokinins are accumulated resulted in group specific mass fingerprints. These fingerprints and the complete sequences of CAPA-periviscerokinins were sampled from 80 Mantodea species; 20 of those belong to the frequently modified genus *Miomantis* SAUSSURE, 1870. The data confirmed the monophyly of Mantodea. In contrast to Blattoptera, Mantodea have very similar CAPA-periviscerokinin sequences and do not express CAPA-Pyrokinnin. The specificity of the mass fingerprints was subsequently used to calibrate morphological characters, and both characters were included in a determination key. Herewith an instrument is given to distinguish living or frozen individuals to populations and species, independent from their larval status or sex.

Near intron pairs and the metazoan tree

JÖRG LEHMANN (University of Leipzig), PETER F. STADLER (University of Leipzig), VEIKO KRAUSS (University of Leipzig)

Gene structure data can substantially advance our understanding of metazoan evolution and deliver an independent approach to resolve conflicts among existing hypotheses. Here, we used changes of spliceosomal intron positions as novel phylogenetic marker to reconstruct the animal tree. This kind of data is inferred from orthologous genes containing mutually exclusive introns at pairs of sequence positions in close proximity, so-called near intron pairs (NIPs). NIP data were collected for 47 species and utilized as binary genome-level characters in maximum parsimony analyses to reconstruct deep metazoan phylogeny. Our analysis supports e.g. Bilateria, Protostomia, Deuterostomia, Ecdysozoa, Platyhelminthes, Pancrustacea, Chordata, and Vertebrata. Arthropoda, however, were not recovered, as the mite Ixodes was placed more basal than expected within the tree. Some other, problematic branchings can be explained by the paucity of synapomorphic changes of intron positions shared between some genomes. In addition, we obtained an assemblage of Cnidaria, Demospongia, and Placozoa as sister group of bilaterian animals, a disputable, but remarkable result. We conclude that NIPs can be used as phylogenetic characters also within a broader phylogenetic context, given that they have emerged regularly during evolution irrespective of the large variation of intron density across metazoan genomes.

Abstracts of talks & posters (continued)

Sacculina carcini – a crustacean genome masked in a fungus-like body

PETER LESNY (University of Bonn), LARS PODSIADLOWSKI (University of Bonn)

Adults of the parasitic barnacle *Sacculina carcini* have lost all features commonly found in arthropod body structure. *Sacculina* grows a fungus-like rootlet system in their hosts body cavity. Nevertheless the complexity of genome and transcriptome seems not to have changed that dramatically. Our comparative genomics approach tries to characterize genomic changes associated with the evolutionary steps towards a sessile (Cirripedia) and parasitic lifestyle (Rhizocephala).

The small set of arthropod collagens and collagenases

SEBASTIAN MARTIN (University of Bonn), LARS PODSIADLOWSKI (University of Bonn)

In a comparative genomics approach we performed a comprehensive review of arthropod collagens and associated genes (matrixins, TIMPs). In comparison to deuterostomes, Lophotrochozoa and even nematodes, there are relatively few members of these genes in arthropods. Especially the fibrillar collagens are much less divergent here. Due to a low amount of sequence similarity and incompatibility to the vertebrate collagen families, there are inconsistencies in nomenclature and orthology assessment. Thus, there is a need for a revision of the arthropod collagen superfamily.

Co-phylogenetic analysis of tick-transmitted *Orbivirus*

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We completed genome sequences of Tribečvirus (TRBV) and Kemerovo virus (KEMV), two tick-transmitted Orbiviruses that can cause diseases of the central nervous system and that are currently classified into the Great Island virus serogroup. VP2 proteins of TRBV and KEMV show very low sequence similarity to the homologous VP4 protein of tick-transmitted Great Island virus (GIV). The new sequence data support previous serological classification of these Orbiviruses into the Kemerovo serogroup, which is different from the Great Island virus serogroup. Genome segment 9 of TRBV and KEMV encodes several overlapping ORF's in the +1 reading frame relative to VP6(Hel). A co-phylogenetic analysis indicates a host switch from insect-borne Orbiviruses toward Ixodes species, which is in disagreement with previously published data.

Abstracts of talks & posters (continued)

Image annotation in MorphDBase

SANDRA MEID (Zoological Research Museum Alexander König, Bonn), PETER GROBE (Zoological Research Museum Alexander König, Bonn), LARS VOGT (Zoological Research Museum Alexander König, Bonn)

MorphDBase is an online web portal and data repository, which allows the archiving, sharing and dissemination of morphological data. It manages entries about taxa, biological specimens, media, literature and morphological character matrices. In MorphDBase's current version it is already possible to annotate single images. With the ongoing project we want to implement a new functionality that will also allow the annotation of image series.

Convergent evolution of defense mechanisms in oribatid mites (Acari, Oribatida) shows no "ghosts of predation past"

PATRICK PACHL (University of Göttingen), KATJA DOMES (Darmstadt), GARVIN SCHULZ (University of Göttingen), ROY A. NORTON (State University of New York), STEFAN SCHEU (University of Göttingen), INA SCHAEFER (University of Göttingen), MARK MARAUN (University of Göttingen)

Oribatid mites are diverse and abundant terrestrial soil arthropods that are involved in decomposition of organic matter and nutrient cycling. As indicated by fossils starting from the Devonian, they evolved varied mechanisms and structures for defense from predators. We investigated four of these defensive structures (ptychoid body, hologastrы, mineralization and opisthonotal glands) and used ancestral character state reconstruction to determine whether they evolved convergently and how many times this may have happened. Phylogenetic trees based on 18S rDNA were constructed for 42 oribatid mite species and two outgroup taxa using likelihood and Bayesian algorithms. The results suggest that at least three of the four defensive structures evolved convergently several times, for opisthonotal glands convergent evolution remain equivocal. This high level of convergence indicates that predation has been an important factor throughout the evolution of oribatid mites, contributing to morphological diversity and potentially also to species richness, as there are indications that some taxa radiated after the evolution of defense structures. Despite the ancientness of oribatid mites, defense structures presumably have rarely been lost suggesting that they still are functional and necessary to reduce predation, rather than being 'ghosts of predation past'.

Abstracts of talks & posters (continued)

Analyses of the genomic structure of α -glycerotoxin

SANDY RICHTER (University of Leipzig), JÖRG HETMANK (University of Leipzig), LARS HERING (University of Leipzig), GIAMPIETRO SCHIAVO (Cancer Research UK London Research Institute), CHRISTOPH BLEIDORN (University of Leipzig)

Glyceridae (bloodworms) are carnivorous polychaetes which use their eversible pharynx for prey catching. The pharynx is equipped with four teeth which are connected with venom producing glands. Venom systems evolved in a broad phylogenetic range of animals and are used for defense or predation. Venoms consist of mixtures of bioactive molecules, including proteins, organic molecules (such as neurotransmitters and amino acids), and salts. Active components are usually described as toxins. The investigation of such toxins often leads to the discovery of agents which could be very relevant for the development of new medications in medicine. In a study (Meunier et al. 2002, EMBO J 21: 6733-6743) it has been found, that some bloodworm species are able to produce a currently unique neurotoxin. This α -glycerotoxin is characterized by its specific effect on the nervous system in stimulating CaV2.2. channels with a high specificity. Additionally its effects are completely reversible. The combination of the high specificity and reversibility of α -glycerotoxin could it make to an important tool in medicine.

We conducted mRNA-seq, as well as whole genome shotgun sequencing of gland tissue from *Glycera tridactyla* using Illumina sequencing technology. Using amino acid data from protein sequencing of short fragments of purified glycerotoxin we were able to identify a 3000bp coding sequence of the 3' end of α -glycerotoxin in our sequence data, which might span 30% of the 320kDA protein. Based on this data set, specific primers were designed which made it possible to amplify a nearly 6kb fragment from genomic DNA. So far, sequencing revealed the existence of at least three introns within our fragment. Moreover, we were able to identify a 1000bp coding region of α -glycerotoxin in other *Glycera* species. Using a phylogenetic approach, we show that all currently identified glycerotoxin-bearing species form a monophyletic group.

Abstracts of talks & posters (continued)

Niche differentiation of the parthenogenetic oribatid mite *Oppiella nova* (Acari, Oribatida) investigated by molecular markers

HELGE VON SALTZWEDDEL (University of Göttingen), INA SCHÄFER (University of Göttingen), STEFAN SCHEU (University of Göttingen)

Parthenogenetic species are doomed to extinction due to their limited adaptive potential to environmental changes. Yet, the cosmopolitan oribatid mite species *Oppiella nova* (Acari, Oribatida) reproduces parthenogenetically and occurs in a variety of habitats: in temperate forest soils, on mosses, lichens, dead wood, rocks, the bark of trees and also in grasslands. To explain the evolutionary success of parthenogenetic taxa two hypotheses have been proposed. The “Frozen-Niche Variation” (FNV) theory states that parthenogenetic organisms consist of several genotypes that each occupies a narrow niche. In contrast, the “General Purpose Genotype” (GPG) theory postulates that a single clonal lineage with broad ecological amplitude dominates in a range of habitats. Using phylogenetic methods we investigated whether the genetic structure in *O. nova* populations is conform to the FNV or GPG theory. Different clonal lineages were determined, based on intraspecific variance of the mitochondrial COI gene; additionally, the D3 region (28S rDNA) was used as species marker. *Oppiella nova* was collected at five different locations in Germany. At each locality two habitats were investigated, grassland and forest. The results show that conform to the FNV theory the two habitats were inhabited by different lineages of *O. nova*. High genetic distance of 14% between forest and grassland haplotypes suggests that the lineages separated 6 – 9 million years ago. Congruent with habitat-specific molecular haplotypes, individuals from forest and grassland sites differed significantly in body size, indicating that in spite of parthenogenetic reproduction *O. nova* lineages adapted to different environments. This suggests that parthenogenetic species evolve in a similar way as sexual species. Propagation of well adapted genotypes via parthenogenesis likely is the reason for the evolutionary success of *O. nova*.

Abstracts of talks & posters (continued)

Phylogeny of Onychophora (velvet worms) based on mitogenomics

STEFAN SCHAEFFER (University of Leipzig), LARS HERING (University of Leipzig), CHRISTOPH BLEIDORN (University of Leipzig), GEORG MAYER (University of Leipzig)

Currently, the phylogeny of Onychophora is unresolved and even the monophyly of the two major onychophoran subgroups, Peripatidae and Peripatopsidae, is uncertain. Previous studies of complete mitochondrial genomes have shown the utility of the mitochondrial data sets for clarifying the internal relationships of Onychophora. However, large-scale approaches, including species from different geographical regions, are still missing. We therefore conducted a phylogenomic approach based on whole genome shotgun libraries and nearly complete mitochondrial genomes of onychophoran species from Chile, South Africa, mainland Australia, Tasmania, New Zealand, Vietnam and Costa Rica. Assemblies of the raw data revealed large contigs spanning the mitochondrial genomes. Protein-coding gene sequences from these genomes were concatenated into a supermatrix and analysed using Maximum Likelihood. This approach recovered a tree with high support values for most nodes. The monophyly of Peripatidae and Peripatopsidae is strongly supported. Furthermore, the phylogeny within these two groups is in good concordance with the biogeographic distribution of taxa studied. An analysis of the mitochondrial gene order among onychophorans revealed that the gene arrangement is conserved in representatives of Peripatopsidae but highly diverse in the Peripatidae species.

Bird phylogeny and the activity of avian SINE retroposons

ALEXANDER SUH (University of Münster), Sandra Bachg (University of Münster), STEPHEN DONNELLAN (South Australian Museum Adelaide), LEO JOSEPH (Australian National Wildlife Collection), JÜRGEN BROSIUS (University of Münster), JAN OLE KRIEGLS (LWL-Museum für Naturkunde Münster), JÜRGEN SCHMITZ (University of Münster)

Short interspersed elements (SINEs) are non-autonomous retroposons that make up about 13% of the human genome size and total about ~1.5 million copies. This is in strong contrast to the situation in the available bird genome sequences: Both the chicken and the zebra finch genomes harbor slightly less than 3,000 SINEs related to mammalian-wide interspersed repeats (MIRs). These SINE insertions appear to be the result of very ancient retroposition. Additionally, the zebra finch genome contains almost 3,000 SINEs that are of a more recent origin and have been mobilized by long interspersed elements (LINEs) of the chicken repeat 1 (CR1) subfamily. We investigated the presence/absence patterns of these avian SINE insertions across the avian tree of life and reconstructed the temporal impact of SINEs on avian genomes. Furthermore, we report a previously unknown avian SINE retroposon, indicating that much of the diversity of avian retroposons has yet to be uncovered.

Abstracts of talks & posters (continued)

Why phylogeneticists should do phylogenetics and philosophers philosophy

LARS VOGT (University of Bonn)

I will start by giving a short introduction into basic philosophical concepts, including (i) the distinction of different epistemic virtues and their corresponding styles of reasoning and (ii) basic modes of inference and their application to causality, resulting in different types of causal empirical arguments. Then I will talk about Popper's falsificationism in general, his incentives and early criticisms, and will explain Popper's terms of "empirical content", "degree of falsifiability", "falsification", "degree of testability", "potential explanatory power", "degree of corroboration", and "severity of test". I will show why it is tempting for scientists to refer to Popper's theory whenever they attempt to establish their scientific discipline or a specific theory or hypothesis as belonging to the so called 'hard' sciences. Finally, I will talk about phylogenetics and why Popper's falsificationism is ill-suited as a normative reference system for justifying a preference between different types of analytical algorithms such as parsimony and likelihood.

Reconstruction of annelid phylogeny using next generation sequencing data

ANNE WEIGERT (University of Leipzig), MATTHIAS MEYER (Max Planck Institute for Evolutionary Anthropology, Leipzig), BIRGIT NICKEL (Max Planck Institute for Evolutionary Anthropology, Leipzig), NATASCHA HILL (Berlin), TORSTEN H. STRUCK (Zoological Research Museum Alexander König, Bonn), CHRISTOPH BLEIDORN (University of Leipzig)

Annelida is a highly diverse animal phylum with over 15,000 described species. Whereas the monophyly of the approximately 80 higher ranked taxa usually classified as families was well established, relationships between those taxa remained controversial. Recent studies have investigated annelid relationships supporting two major groups, the Errantia and Sedentaria. Additionally, Chaetopteridae, Myzostomida, and Sipuncula grouped outside this core Annelida now named Pleistoannelida, in the basal part of the tree. To investigate the possible basal position of Oweniidae and Magelonidae within the Pleistoannelida, we conducted ML- and Bayesian analyses of a phylogenomic dataset based on Sanger ESTs and next generation sequencing mRNAseq data. With extended taxon sampling we recovered a well-supported phylogeny with strong support for two major splits (Errantia and Sedentaria) including the biggest fraction of annelid diversity, indicating that life-history characters are phylogenetically informative. Moreover, we found additional support for a position of Chaetopteridae, Myzostomida, and Sipuncula grouping together with Oweniidae and Magelonidae outside the core Annelida.

Abstracts of talks & posters (continued)

A survey of Hox gene expression in adult *Owenia cf. fusiformis*

ANNE WEIGERT (University of Leipzig), TORSTEN H. STRUCK (Zoological Research Museum Alexander König, Bonn), CHRISTOPH BLEIDORN (University of Leipzig)

Hox genes are known to play a key role in body plan formation and often show expression patterns along the anterior-posterior axis during larval development. Numerous studies have explored Hox gene expression in larval development and genome organization in various taxa, but little is known about expression patterns and their function in adult stages. We discovered that the segmented annelid *Owenia cf. fusiformis* (Oweniidae) expresses Hox genes not only during larval development but also in adult stages. We identified 9 out of 11 expected Hox gene transcripts in an Illumina mRNA-seq library of only adult stages of *Owenia cf. fusiformis* using local Blast algorithms. Using ML-based phylogenetic analysis including Hox genes from 23 additional taxa paralog groups have been identified for our transcripts. These results are a pre-requisite for further studies using in-situ-hybridization, to investigate hox gene expression patterns in adult and larvae stages.

Comparative analyses of the evolution of metazoan chitin synthases

ANNE ZAKRZEWSKI (Sars International Centre for Marine Molecular Biology, Bergen), CONRAD HELM (University of Leipzig), STEPHAN Q. SCHNEIDER (University of Oregon), CHRISTOPH BLEIDORN (University of Leipzig), FLORIAN RAIBLE (Max F. Perutz Laboratories, Vienna), HARALD HAUSEN (Sars International Centre for Marine Molecular Biology, Bergen)

Chitin synthases are membrane-bound enzymes that catalyze the polymerization process of single N-acetyl-glucosamine subunits to a growing chain of a chitin polymer. Chitin is highly abundant in nature and is present in a variety of taxa, but until now, there has not been an evolutionary analysis of chitin synthases that comprised more than the so far best-studied chitin synthases of arthropods, nematodes and Fungi. We isolated several novel chitin synthases from newly established transcriptomes and conducted the first densely sampled analysis of chitin synthase evolution among the major metazoan taxa, such as Lophotrochozoa, Ecdysozoa, Cnidaria, Porifera, and the chitin-lacking Chordata. This reveals a complex evolutionary history of the chitin synthase gene family. Gene expression studies in some metazoan representatives show remarkable tissue specificity for their chitin synthase expression. This spatio-temporal characterization of chitin synthases promises to be the first step towards unravelling the exact functions of chitin synthases.

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