

it is also turning into an essential model system in comparative genomics. However, to fully exploit this opportunity, it is necessary to use these tools to assay the genome, transcriptome and epigenome of more cephalochordates. To this end, we have sequenced three different genera of cephalochordates, complementing the ongoing sequencing of several species belonging only to the Branchiostoma genus. We have performed comparative analysis of RNA-seq and small RNA-seq data from *Branchiostoma lanceolatum*, *Asymmetron* and *Epigonychthis*. Using a combination of available and new computational analyses, we performed de novo assemblies and mapping of replicated datasets for each genus. The objective was to reliably reconstruct the molecular basis of mild but distinctive morphological differences between the three cephalochordate genera. Our results suggest that such morphological differences, although mild, might have been critical for elaborating the definitive vertebrate body plan, as we find they are linked to differentially expressed transcripts between the three cephalochordates studied.

**P-023 Comparative expression analyses of homeobox genes in mollusks**

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Mollusca are the most speciose lophotrochozoan phylum and its representatives exhibit diverse body plans from creeping worm-shaped aplousobranchs to highly mobile cephalopods with complex brains. Up to date only little is known concerning the developmental mechanisms that have led to the diversification of molluscan body plans during evolution. Homeobox genes such as parahox genes and pair-rule genes are involved in body plan patterning of many bilaterian clades. Previous studies on these genes have mainly focussed on ecdysozoan and vertebrate model species. Within the highly diverse Mollusca, however, only one gastropod and cephalopod species have been investigated. The present study focuses on the expression of the parahox gene *gsx* in the pygmy squid *Idiosepius notoides*, the scaphopod *Antalis entalis*, and the polyplacophoran *Acanthochitona crinitus*. A previous study showed that *gsx* is expressed around the gastropod mouth, in the apical organ, and in putative neuroectodermal cells. Besides taxon-specific expression domains in all three species, *gsx* is expressed in the cephalopod brain, the scaphopod and gastropod larval apical organ and probably neuroectodermal cells in scaphopods and polyplacophorans. In addition, expression of *otx*, *pax2/5/8*, and *gbx* was investigated in embryos of the cephalopod *I. notoides* and

pericalymma larvae and settled postmetamorphic specimens of the protobranch bivalve *Nucula tumidula*. In this talk homeobox gene expression in mollusks will be discussed with focus on the evolution of molluscan-specific organs.

**P-024 Comparative transcriptomics to study habitat change and adaptive radiation in water striders**

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Gerromorpha offer a good model to study the developmental genetic changes associated with the invasion of water surface habitat and their radiation into a diverse array of niches, from small ponds to open oceans. This ecological transition and subsequent specialization have been facilitated by substantial changes in morphology to meet the challenges and exploit the opportunities of the new environment. These morphological changes and specialization have captured a broad interest making Gerromorpha historically established models for ecology, evolution and biophysics. In particular, it is well established that the ability of this group to walk on water is mainly based on two traits: leg length and the hydrophobic bristles that cover the contact surface between the leg and water. However, despite the body of knowledge of the biogeography, phylogeny and biomechanics of water walking insects, the genetic changes underlying the invasion and radiations in water surface habitats are poorly understood. Here we generated and annotated the transcriptome of the water strider *Limnoporus dissortis* to study the genetic basis of leg morphology and specific adaptation associated with water surface locomotion. Using next generation RNA sequencing we identified the set of genes expressed in the legs during embryogenesis and tested for genes known to be involved in both bristle and leg development. Finally, after transcriptome data validation, we identified and analyzed a list of new genes potentially involved in second and third thoracic legs' length differences.

**P-025 Composition of pre-nervous serotonergic signaling system in early embryonic development of sea urchin, clawed frog and mouse**

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Neurotransmitters, such as serotonin, catecholamines and acetylcholine have numerous non-neuronal functions in addition to their classic one, and functionally active during early embryonic development,

picture is not as clear: the expression patterns of early developmental genes cannot be explained by the interactions between them that are known so far. This suggests that there are many components still to be discovered in this GRN. We have carried out a series of knockdowns of early patterning genes and followed the effects of the knockdown of one gene on the expression of other genes in the *Oncopeltus* blastoderm GRN. Among our results, we show that the genes orthodenticle and even-skipped play important roles in early embryogenesis: the knockdown of these genes leads to the most significant changes in the expression patterns of other genes. These results are different from what we know from *Drosophila*, where *otd* and *eve* have minor roles in initial patterning of the embryo. We are in the process of elucidating additional interaction, and hope to be able to ultimately reconstruct the complete blastoderm GRN in *Oncopeltus*, including distinguishing between direct and indirect interactions.

**P-020** **Cis-regulatory evolution and functional diversification of gene duplicates**

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Gene duplication plays a major role in evolution of novel gene functions as it provides a material basis for variation and selection. We are interested in how *cis*-regulatory changes contribute to functional diversification ensuing gene duplication. To address this question we are studying the Ly6 gene family in insects. Members of this family encode different GPI-anchored membrane proteins and are fully conserved across drosophilids. Our analyses of the sequenced insect genomes indicate that a subset of these genes is unique to higher dipterans. We are focusing on seven paralogues in *Drosophila*, which we found to derive from sequential duplications of a single orthologue. By characterizing the embryonic tissue-specificities of the paralogues and their unduplicated orthologues in six insect species representing various stages of duplication, we determined how the original function of the unduplicated orthologue progressively diversified. Our results show that at each node of duplication, one paralogue inherited the tissue-specificities of the unduplicated orthologue, while the other paralogue acquired novel expression domains suggesting neofunctionalization. Moreover, we also found many instances of lineage-specific gains of tissue-specificities. We are currently identifying the *cis*-regulatory elements of some the duplicates and the

unduplicated orthologues to elucidate the *cis*-regulatory mechanisms underlying the evolution of divergent expression patterns.

**P-021** **Commissureless regulation of Slit-Robo signalling in insects**

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Slit-Robo signaling is a key mediator of axon guidance decisions in organisms ranging from planaria to vertebrates. Not surprisingly, Slit and Robo homologues can be identified in all insect genomes sequenced to date. 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. We are investigating the evolution of Comm-like genes and regulation of Slit-Robo signaling in insects. Bioinformatic studies suggest that Comm-like genes are present in all sequenced 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 to date not outside of insects. The presence of a Comm-like gene in many insect orders suggests this gene was present early in insect evolution. There is evidence for three independent losses of this Comm-like gene: (1) the absence from all sequenced Lepidopteran genomes, (2) the absence in *Tribolium* but presence in more basal Coleopteran genomes, and (3) the presence in basal Hymenoptera, like the sawfly *Athalia rosae*, and absence in more derived Hymenoptera including ants and bees. In ongoing experiments, we are addressing 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-022** **Comparative cephalochordate transcriptomics: Linking genotype and phenotype at the root of chordate evolution**

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The basal chordate amphioxus is a key model system for understanding the evolutionary genesis and radiation of vertebrates. In this context, it has been long used in comparative anatomy and developmental biology. More recently, since the arrival of next generation sequencing,