

Session 2: Evolutionary and ecological omics

09 | Signatures of adaptive evolution in Collembola Genomes

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Collembola (springtails) represent a soil-living lineage of hexapods in between insects and crustaceans. Consequently, their genomes may hold key information on the early processes leading to evolution of Hexapoda on land. Recently, we generated transcriptomes and very high quality reference genomes for two collembolan species, *Folsomia candida* and *Orchesella cincta*, using Illumina and Pacific Bioscience sequencing platforms. Total size of *O. cincta*'s genome is 280 Mbp, while *Folsomia*'s genome is about 60 Mbp smaller in size. In contrast, *F. candida* contains 28.734 genes, while *O. cincta* contains about 20.459 genes, indicating that the two genomes diverged in terms of gene content. Extensive gene family expansions and contractions seem to have driven this divergence. Moreover, several expanded gene families could be linked to evolution of stress tolerance in the soil ecosystem. Annotations could be retrieved for about 60% of the genes. However, about 30% of gene clusters did not show any homology to organisms in genome databases, suggesting that they evolved *de novo* in springtails. About 1.5-1.8% of the genes have evolved after horizontal gene transfer (HGT) events. Remarkably, a gene cluster resembling a complete functional antibiotic biosynthesis pathway could be identified among HGT genes in *Folsomia*, and active β -lactam compounds could be detected *in vivo*. This is in line with previous observations that *Folsomia* is very resistant to microbial pathogens, which are quite abundant among soil microbial communities. Finally, an unusual high number of HGT genes in both springtail genomes seem to originate from fungal sources. They mostly code for enzymes involved in cell wall degradation, suggesting that they were instrumental in adaptation to specific food resources in the soil ecosystem. I will discuss these findings in the context of arthropod evolution.

10 | Inferring demographic histories from whole genome data

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Genomes contain a wealth of information about past demographic events. While we now have access to vast volumes of genomic data, extracting the relevant demographic information remains a difficult challenge. Many current inference methods either ignore linkage information or simply do not scale to genomic data. I will describe a new inference framework that uses the full configuration of mutations in short blocks of sequence to understand the past history of species and populations. For small samples of genomes and simple demographic models, likelihoods can be calculated analytically using a recursion for the generating function of the genealogy. For more detailed histories and larger samples, we have recently developed an efficient approximate likelihood method based on coalescent simulations. These methods make it possible to fit arbitrary demographic histories to genomic data and address fundamental questions about speciation and the evolution of biological communities. I will discuss example applications including the Pleistocene history of the Orang Utan and species divergence in *Heliconius* butterflies.

11 | Genetic and plastic responses in *Daphnia magna*: comparison of clonal differences and environmental stress induced changes in alternative splicing and gene expression

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The water flea *Daphnia magna*, a small aquatic crustacean, is often a key species in lentic habitats, forming a central part of the food web throughout the northern hemisphere. It has long been regarded as a model organism for ecosystem health and ecotoxicology. The small body size, short generation time and cyclic parthenogenetic life cycle lends itself well to analyzing interactions of genes and environment. A high quality draft genome (GenBank LRGB00000000) and genome-wide transcriptome profiling, carried out by the STRESSFLEA consortium, has allowed us to characterize the role of alternative splicing in this ecologically relevant model species. Two inbred genotypes, originally collected from ecologically distinct habitats; an ephemeral rock pool on an island near Tvärminne, Finland (Xinb3) and a fish-rearing pond near Munich, Germany (linb1) were exposed to seven environmental perturbations, and sequenced with Illumina HiSeq2000, generating over 6 billion read pairs for 49 samples. We analyzed stress induced changes in alternative splicing and gene expression as well as clone-specific differences by mapping the RNA-seq reads to de-novo assembled transcripts that were annotated in the genome using Bowtie2. The expression levels of the transcripts were estimated using BitSeq (<http://bitseq.github.io/>). The alternative splicing events were distinguished from SNP and indel variation using KisSplice (<http://kissplice.prabi.fr/>), by quantifying the reads that cause forks/bubbles in the De Bruijn graph of the assembly. We found that environmental stress triggered a relatively modest number expression and splicing changes (300 on average), which were mostly unique to each stress condition and also specific to each clone. However, the clone-specific responses had a high degree of overlap in the gene functions suggesting that paralogous genes with similar functions may be used to respond to the same stress conditions in different clones. On the other hand, the gene expression profiles of the two clones differ substantially from each other, even in their baseline expression without stress treatment. More than 70% of transcripts were differentially expressed, with more than 80% of the DE transcripts having higher than 2 fold difference between the clones. Almost half of differential expression between the clones resulted from alternative splicing, with one genotype favoring a different isoform. This may significantly impact genotypic differences and local adaptations.

12 | Hook a worm to catch a man

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The pre-European Amazon has historically been regarded as a pristine forest. This has now been thoroughly refuted, using evidence from a number of well-characterised archaeological sites, that date back to ~9000 years BP. The ancient human cultures that have lived in this region have had a measurable impact on the Amazon, including the adoption and transport of a number of cultivated plant species. It is also possible that the indigenous Amerindian groups transported soil animals, such as earthworms, along with their crops. This process of human-mediated transport would explain the distributions that are observed in Brazilian worm species such as *Pontoscolex corethrurus*. *P. corethrurus* has been linked to human movements elsewhere in the world, and as the species is so widely spread throughout South America, it seems likely that this is also the case in South America. This project aims to use genomic approaches to track the movement of *P. corethrurus* across Amazonia, and investigate if this information can be used to test between competing hypotheses of

ancient human migrations across this region. Here, I report on the progress of this project, including preliminary results on the development of genomic resources.

13 | Field-realistic levels of neonicotinoids: assessing gene-networks in honeybees

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Evolutionarily new environmental stressors such as the neonicotinoid class of crop-protecting agents have been implicated in the population declines of pollinating insects, including honeybees (*Apis mellifera*). We explore if field-relevant levels of imidacloprid and thiamethoxam can influence gene expression and lipid profiles of honeybee workers. Within a catalogue of 300 differentially expressed transcripts in larvae from imidacloprid-exposed hives, we detect significant enrichment of genes functioning in lipid-carbohydrate-mitochondrial metabolic networks. Altered metabolism is also implied by our lipid profiling results, where we observed significant differences in ratios of around 15% of the sampled lipid metabolites between imidacloprid-exposed and unexposed larvae. Collectively, we identify a multifaceted, physiological response of worker bee larvae to an evolutionarily novel stress factor. We are currently analysing potential changes in gene-expression levels in brains of adult worker bees, which have been exposed to different concentrations of thiamethoxam. We discuss how pesticide exposure in early life could lead to persistent changes in gene expression patterns that are mediated by epigenetic programming mechanisms.