

Revealing the genomic innovations during evolution of holometaboly

Gregor Bucher (Uni Göttingen)
Mario Stanke (Uni Greifswald)

Holometaboly is a key innovation within insects and led to a very successful and diverse clade, the holometabolous insects, which have conquered all habitats and include important pests and vectors. However, many aspects of the evolution of holometaboly remain enigmatic. Do holometabolous larvae correspond to hemimetabolous embryos or nymphs? How did the simplified morphology of first instar larvae evolve? How did immature developing brains become functional in first instar larvae? What is the genetic control of shifted developmental timing (heterochrony)? What genes are specifically required for metamorphosis leading to the pupa, a novel stage? Genetic studies have so far mainly relied on the fly *Drosophila melanogaster*, which shows a quite derived mode of metamorphosis.

We want to develop and apply a genome-wide bioinformatics approach comparing hundreds of insect genomes to identify genes that show signs of increased sequence evolution at the base of holometabolous insects. Subsequently, we test the functions of the genes emerging from this analysis in the red flour beetle *Tribolium castaneum*, an insect with insect typical metamorphosis. This approach has become possible only recently, as a large number of high quality insect genome sequences have become available and since genome wide functional screening was established in an insect with typical metamorphosis.