

Summary

The occurrence of evolutionary events and mutations are precursors to the origination of species and diversity. The subject of the presented work is the analyses of different Hymenoptera-genomes to get insights into the evolution of haplodiploid sex-determination and the formation of eusociality with its different shapes.

The highly conserved genes *feminizer* (*fem*, *transformer*) and *doublesex* build the core of the sex-determining gene cascade, while the different initial signals can largely vary. Within the examined species, *doublesex* shows only few differences in its amino acid composition. However, *feminizer* expresses marked differences in its functional motifs. These differences are mainly found between *Apis* and non-*Apis* species and give indications to a modified gene function. Further it was shown that the co-factor *transformer2* in *Apis*, co-evolving with *feminizer*, has developed in a different way than in other genera and has an altered binding specificity.

The primary signal of the sex-determination in *Apis* is the gene *complementary sex determiner* (*csd*). It has developed a novel function in *Apis* and shows such a high variability that even within the genus huge differences can be found. A closer examination of *csd* in *Apis florea* revealed a less complex composition compared to other *Apis* species, which promotes a more rapid formation of new allele specificities. This accords to the life cycle and demographic circumstances. Further it correlates to the theory of continuous bottleneck events acting on *A. florea* populations. Moreover *csd* and *fem* show modified functional motifs, which emphasizes its defined status within the genus *Apis*.

The analyses of different Hymenoptera genomes regarding the evolution of eusociality revealed the development of regulatory gene networks as fundamental similarity. An increasing complexity of such gene networks correlates with the evolution of advanced social organization of species.

A detailed examination of the genomes of the agriculturally relevant species *Bombus terrestris* and *Bombus impatiens* verified the correlation of gene networks and eusociality and gave further insight into their evolutionary development. Social organization is not a consequence of a few major changes, but of many lesser evolutionary events which can be reconstructed by the analyses of complex regulatory gene networks.