

## **SFB 680**

## Molecular Basis of Evolutionary Innovations

Molekulare Grundlagen evolutionärer Innovationen

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## Signatures of selection and insights into the history of honey bee populations: Lessons from the sex determining gene *csd*

Our understanding of the impact of evolutionary forces such as selection, recombination and genetic drift on nucleotide evolution is still limited. The gene *complementary sex determiner* (*csd*) determines sex in the honey bee *Apis mellifera* by its allelic composition and serves as an excellent example to study the impact of these forces on sequence evolution. The *csd* gene evolves under a well know mode of strong heterozygote advantage. Consequently, high numbers of *csd* alleles segregate in honey bee populations and are maintained over an extended period of time when compared to neutral polymorphism (balancing selection). I will present the signs of balancing selection we observed from the analysis of nucleotide polymorphism and provide insights into the longer term evolutionary history of honey bee populations we deduced from a first analytical model of *csd* coalescence. The gene *feminizer* (*fem*) is the ancestrally conserved progenitor from which *csd* arose by a recent gene duplication, followed by positive selection and gained a new function in the honey bee lineage. This system of duplicated genes served as informative example to study how under the model of neofunctionalization the origin of a new gene function influences the evolution of other genes. I foresee with the honey bee and its rich repertoire of phenotypic characteristics a great organism to study fundamental evolutionary processes on the genomes of populations.

June 29, 2011, 2:00 p.m.

Biocenter, Zülpicher Str. 47b, Lecture Hall, Ground floor

Host: Thomas Wiehe

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