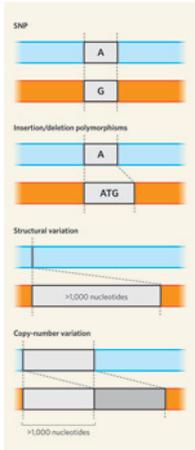


## Genomics of Host-Parasitoid interactions

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### Background

Natural variation in the genome is the raw material for evolutionary change. It comprises, among others, point mutations, multiple copies of a gene, and mobile genetic elements. Until the start of the genomic era, it was impossible to measure the genomic variation among natural populations, implying that the core element of evolution was a black box. Only now, with the latest advances in genomic and sequencing technology, we have the tools available to measure genomic variation and associate it with complex ecological traits.

### Approach

The aim of our research is to assess what genomic variation is exploited for rapid evolutionary changes, using the parasitoid-host interaction as a model system. The parasitoid-host interaction is particularly suitable for studying evolutionary responses, because parasitoids are important in nearly all terrestrial ecosystems, several insect species have evolved potent immune defenses to kill the parasitoid eggs, and natural variation in host immune function is widespread. In our research we investigate genomic variations associated with the rapid acquiring of resistance to parasitism in the fruit fly *Drosophila*. For this we use natural and artificially selected populations and the 12 sequenced *Drosophila* species. We have obtained genome-wide expression profiles and the complete genomic sequences for *Drosophila* strains and species that differ in their immunological resistance to parasitoids. We study the link between these genomic data and phenotypic traits.

### Master projects

Within our group are many possibilities for master projects, using a variety of techniques:

- Behavioural assays: e.g., behaviour of parasitoids on hosts with different levels of resistance
- Population genetics: e.g., inbreeding depression in immunological resistance traits
- Molecular genetics: e.g., measuring or manipulating expression of candidate resistance genes
- Functional genomics: e.g., involvement of microRNAs in different levels of resistance
- Comparative genomics: e.g., identifying genomic regions/genes under positive selection

Please, come and talk to us if you want to explore the possibilities!