Universität Basel

# Research Project

# Testing predictions of Red Queen coevolution

## Third-party funded project

**Project title** Testing predictions of Red Queen coevolution
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Testing predictions of Red Queen coevolution, by Dieter Ebert, Universitat Basel

SUMMARY
It is believed that many biological phenomena (e.g. the evolution of sex, Batesian mimicry, and immune response) have evolved as a consequence of host-parasite coevolution. The leading hypothesis for such coevolution is based on time-lagged negative frequency dependent selection (NFDS), also known as Red Queen coevolution. Evidence from population genetics (e.g. high genetic diversity and balancing selection at disease loci) is consistent with the idea that NFDS drives coevolution in host-parasite systems, but other models of coevolution (e.g., selective sweeps) cannot be easily excluded. Here I propose to test the predictions of the Red Queen coevolution hypothesis by analysis of hosts and parasite dynamics in one well-characterized population. In this Daphnia magna population we observe yearly strong epidemics of the bacterial parasite Pasteuria ramosa. I propose to test the hypothesis that coevolution in this system is driven by NFDS.

Subproject A aims to identify the host genes that prevent parasite attachment in one particular population ("The Swisspond"), which has yearly strong epidemics of Pasteuria ramosa. We plan to compare different host-genotypes by sequencing from each resistotype multiple genomes and conduct genome-wide association mapping. In a next step we aim to pinpoint the exact genes responsible for the resistance polymorphism by employing molecular tools (CRISPR/Cas9) to knock down candidate genes in the regions of interest. The cloned offspring of the knock down genotypes will be tested for phenotypic effects in response to multiple parasite clones.

Subproject B continues our efforts to find the infectivity genes in the bacterial pathogen Pasteuria. This parasite has now been fully sequenced and genomes from different isolates with known infection characteristics will be compared. As a further step we plan to do a proteomics approach, to identify the proteins which are expressed on the spore surface and which are responsible for the attachment of the parasite to the host.
Subproject C aims to uncover the genetic interaction matrix between host and parasite genotypes. Host and parasite isolates from the field will be cloned in the laboratory and the mode of inheritance of resistance will be worked out by conducting genetic crosses among hosts. At the same time, infected hosts will be collected across the course of an epidemic in the field and will be genotypes for candidate genes at host resistance loci and parasite infectivity loci. This "co-genotyping" will allow estimating the strength of genetic host-parasite interactions during natural epidemics and enable us to estimate the strength of selection acting on different genotypes.

Expected value of the research: This research aims to provide a convincing case study on the validity and predictions of the Red Queen coevolution hypothesis, offering urgently needed genetic data for theoretical and empirical research in evolution, epidemiology and disease biology. It has implications for our understanding of how coevolution shapes genetic diversity and genomes.

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**Add publication**

**Add documents**

**Specify cooperation partners**