Universität Basel

Research Project

Testing genetic assumptions and predictions of Red Queen coevolution

Third-party funded project

Project title Testing genetic assumptions and predictions of Red Queen coevolution
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Organisation / **Research unit**
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Department
Project Website http://www.evolution.unibas.ch/ebert/
Project start 01.04.2013
Probable end 31.03.2016
Status Completed
Testing genetic assumptions and predictions of Red Queen coevolution

Grant proposal for the Swiss Nationalfonds by Dieter Ebert, Universität Basel

Background: 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 specific predictions of Red Queen coevolution by undertaking a genetic analysis of the genes under selection and their evolutionary dynamics, focusing on the genetic interactions of *Daphnia magna* and its bacterial parasite *Pasteuria ramosa*. I will test my main hypothesis—that coevolution in this system is driven by NFDS—by exploring the genetic interaction matrix of host and parasite, characterizing the genes involved in these interactions, and tracing their dynamics over a 50-year period in pond sediments that contain layered archives of host and parasite populations.

Subproject A aims to uncover the genetic interaction matrix between host and parasite genotypes. We focus on the attachment step of *Pasteuria,* because polymorphism in attachment genes explains most of *Daphnia's* variation in resistance.

Subproject B aims to identify the host genes that prevent parasite attachment. We have already mapped the location of these genes to a small genomic region. I suggest using association mapping in natural populations to further narrow down this region. Next, we will employ molecular evolution tools to test the prediction that allelic variants at these loci are old and under balancing selection. Furthermore, we will trace temporal changes at the candidate loci and of resistance phenotypes in layered pond sediments that harbour resting stages of host and parasite. This will enable us to observe if there is a signature of fluctuating selection on resistance genes.

Subproject C will focus on identifying the infectivity genes in *Pasteuria.* This parasite shows frequent recombination, allowing us to use a genome-wide approach to analyse genetic diversity in several *Pasteuria* genomes from different infectotypes (carrying different attachment genes). The candidate regions in the genome will then be tested for associations with the parasite's attachment phenotypes using material from natural populations. Next, the prediction of rapid allele frequency changes will be tested in sediment cores. Finally, we will test the prediction that parasite infectotypes track host resistotypes by combining the sediment core results of Subprojects B and C.

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 control. It has implications for our understanding of how coevolution shapes the phenomena related to host-parasite interactions.

Keywords coevolution, host-parasite interactions, Red Queen
Financed by
Swiss National Science Foundation (SNSF)

Follow-up project of 241885 Processes and genetic mechanisms of host-parasite coevolution.

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