

Research Project

Processes and genetic mechanisms of host-parasite coevolution.

Third-party funded project

Project title Processes and genetic mechanisms of host-parasite coevolution.

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Organisation / Research unit

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Department

Project Website <http://www.evolution.unibas.ch/ebert/>

Project start 01.04.2010

Probable end 31.03.2013

Status Completed

The research I am proposing continues the work of my group on the outgoing grant "Processes and mechanisms of antagonistic host-parasite coevolution" (Nr. 31003A-116029).

For the parasite-host systems my group has been focussing on we now have good evidence that rapid coevolution is taking place: parasites track the locally abundant host genotypes and hosts evolve resistance. What we lack is an understanding of the underlying genetic mechanism and with it, the best model to explain the processes at work. Here we focus on discovering the genetic mechanisms underlying the host-parasite interactions because this knowledge will allow us to identify the model to best explain coevolution. The two most often discussed models are time lacked negative frequency dependent selection (the Red Queen hypothesis) and coevolution by selective sweeps. Knowing the genetics would allow us to pinpoint the appropriate coevolutionary model.

The Pasteuria-Daphnia model

Pasteuria ramosa is an endoparasitic bacterium infecting several *Daphnia* species as well as some other Cladocera. Despite of *Pasteuria*'s seemingly low degree of specificity on the host species level, this bacterium shows a remarkable degree of host genotype specificity. The same clone of *Pasteuria* shows high specificity in infection for only certain clones of *D. magna*, but is also specific to certain clones of other species, e.g. *D. longispina* or *D. pulex*. I am proposing that one Ph.D. student project continues to work on the genetic interactions between *Daphnia* and parasite clones. The aims of this work would be 1) Conduct multiple crosses between *Daphnia* clones and elucidate the segregation patterns of resistance. 2) Test for linkage among resistance loci. 3) To determine whether resistance loci show epistasis, i.e., if combinations of alleles result in different phenotypes than their effects alone would suggest.

The postdoc project proposed here focuses on the population genetic structure of *Pasteuria ramosa*. For this we plan to sample *Pasteuria* from different spatial and temporal scales and obtain sequence data on putative resistance loci and house-keeping genes. This project has three parts: 1) Global scale: With *Pasteuria* samples across Europe and North America. 2) Intermediate temporal scale: Using *Pasteuria* samples from the layered sediments of lakes (sediment cores), we plan to reconstruct the temporal changes of the *Pasteuria* populations over periods of about 30 years. 3) Short temporal scale: To link the changes in allele frequencies expected from the sediment cores with events during natural selection, we will collect time series of *Pasteuria*-infected *Daphnia* during epidemics in natural populations. These data will allow us to follow the microevolutionary changes during coevolution and to quantify the strength of selection acting on candidate genes.

The Octosporea-Daphnia model

Octosporea bayeri is a microsporidian parasite with both vertical and horizontal transmission. Preliminary data suggest, that *O. bayeri* adapts by means of epigenetic genome modification. The second Ph.D. project for which I seek funding with this proposal is to verify or reject the epigenetics hypothesis for *O. bayeri*. First we will carry out detailed experiments to test for epigenetic adaptation. If these experiments suggest that epigenetic effects are likely to play a role for parasite adaptation, we will use "bisulfite sequencing" to obtain methylation patterns of *O. bayeri* kept in different host environments. This would allow us to find candidate genes responsible for parasite adaptation to its host clones. The topic of parasite adaptation by means of epigenetics has received little attention by evolutionary biologists, but promises an exciting field for understanding host-parasite coevolution.

Keywords coevolution, infectious diseases, epidemiology, genomics

Financed by

Swiss National Science Foundation (SNSF)

Follow-up project of [5914 Processes and mechanisms of antagonistic coevolution](#)

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