Universität Basel

Research Project

Processes and mechanisms of antagonistic coevolution

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Processes and mechanisms of antagonistic coevolution

The research I am proposing addresses basic aspects of the coevolution between hosts and their parasites. Many biological and medical phenomena have been explained to be a consequence of reciprocal host-parasite coevolution. Some of these explanations require specific and rapid antagonistic coevolution to take place. Experimental coevolution of viruses in bacteria or cell cultures gave evidence for coevolution by selective sweeps, but we have little, and mostly indirect evidence for coevolution with plant and animal hosts. However, population genetic consideration suggests that rapid antagonistic coevolution in plant and animal host systems should be dominated by negative frequency dependent selection. In this proposal I ask for funds to carry out experiments with populations of the waterfleas Daphnia magna and its microparasites to deepen our understanding of the genetic processes and mechanisms of coevolution. D. magna reproduce sexually and clonally, the later with a generation time of only 10 days. Two parasites, the microsporidium, Octosporea bayeri, and the bacterium, Pasteuria ramosa, will be used in the experiments.
I propose a project with 3 sub-projects to elucidate the mechanisms and patterns of host-parasite coevolution. Sub-Project A aims to find direct experimental evidence for rapid and specific coevolution with Daphnia and a microsporidian parasite under natural conditions. This will include time-shift cross-infection experiments using hosts and parasites stored at different times of the coevolution. Sub-Project B is about finding the infectivity genes in the bacterial parasite, Pasteuria. Sub-Project C proposes experiments to elucidate the mechanisms at work shaping the genetic epidemiology and coevolution of Pasteuria with its waterflea host.
With my research I hope to establish a case study, which would provide urgently needed data to test assumptions and to estimate parameters for epidemiological and (co-)evolutionary models of infectious diseases. It would allow streamlining treatments against pests and parasites and to make more accurate predictions about infectious diseases evolution. It will further provide insight into natural phenomena, which are suggested to be a consequence of rapid antagonistic coevolution.

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