Universität Basel

Research Project

A genomic perspective on host-parasite coevolution

Third-party funded project

Project title A genomic perspective on host-parasite coevolution
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Studies in diverse biological systems have led us to believe that host–parasite coevolution is responsible for the extraordinary genetic diversity seen in some genomic regions, such as MHC genes in jawed vertebrates and R-genes in plants. What is still missing, however, is the functional link between genetic variants for host resistance and parasite infectivity on the level of individual interactions and genomic signatures that are predicted to result from these interactions. In this research proposal—a continuation of my previous SNF grant—I address this topic, focusing on a well-established host–parasite system: the water flea Daphnia magna and its virulent bacterial parasite Pasteuria ramosa. This model system has the potential to reveal the mechanistic connection between resistance and infectivity on the individual level and genomic variation at the species level. Our work may thus serve as a case study for demonstrating how selection on specific host– parasite interactions creates genomic patterns of long-term balancing selection and trans-species polymorphism. The proposed research has three main aims, each with two subprojects (SPs):

Aim 1: Identify resistance and infectivity genes: We will use genomic approaches to screen hosts (SP1) and parasites (SP2) for loci related to their interactions, with the overarching aim of understanding how these genes interact to produce phenotypic variation. Specifically, we will map genes for polymorphisms in host resistance and parasite infection using stratified genome-wide association studies (GWAS).

Aim 2: Long-term consequences of coevolution: Here we will analyse genomes of D. magna and two related species, D. similis and D. sinensis, for long-term balancing selection and trans-species polymorphism (TSP). SP3 will focus on a known host supergene for resistance, a gene so diverse that it requires a haplotype approach, using long-read sequencing. SP4 will employ candidate-free genome scans to search for signatures of balancing selection and TSP in genotypes of the three species collected over a broad geographic scale.

Aim 3: Short-term dynamics of coevolution: Genomes of naturally infected hosts will be sequenced together with those of the infecting parasite. These data will be used to test directly for genetic interactions between host and parasite loci, i.e. interspecies linkage disequilibrium (SP5). Variation at the resulting host and parasite candidate loci will then be tracked over two years in longitudinal samples from a natural population and also in sediment cores taken from the same population (SP6). This will allow us to follow coevolution at the interacting genes over time spans from years to decades. SP6 depends on results from SP5.

These subprojects complement each other, promising to create a comprehensive picture of the nature and dynamics of the genes that underlay coevolutionary interactions of this system over both the short-term (via patterns of parasitism and selection) and the long-term (via genomic signatures). The proposed research will close the gap between theory, individual level patterns of disease and genomic signatures

at disease loci. This is important not only for this system, but for many other host-parasite systems undergoing antagonistic evolution, including humans and their parasites.

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