

Coevolutionary interactions in the Linum-Melampsora host-pathogen system

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Antagonistic coevolution is a critical force driving the evolution of host and pathogen diversity, yet the selective processes underpinning reciprocal adaptive changes are still not well understood. Thus, we have little knowledge of the relative importance of fluctuating selection vs. arms-race dynamics in maintaining polymorphism in host-pathogen interactions or how these are impacted by host resistance structure, pathogen life-history, and spatio-temporal environmental variation. I discuss these issues with a particular focus on the wild association between *L. marginale* and *M. lini* which we have studied for more than 20 years. I first provide an overview of epidemiological, experimental and modeling studies within a single metapopulation that reveal significant spatial structure in the

distribution of resistance and infectivity. I then describe extensive cross-year epidemiological, infection and genetic studies of multiple wild host and pathogen populations which demonstrate asynchronous phenotypic fluctuations in resistance and infectivity among demes. Changes in allelic frequencies at pathogen infectivity loci, and in host recognition of these genetic variants, correlate with disease prevalence during natural epidemics. These results strongly support reciprocal coevolution maintaining balanced resistance and infectivity polymorphisms and highlight the importance of characterising spatial and temporal dynamics in antagonistic interactions. Finally, at larger regional scales, I discuss evidence for the existence of two genetically distinct pathogen lineages which differ in geographic ranges and mating systems, as well as key life history features that are likely to have a profound impact on coevolutionary outcomes. I conclude with some general comments and highlight some future research directions.

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