

The adaptive dynamics of fungal speciation

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The literature contains numerous examples of fungal morphospecies within which partially or totally reproductively isolated sub-groups (sibling species) have been identified [1].

The evolution of sibling fungal plant pathogens is not well understood and due to their morphological and genetic similarities it is possible that they have evolved from a common ancestor. Identification of ecological and epidemiological mechanisms that lead to evolutionary divergence in fungal pathogens is an important problem. Evolutionary changes in fungal pathogens can occur over relatively short time scales, measured in years or decades [1], providing a good model for scientific studies of evolution. Furthermore understanding the effects of disease management on fungal evolution could substantially improve strategies for control of emerging or reemerging diseases.

Within the frame of natural selection we focus on the role of ecological niches [1] and the pathogen's success in occupying these niches [3] in the speciation process. Therefore a mathematical model of host-host-pathogen interactions is developed to investigate the role of the presence of different host species and differences in the ability of the pathogen to infect these hosts in the evolution of sibling plant pathogens. We assume a trade-off relationship between the pathogen's infectivity to the two hosts where an increase in the pathogen's infectivity to one host carries a cost in terms of its infectivity to the other host. Using the method of adaptive dynamics [2], we investigate the evolution of pathogen's infectivity and the outcomes are discussed in the context of fungal speciation.

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