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Pathogen invasion assisted by evolution: a spatially explicit model for a multilocus gene-for-gene system

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There is little knowledge of how spatial factors influence the evolution of pathogen virulence in gene-for-gene (GFG) interactions. In agrosystems, the problem of the emergence and spread of pathogen genotypes carrying multiple virulence genes requires understanding pathogen evolution in spatially realistic situations.

In order to study the invasion process of a genetically diverse host population by recombinant multiple virulence, we incorporate genetics into a general epidemiological model based on reaction-diffusion system. The built model describes m-locus GFG interactions between 2^m distinct host and pathogen genotypes spatially distributed in a two-dimensional domain. The host population does not evolve. The pathogen population is assumed to be a haploid organism with diffusive dispersal. The emergence of multiple virulence is provided only by genotype recombination. A nonlinear mating function governs sexual and asexual stages of pathogen reproduction. We do not model the locus mutation from avirulence to virulence.

Linking genetics and population dynamics, the model shows how genetic host diversification coupled with spatial patterns governs the pathogen evolution and spatial dynamics of multi-virulent genotypes. In particular, numerical solutions reveal that, for certain patterns, multigenic resistance and a mixture of singly resistant genotypes have the same effects on the genetic composition of the pathogen population and its density.

To our knowledge this is the first population-genetic model that allows studying the evolution of virulence in a pathogen population followed by sequential invasion across a landscape with a genetically and spatially heterogeneous host. We discuss the model implementation for the development of resistance gene deployment strategies.

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