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# Virulence evolution in multilocus gene-for-gene systems: the effects of spatial arrangement of resistant host genotypes

Natalia Sapoukhina, Charles Eric Durel, Bruno Le Cam

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## Abstract feedback

Salutation Dr.  
Surname SAPOUKHINA  
First Name Natalia  
Email Natalia.Sapoukhina@angers.inra.fr  
Institution INRA UMR077  
Author(s): N. SAPOUKHINA, CH-E. DUREL, B. LE CAM  
Title of your presentation VIRULENCE EVOLUTION IN MULTILOCUS GENE-FOR-GENE SYSTEMS: THE EFFECTS OF SPATIAL ARRANGEMENT OF RESISTANT HOST GENOTYPES  
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Abstract

Nowadays, the longevity of multilocus gene-for-gene resistance is a major challenge in the deployment of resistant cultivars for pest and disease management. The successive pathogen adaptations to hosts possessing different resistant genes and their combinations have been already reported for several plant-pathogen systems. In order to investigate the invasion process of a genetically diverse host population by recombinant multiple virulences, we develop a two-dimensional spatially explicit model for multilocus gene-for-gene interactions between host and pathogen genotypes. The pathogen population is assumed to be a haploid organism with diffusive dispersal. The host population does not evolve. We do not model the locus mutation from avirulence to virulence. The emergence of multiple virulence is provided only by genotype recombination. A nonlinear mating function governs sexual and asexual stages of pathogen reproduction. For the sake of simplicity, we consider dynamics of two-locus host-pathogen system. The host population includes a susceptible genotype, two singly resistant genotypes possessing different resistance genes, and a resistant genotype carrying the combination of these genes. There are correspondingly four pathogen genotypes: universally avirulent, two singly virulent genotypes, and doubly virulent. We perform numerical experiments that mimic the year-to-year dynamics of the crop host-pathogen system with continuous spatio-temporal dynamics within a growing season and one sexual phase per season. We design five distinct spatial planting patterns where a susceptible genotype is mixed with two singly resistant genotypes or with one doubly resistant genotype. We examine (1) how pathogen responses on the host genetic composition and spatial arrangement of host genotypes; (2) which factors favor invasion by the doubly virulent genotype; (3) which factors can lead to the disease suppression. For given parameter values, we show that if the fitness of a novel multiple virulence is less than the fitness of singly virulent and avirulent genotypes, the resistance can lead to a considerable suppression of the pathogen density. Furthermore, genetic host diversification and spatial patterns govern the pathogen evolution and dynamics of the doubly virulent genotype. In particular, a random mixture of two singly resistant genotypes with susceptibles can prevent the invasion by the doubly virulent genotype, while a random mixture of susceptibles with doubly resistance can lead to the dominance of doubly virulence in the pathogen population. To our knowledge this is the first population-genetic model that is able to exhibit 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.

Keywords

spatially explicit model, recombinant multiple virulence, resistance, gene-for-gene, host heterogeneity