

Spatially explicit modeling of pathogen adaptation to hosts with multiple resistance genes

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ABSTRACT

One of the control strategies of fungal crop diseases is planting highly resistant varieties. However selection pressure on the pathogen, imposed by major resistance genes, leads to the development of new virulent races. In most cases breakdown of resistance has been reported for crop-pathogen systems with a genetically uniform crop distributed over large areas [2].

To derive strategies leading to durable resistance we focus on studying the role of recombination of pathogen genotypes and their spread in the process of successive breakdowns of resistant hosts carrying different major resistance genes and their pyramids.

We developed a dynamical model for the evolution of pathogen virulence under a multilocus gene-for-gene interaction with hosts in a two-dimensional domain. The model was verified by applying to the epidemic development of apple scab, caused by the fungus *Venturia inaequalis*, in France [1] and Denmark.

Combination of population dynamics and genetics [3], providing an explicit simulation of the spatial patterns of disease propagation, allows us to test different hypothesis concerning prevention of the invasion of a virulent pathogen strain. In particular, we can compare the efficacy of heterogeneity introduced to the pathosystem at the genetic or population level. What is better to pyramid several resistance genes into a single cultivar or to plant mixtures of cultivars with different resistance genes? The effective long-term strategies against pathogens are discussed.

Key Words: gene for gene, resistance, virulence, spatial spread, recombination

References

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