

Spreading of virulence regarding spatial distribution resistant cultivars inferred from population modeling coupled with genetics

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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]. Des choix stratégiques en matière de construction et de déploiement de génotypes résistants combinant des gènes de résistance se pose aujourd'hui de manière aigüe afin de tendre vers une agriculture à résistance durable. To reach this objective, we start a study that combined population modeling with genetics to (1) identify keys traits of life of the pathogen involved in resistance breakdown (2) simulate virulence spreading regarding spatial host distribution.

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 habitat. The model was verified by applying to the epidemic development of apple scab, caused by the fungus *Venturia inaequalis*, in Denmark [1].

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.

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