

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

Natalia Sapoukhina¹, Pierre Gladieux¹, Hanne Lindhard Pedersen⁴,
Charle-Eric Durel², Christian Lannou³, Bruno Le Cam¹

¹UMR PaVé, ²UMR Genhort, INRA Centre d'Angers
Rue Georges Morel, BP 57, 49071 Beaucouzé Cedex, France
e-mail: Natalia.Sapoukhina@angers.inra.fr

³Pathologie Végétale, INRA
R78850 Thiverval-Grignon, France

⁴Department of Horticulture, Research Centre Aarslev
Kirstinebjergvej 10, DK-5792 Arslev, Denmark

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 [3].

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 France [1] and Denmark [2].

Combination of population dynamics and genetics [4], 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, heterogeneity

References

- [1] Guérin, F., and B. Le Cam. 2004. The breakdown of the scab resistance gene Vf in apple leads to a founder effect in populations of the fungal pathogen *Venturia inaequalis*. *Phytopathology* 94: 364-369.
- [2] Lindhard Pedersen, H., and M. Bertelsen. 2002. Alleyway groundcover management and scab resistant apple varieties. ECO-FRU-VIT. 10th International Conference on Cultivation technique and Phytopathological problems in Organic Fruit-Growing and Viticulture. P. 16-21.
- [3] McDonald, B.A., and C.C. Linde. 2002. Pathogen population genetics, evolutionary potential, and durable resistance. *Annual Review of Phytopathology* 40: 349-379.
- [4] Svirezhev, Yu.M., and V.P. Pasekov. Fundamentals of mathematical evolutionary genetics. Moscow, Nauka. 1982 (In Russian), Dordrecht, Kluwer Academic Publishers, 1990.