Improving the durability and efficiency of plant resistance deployment using eco-evolutionary modelling

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Genetically-controlled plant resistance can reduce the damage caused by pathogens. However, pathogens have the ability to evolve and overcome such resistance. This often occurs very quickly after resistance is deployed, resulting in significant crop losses and a continuing need to breed new resistant cultivars. To tackle this issue, several strategies have been proposed to constrain the evolutionary potential of pathogen populations and thus increase resistance durability. These strategies mainly rely on using different combinations of resistance genes (e.g. qualitative and/or quantitative resistance) in time, space, or both (e.g. via gene pyramiding, cultivar rotations, cultivar mixtures, field mosaics). However, experimental assessment of the efficiency (i.e. ability to reduce disease impact) and the durability (i.e. ability to limit pathogen evolution and delay resistance breakdown) of different deployment strategies presents a major challenge.

Therefore, we developed a spatially-explicit stochastic model to assess the epidemiological and evolutionary outcomes of the major deployment options described above, for both qualitative (major resistance genes) and quantitative resistance (e.g. QTLs affecting different pathogen life-history traits). In addition, we analysed the impact of landscape organisation (as defined by the proportion of fields cultivated with a resistant cultivar, and their spatial aggregation) and epidemiological or evolutionary parameters (e.g. mutation probability, cost of infectivity).

The model was first parameterised for cereal resistance to rusts (caused by fungi of the genus *Puccinia*), and is destined to be applied to other pathosystems including especially viruses of vegetable crops. Our main results on resistance to rusts indicate that evolutionary and epidemiological control are not necessarily correlated, and that no deployment strategies is universally optimal.

Key words: deployment strategy, durable resistance, gene-for-gene, plant disease, quantitative resistance, spatially-explicit modelling.