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GENETIC DRIFT AS A TOOL TO INCREASE THE DURABILITY OF PLANT QUALITATIVE RESISTANCE TO VIRUSES

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BACKGROUND and OBJECTIVES

Plant qualitative (i.e. total) resistance to viruses is an efficient way of protecting crops, but it is often broken down by the emergence of adapted virus variants, able to infect those resistant plants. This evolutionary phenomenon can occur particularly quickly in monocultures deployed in vast areas. Different strategies have been studied, aiming at increasing the durability of resistant crops, such as the use of multiline cultivars or cultivar mixtures in space and time. Here we study a complementary strategy that can yield interesting results in terms of yield increase and resistance durability. It exploits the evolutionary principles governing virus populations for the management of plant resistance, particularly regarding the effect of genetic drift on the evolution of plant viruses.

MATERIAL and METHODS

We have developed a stochastic plant epidemic model at the field scale, coupling epidemiology and population genetics. It allowed to study the effect of genetic drift controlled by quantitative (i.e. partial) resistances on qualitative resistance durability. Our model yields predictions of the added value of pyramiding quantitative resistances controlling virus effective population sizes, and thus the intensity of genetic drift, on crop damage reduction. We investigated the role of field features - such as the intensity of epidemics or the proportion of resistant plants -, and of population genetics features - such as virus bottlenecks sizes and their evolutionary equilibrium within hosts - on yield benefit.

RESULTS

The model provided insightful guidelines for the management of cultivars pyramiding qualitative and quantitative resistances controlling virus effective population sizes. Notably, those quantitative resistances should be particularly helpful when the qualitative resistance gene is not highly efficient, or when the adapted variants are not already present at high frequency in the landscape. Two additional points emerged from the simulations in our framework, (i) it is often preferable to deploy a large proportion of resistant cultivars and (ii) when helpful, it is better to choose quantitative resistances leading to the smallest virus effective population sizes, hence to the strongest genetic drift.

CONCLUSIONS

This model is, to our knowledge, the first one to depict the impact of genetic drift on plant disease resistance durability. We decided to build it as simple as possible, to be able to discriminate which underlying processes enhance durability. It provided promising qualitative results, encouraging further finer research on this subject. In all, we were able to prove the interest of introducing quantitative resistances controlling virus effective population sizes in breeding strategies to increase the durability of plant qualitative resistances.

Building bridges between disciplines for sustainable management of plant virus diseases



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