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Modelling plant resistance deployment: the R package landsepi

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Owing to their evolutionary potential, plant pathogens are able to rapidly adapt to genetically-controlled plant resistance, often resulting in resistance breakdown and major epidemics in agricultural crops, as well as a continuing need to breed new resistant cultivars. Several strategies (e.g. gene pyramiding, crop rotations and mixtures, landscape mosaics) have been proposed to improve resistance deployment. They rely on the careful selection of resistance sources and their sensible combination at various spatio-temporal scales. However, experimental assessment of their efficiency (i.e. ability to reduce disease impact), durability (i.e. ability to limit pathogen evolution and delay resistance breakdown) and cost-efficiency (i.e. ability to maximise profit) at large spatio-temporal scales presents a major challenge (1). The R package landsepi provides a general modelling framework to help compare deployment strategies and understand the impact of epidemiological, evolutionary and genetic factors for a wide range of pathosystems. The model is based on (i) a spatial geometry for describing heterogeneous landscape and allocating different cultivars, (ii) a dispersal kernel for the dissemination of the pathogen, and (iii) a stochastic SEIR ('Susceptible-Exposed-Infectious-Removed') structure with a discrete time step for the description of the host-pathogen interaction, which involves both with qualitative and quantitative resistance genes. It accounts for pathogen evolution (e.g. via mutation, selection, drift, sexual reproduction) and provides epidemiological, evolutionary and economic outputs to assess the performance of the simulated deployment options. The model has initially been calibrated to represent spore-borne pathogens as typified by rust fungi of cereal crops (genus *Puccinia*); parameterization of other pathosystems including downy mildew on grapevine (caused by the oomycete *Plasmopara viticola*) and two viral diseases of pepper (caused by *Potato virus Y* and *Cucumber mosaic virus*) is ongoing.

Reference

(1) Rimbaud, L., et al. (2021). Annu. Rev. Phytopathol., 59: 125-152