O.60 - A mathematical approach towards durable deployment of host resistance

Sapoukhina, N.[1], Kessel, G.J.T.[2], Pinnschmidt, H.O.[3], Durel, Ch.E.[4]

[1] UMR INRA/AgroCampus Ouest/UA - Plant Pathology, INRA Angers, BP 60057, F-49071 Beaucouzé, France
[2] Plant Research International. P.O.Box 69, 6700 AB Wageningen, the Netherlands
[3] Faculty of Agricultural Sciences, Department of Integrated Pest Management, University of Aarhus, 4200 Slagelse, Denmark
[4] UMR INRA/AgroCampus Ouest/UA - Genetics and Horticulture, INRA Angers, BP 60057, F-49071 Beaucouzé, France

Contact: Natalia.Sapoukhina@angers.inra.fr

Abstract

The current use of defeated resistance genes in varietal selection requires to develop strategies for durable cultivation of novel resistance carrying combinations of defeated resistance-genes with quantitative form of resistance. Here, we present a modelling framework coupling three modelling approaches and empirical biological data on differential selection exerted by host resistance. The proposed integrated approach is applicable to a broad range of spatial and temporal scales and it can be used for designing well-suited strategies for the most appropriate deployment of plant genetic resistance.

Plant pathogens overcoming host plant resistance are a recurring problem in crop protection. Durable deployment of host plant resistance is therefore a challenge requiring custom-made solutions for different types of pathogens and host resistance. Examining the efficiency of various scenarios, mathematical modelling can provide an intelligent spatio-temporal deployment of resistant cultivars carrying different types of resistance (major resistance genes vs QTLs) and combinations thereof. Here, we present an integrated framework of the RA4.2 modelling group coupling three modelling approaches (WU, INRA, AU) and empirical biological data (AU, CNR, INRA, IHAR, RRES) on differential selection exerted by host resistance. The ultimate goal of the RA4.2 modelling team is to identify effective strategies of resistance deployment in time (crop rotation) and/or space (field and landscape scales) allowing durable cultivation of resistant cultivars by a significant reduction of pathogen population density. The numerical experiments testing the effectiveness of R-gene and QTL deployment in time and space are based on qualitative information of the fitness balance within pathogen populations provided by empirical studies. A schematic representation of integrating the various modelling approaches is shown in Figure 1.

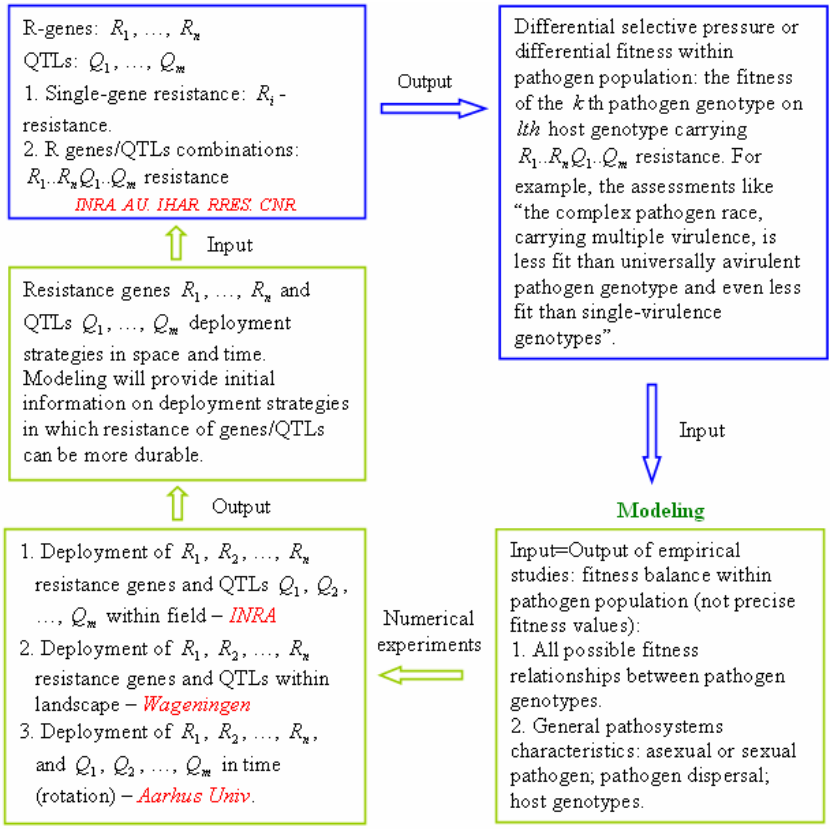

Figure 1. An integrated modelling approach towards durable resistance deployment.

The results of numerical experiments underline the crucial effect of differential fitness within pathogen population on the success of cultivar diversification including both complete specific and partial non-specific resistance and give some guiding threads for optimizing temporal and spatial resistance deployment. In particular, models showed that if pathogen invasion is to be controlled by cultivar diversification, fine-grained spatial arrangement of cultivars (at the field or larger scale) is more effective than coarse-grained one.

The proposed integrated approach provides theoretical support for studying the rapid emergence and spread of novel plant pathogenic genotypes carrying multiple virulence factors. It has practical applicability for designing innovative strategies for the most appropriate deployment of plant genetic resistance.

References

Hovmøller MS, Østergård H, Munk L, 1997. Modelling virulence dynamics of airborne plant pathogens in relation to selection by host resistance in agricultural crops. In: Crute IR, Burdon JJ, Holub EB, The Gene-for-Gene Relationship in Host–Parasite Interactions. Wallingford, UK: CAB International, 173–90.

Sapoukhina N, Durel Ch-E, Le Cam B. 2009. Spatial deployment of gene-for-gene resistance governs evolution and spread of pathogen populations. Theoretical Ecology. DOI: 10.1007/s12080-009-0045-5 (in press).

Skelsey P. Kessel GJT, Rossing WAH, van der Werf W, 2009. Parameterization and evaluation of a spatio-temporal model of the potato late blight pathosystem. Phytopathology 99, 290-300.