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Many different recipes but one flavor: A universal nested structure of quantitative interactions between plant genotypes and their parasites, including viruses

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Understanding the relationships between host range and pathogenicity for parasites, and between the efficiency and scope of immunity for hosts are essential to implement efficient disease control strategies. In the case of plant parasites, most studies have focused on describing qualitative interactions and a variety of genetic and evolutionary models has been proposed in this context. Although plant quantitative resistance benefits from advantages in terms of durability, we presently lack models that account for quantitative interactions between plants and their parasites and the evolution of these interactions.

Nestedness and modularity are important features to unravel the overall structure of host-parasite interaction matrices. We analysed these two features on 32 matrices of quantitative pathogenicity trait data gathered from 15 plant-parasite pathosystems including viruses, fungi, oomycetes, bacteria, nematodes, and insects. We observed significant modularity in only six of the 32 matrices, with two or three modules detected. In contrast, we found high and significant nestedness in 30 of the 32 matrices. Consistent with the widespread nestedness, we showed additionally that: (i) pathogenicity trait values can be mostly explained by a parasite strain effect and a plant accession effect, with minor parasite-plant interaction effect; (ii) there are positive correlations between the efficiency and scope of the resistance of plant genotypes and (iii) between the host range breadth and pathogenicity level of parasite strains. This latter result questions the efficiency of strategies based on the deployment of several genetically-differentiated cultivars of a given crop species in the case of quantitative plant immunity.