

ArchiV

Genetic architecture of quantitative traits in plant-virus interactions: Consequences for the management of resistant and/or tolerant varieties at the landscape scale

Studies of plant defense against parasites have focused mainly on qualitative resistance, which inhibits almost completely plant infection and is controlled by major-effect genes. Such resistance is often compromised by the counter-adaptation of the targeted parasite, resulting into resistance breakdown, with heavy economic losses and a waste of genetic resources.

The ArchiV project deals with understudied and widespread plant genetic resources to control diseases: quantitative resistance and tolerance. It aims

- to phenotype both quantitative resistance and quantitative tolerance and to map the corresponding quantitative trait loci (QTLs) in the plant genome,
- to identify the genetic determinants of pathogenicity traits (virus load, aggressiveness and plant-to-plant transmission capacity) in viruses and their interactions with plant resistance and tolerance QTLs and
- to estimate the durability potential of quantitative resistance and tolerance in the field.

The biological models consist in two economically-important viruses (Potato virus Y and Cucumber mosaic virus) that are also models in basic research and one of their crop host plant, pepper (*Capsicum annuum*). The contrast between the genome structure (monopartite vs. segmented genome) and evolutionary mechanisms (rare vs. frequent genetic exchanges) of these two viruses is expected to have consequences on the genetic architecture of their pathogenicity traits and adaptation capacity.

Modelling approaches will explore the consequences of these genetic architectures on virus evolution and on the efficiency and durability of management strategies of resistant and/or tolerant cultivars in agricultural landscapes. The modelling framework will allow comparison of strategies dedicated to the sustainable control of different kinds of plant pathogens (notably microbes). These management strategies will include pyramiding of different QTLs in a same cultivar, rotations, within-field mixtures and mosaics of fields with cultivars carrying different QTLs.

The project will impact both the scientific areas of virus evolution and virus-plant interactions and stakeholders of the horticultural sector.