

## Adaptation of downy mildew to grapevine partial resistance

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Invasions by plant pathogens are responsible for tremendous damage in crops and are increasing in frequency. Consequently, population genetics studies of pathogens are of great interest to understand invasive population dynamics and adaptation to new hosts (e.g. resistant cultivars) and environments. *Plasmopara viticola* is a heterothallic oomycete responsible for grapevine downy mildew, a major and costly disease worldwide. It has been introduced very recently (around 150 years ago) from North America in Europe and has subsequently invaded European vineyards in a few years. In the last two decades, resistant grapevine cultivars have been used to control the disease, but *P. viticola* populations quickly adapted to this resistance.

The genome of *P. viticola* has been sequenced with PacBio long reads, resulting in a high quality assembly covering 85% of the estimated genome size (BUSCO pipeline: 95.7% completeness). A total of 63 European isolates collected on sensible and resistant grapevines (harboring the Rpv3 QTL) have been resequenced and phenotyped for aggressiveness traits. While isolates collected on sensible grapevines were not structured geographically, isolates from resistant cultivars, in addition to being more aggressive, were genetically differentiated in three separated groups. This suggested the existence of multiple independent adaptations to grapevine resistance. Detection of genomic regions linked to adaptation to cultivated grapevine and resistant cultivars, as well as genes responsible for the determination of mating type, are currently on-going.

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