

FROM TRANSCRIPTOME ANALYSIS TO DISEASE FORECASTING MODELS: A RESEARCH APPROACH FOR A SUSTAINABLE MANAGEMENT OF GRAPEVINE DOWNY MILDEW

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The oomycete *Plasmopara viticola* (Berk. et Curt.) Berl. and de Toni, the grapevine downy mildew agent, caused limited damages when first introduced from North America into Europe. In about thirty years, the pathogen adapted to the Italian climate causing dramatic yield losses. The adaptation to the host is a crucial point: plants and pathogen evolve in response to each other. This co-evolutionary arms race is controlled by genetic variation, which promotes the recognition of pathogen proteins by the host and the overcoming of host defenses by the pathogen. In light of the increasing need to control a pathogen with an incredible variability, novel and sustainable disease management strategies were explored. The screening of a large collection of *Vitis vinifera* germplasm revealed the existence of the first resistant Eurasian cultivar, named ‘Mgaloblishvili’. Transcriptomic analyses allowed to identify the *V. vinifera* resistance/susceptibility genes and *P. viticola* genes, encoding effectors, that are at the bases of the molecular interaction between the host and the pathogen. The drawbacks of disease-resistant varieties is the selection of strains able to overcome plant resistance. To provide indication on the pathogen adaptability, the genetic variability of the *P. viticola* Italian population was investigated. This analysis indicated an adaptive evolution for the presence of two separate genetic clusters, with little, but significantly different, distribution according to geography and climatic conditions. The pathogen adaptability must be taken into consideration in the implementation of the disease control methods for preserving the durability of plant resistance and avoiding fungicide resistance in open field. In this view, the EPI forecasting model was validated in field trials to define a rational treatment strategy. These results open the way to new perspectives in molecular breeding to obtain *P. viticola* resistant grapevine which, integrated with the forecasting model, could allow to achieve a sustainable disease control.