

Adaptation of Plasmopora viticola isolates against defense mechanisms conferred by different resistance genes in grapevine.



De Freitas, Fábio Ribeiro¹; Bitencourt, Camila¹; Dal Vesco, Lirio Luiz²; Dellabruna, Emilio³; de Souza, André Kulkamp⁴; Trapp, Oliver⁵; Stefanini, Marco⁶; Nodari, Rubens Onofre¹, Welter, Leocir José^{1*}

- 1 Plant Genetic Resources Graduate Program, Federal University of Santa Catarina (UFSC), Florianópolis, Brazil 2 Agricultural and Natural Ecosystems Graduate Program, Federal University of Santa Catarina (UFSC), Curitibanos, Brazil 3 Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina (EPAGRI), Urussanga, Brazil 4 Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina (EPAGRI), Videira, Brazil
- 5 Institute for Grapevine Breeding Geilweilerhof, Julius Kühn Institute (JKI), Siebeldingen, Germany 6 Fondazione Edmund Mach (FEM), Genomics and Biology of Fruit Crops, San Michele all'Adige-TN, Italy
- * leocir.welter@ufsc.br

INTRODUCTION

Grapevine breeding for disease resistance is an essential strategy to promote the sustainability of grape and wine production. Resistance durability play a central role particularly for perennial crops, such as grapevine. The resistance durability is dependent on the resistance mechanism of the genes and the evolutionary potential of the pathogen. In the highlands of Santa Catarina the Plasmopara viticola reproduces sexually and asexually (BITENCOURT et al., 2021) and the populations are genetically diverse (TOMAZZETI, 2021). Thus, the main aim of this work was to evaluate the level of adaptation of two Plasmopara viticola populations to resistant grape varieties/genotypes carrying different combinations of R-Gene alleles in Santa Catarina state, Southern Brazil.



Figure 1. Map of Santa Catarina state describing the places where P. viticola were collected.

MATERIAL AND METHODS

P. viticola inoculum was collected from two sites of the Santa Catarina State, Southern Brazil, at the end of the grape season 2020/21. The inoculum was composed of a mixture of sporangia sampled from hosts containing the R-alleles Rpv3, Rpv10, Rpv1+3 and Rpv3+10. Two sporangia suspensions were prepared from each site: 1) A bulking of sporangia collected from all hosts (PC21: Curitibanos; PU: Urussanga); 2) A bulk of sporangia collected from hosts containing the R-allele(s) combination (SPRpv3; SPRpv10; SPRpv1+3; SPRpv3+10). The suspensions were used to inoculate leaf discs of the susceptible variety 'Cabernet Sauvignon' and a panel of ten cultivars/genotypes containing different R-alleles combinations. Seven days after inoculation, the following parameter were measured: disease severity, resistance level (OIV 452-1 descriptor), severity and sporangia production.



Figure 2. Severity analysis by ImageJ software (A), OIV 452-1 scale (B).

Results

- The Rpv12 and Rpv10 R-alleles were the most effective source of resistance. - An erosion of the resistance conferred by Rpv3 haplotypes was observed.

-The combination of Rpv3 with Rpv1, increased the level of resistance.

- Isolates were able to sporulate in hosts carrying Rpv1+3 (in Curitibanos) and Rpv3+10 (in Urussanga), bringing concerns about the resistance durability.

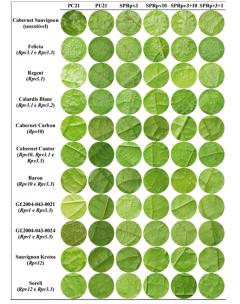


Figure 3. Leaf discs containing different Rpv genes inoculate with populations and subpopulations of P. viticola.

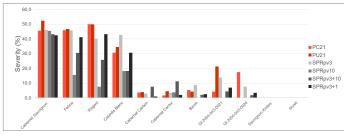


Figure 4. Disease severity resulting from P. viticola isolates inoculation in different genotypes leaf discs.

CONCLUSION

- The results obtained are fundamental to delineate breeding strategies for the development of new varieties with durable resistance to P. viticola.

- The results indicate the presence of isolates that overcome the resistance conferred by Rpv alleles in Southern Brazil.

ACKNOWLEDGEMENT

