

resistance gene, *PdR1*, and used marker-assisted selection (MAS) to introgress *PdR1* into *V. vinifera* cultivars. Using aggressive training and MAS we were able to reduce the seed-to-seed cycle to 2 years and went through four modified backcross (BC) generations to obtain 97% *V. vinifera* hybrids. To avoid inbreeding depression, we used different *V. vinifera* cultivars for each BC generation. In the mBC4 generation we grew out large seedling populations. These were first selected for horticultural characters and high organoleptic quality, and then were repeatedly screened for the highest levels of *X. fastidiosa* resistance. The best were replicated and advanced to small-scale wine making (< 20L). To date, 5 advanced selections have been pre-released to grapevine nurseries for multiplication, and will be ready for commercial use in Summer 2020. Wines have been evaluated with professional tasting panels and judged to be very high quality. These vines are under testing across California in areas with extreme PD pressure, and several mBC3 and mBC2 selections are being tested in Florida, Alabama and Texas. Additional commercial scale plantings are planned for 2018. The next phase of the breeding program involves stacking additional resistance genes to produce PD resistant winegrapes with more broadly based resistance. We are also introgressing powdery mildew resistance from selections with a high percentage of *V. vinifera* and powdery mildew resistance from multiple sources.

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Screening of olive germplasm for resistance to *Xylella fastidiosa* ST53: the state of the art

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Abstract: While different sources of natural resistance to *X. fastidiosa* have been described in grapevines and citrus, lack of solid information exists on possible sources of resistance/tolerance in the cultivars that characterize the wide olive germplasm. Preliminary field observations and laboratory analyses of a few cultivars, have shown that differential responses to *X. fastidiosa* infections exist. To confirm these preliminary findings, a large panel of olive cultivars is being specifically investigated. Currently, the screening procedure relies on field observations looking for symptomless subjects (trees of known cultivars/volunteer seedlings), mechanical inoculations, qualitative and quantitative diagnostic assays (ELISA & qPCR) and, in selected cases, comparative transcriptomic profiling. Field experiments include the planting of the target cultivars/selections in an infected area under high inoculum pressure. All the plots are located in the Apulia Region (Italy) in the demarcated infected area, surrounded by *X. fastidiosa* heavily affected olive groves. A first experimental plot was