

## INNOVATIVE STRATEGIES TOWARDS MARKER-ASSISTED (PRE-) BREEDING FOR DISEASE RESISTANCE IN GRAPEVINE

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Grapevine (*Vitis vinifera* L.) is one of the most valuable crops worldwide, mainly studied for quality and disease resistance traits. Viticulture has often been affected by encounters with new parasites that still represent a major constraint. This is a particularly important issue because, even though some inter-specific varieties (hybrids) between *V. vinifera* and *Vitis* spp. are widely present, the majority of cultivated grapevines are pure *V. vinifera* varieties, which are highly susceptible to pathogen attack. Fungal diseases represent some of the most severe plagues and growers are obliged to use pesticides to prevent serious yield loss.

Within the FEM breeding program, the selection process has been based on the major need of innovation brought up by the grapevine growers. While during the past years this request has been addressed focusing on the increase of the complexity and the originality of wines, in the last decade the need of new varieties resistant/tolerant to the abiotic and biotic stresses is emerging. In order to reach this goal, the FEM (pre-)breeding activity targets the introgression of downy (DM) and powdery (PM) mildew resistance/tolerance into *vinifera* background, to be coupled with grape quality characteristics in the next future. The achievements of this long-term objective can be anticipated by means of early-flowering genotypes and *ad hoc* agronomical practices, such as fruiting cuttings.

The main objective is to create introgression lines in which the dilution of the *Vitis* spp. in the *V. vinifera* genome occurs with a selective and focused method based on the molecular detection of specific chromosome arms. With this aim, we focused on the genetic (190 SSRs) and phenotypic (DM and/or PM resistance) characterization of about 300 *Vitis* hybrids in order to identify selection signatures. Based on SSR profiles, the historical pedigree information has been checked and the trueness-to-type validated for several of the studied hybrids. This allowed to perform the Identity By Descent analysis, tracing the allelic flow through the successive generations. In particular, we

exploited the information derived from the genome sequencing related to the presence of resistance gene analogue clusters along the chromosomes 5, 7, 9, 12, 13, 15 and 18.

The final result of this study will be the release of molecular markers valuable for grapevine Marker-Assisted Breeding, upon their validation in *ad hoc* segregating populations.