

NOVEL APPROACHES TO GENETICALLY AND PHENOTIPICALLY CHARACTERIZE DOWNY MILDEW RESISTANCE IN GRAPEVINE

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Within the FEM grapevine breeding program, re-established in the middle '80s, the selection process has been based on the major need for innovation raised by grapevine growers. During the past years, this request has been addressed to increase the complexity and the originality of wines, while in the last decade the need for new varieties resistant/tolerant to abiotic and biotic stresses has emerged. In particular, among fungal diseases, downy mildew (DM) represents the most severe plague in humid-temperate climate and growers are obliged to massively use pesticides to prevent serious yield loss. In order to reach this goal, novel approaches have been undertaken.

Firstly, new acquisitions from other breeding programs and novel wild genetic material collection - for a total of 264 accessions - were genotypically characterized with 50 highly informative microsatellites, followed by a genetic diversity and pedigree analysis; the overall genetic material was divided into five classes: known and related (38%); unknown and related (21%); known and unrelated (10%); unknown and unrelated (23%); and redundant (8%). The unknown (related and unrelated) genotypes hold great potential as exclusive genetic resources, while the related (known and unknown) genotypes lead to the identification of pedigree-supported parental materials for the creation of segregating populations.

Secondly, most of the overall genetic material was phenotypically characterized to identify the donors of disease resistance traits. In particular, a DM resistance *in vitro* phenotyping protocol and assessment were optimized at leaf disc level, while a novel *in vitro* screening method and annotation procedure were developed at inflorescence level. The latter led to the submission to the *Organisation Internationale de la Vigne et du Vin* (OIV) commission of the new OIV 453-1 descriptor. The study of inflorescence in addition to leaf organ - therefore of DM dual epidemics - was feasible thanks to the optimisation of the fruiting cutting agronomic technique, which turned out to be crucial for the anticipation of the study of late traits under controlled conditions.

Our findings are highly informative to prospective Marker-Assisted Breeding programs for disease resistant traits, as well as preparatory to transcriptomics and metabolomics studies enabling the fine comprehension of the molecular and physiological mechanisms underpinning the dual epidemics phenomenon.