

SUSTAINABLE VITICULTURE: DIFFERENT STRATEGIES TO ENHANCE THE RESISTANCE OF THE VINE TO THE MAIN FUNGAL DISEASES ON SICILIAN CULTIVARS

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This project, funded by Istituto Regionale del Vino e dell'Olio della Regione Siciliana (IRVO), is aimed at the development of novel genotypes characterized by resistance to the grape main fungal diseases like *Botrytis cinerea* (grey mould), *Plasmopara viticola* (downy mildew) and *Erysiphe necator* (powdery mildew).

The project is based on the combination of traditional breeding efforts, whole-genome sequencing and CRISPR/Cas9 genome editing approaches. The breeding program is focused on the most representative cultivars of the Sicilian viticulture: 2 red grape ('Nero d'Avola' and 'Nerello Mascalese') and 3 white grape ('Catarratto', 'Grillo' and 'Carricante').

During the 2022 pollen of previous constituted hybrids, showing resistance to different fungal diseases, provided by the CREA-VE project partner, has been used to pollinate the 5 Sicilian cultivars. After seeds germination, more than 200 seedlings were obtained which are now being evaluated for the presence of resistance genes through molecular analysis.

In parallel, the genome of the five Sicilian cultivars was sequenced (Illumina pair-ends sequencing at a coverage of 50X) to outline genetic similarities and dissimilarities within the five accessions in comparison with the other grapevine genomes available and to decipher the genetic basis of important horticultural traits.

In order to apply genome editing approach, the five cultivars were also evaluated for their regeneration capacity and aptitude for *in vitro* culture. Clusters of flowers were collected from local vineyard at different pollen developmental stage and sterilized. The anthers were cultured on different media for the induction of embryogenic calli, the prerequisite for the application of CRISPR/Cas9 to modify tolerance/resistance genes of fungal diseases. Of the 5 cultivars, up to now 'Nero d'Avola' cultivar has produced embryogenic calli.

The combined approaches of traditional breeding and genome editing will allow the development of novel genotypes combining the positive agronomical traits of the cultivars in analysis and the resistance to the main fungal diseases.