

## Digitalization and valorization of the genotypic and phenotypic information retained within the FEM grapevine germplasm

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### Abstract

The maintenance and valorization of genetic diversity is an undoubtable resource for the viticulture of the future, since the climate crisis is forcing us to think of new, more resilient varieties. For this reason, the grapevine germplasm of the Fondazione Edmund Mach has been continuously expanded in the last decade to a total of 3,120 accessions, whose trueness-to-type has been verified by means of the universal set of nine microsatellites. About two thirds are *V. vinifera* subsp. *vinifera* accessions, while the rest consists of naturalized and selected hybrids, *V. vinifera* subsp. *sylvestris*, and pure species. The genetic material has also been characterized over three consecutive years for ampelographic, vine development, and biotic stress response traits to be exploited for experimental purposes. All the data and metadata have been digitalized and hosted in a SQL database, the FEMVitisDB, developed with an ontology driven paradigm to annotate the deposited information. The database was built following the MIAPPE checklist to ensure data FAIRness. A RESTful WebserviceAPI based on BrAPI and a web frontend were developed to easily explore the information in the repository.

Findings about the captured genetic diversity, the identified unique profiles, and the scouted unknown and therefore novel genotypes will be discussed. The latter enrich the genetic asset of the grapevine community, towards the feeding of international databases. Where feasible, the first degree of parentage relationship has been reconstructed. Finally, the outcomes regarding the inferred phenological core collections will be introduced to provide an information arsenal for future 'omics analyses.

**Keywords:** Database, collection, breeding, kinship, *Vitis*.