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**XIV. International
Symposium on Grapevine
Breeding and Genetics**

■ ■ ■ ■ **ZAGREB CROATIA**

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Book of Abstracts



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**XIVTH INTERNATIONAL
SYMPOSIUM ON GRAPEVINE
BREEDING AND GENETICS**

INFORMATIONS

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POSTER

The FEMVitisDataset: from germplasm collection to an Open FAIR Data resource

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ABSTRACT

The preservation and strategic exploitation of grapevine genetic resources are essential to sustain viticulture under accelerating climatic and phytosanitary pressures. Here we present the FAIR-compliant digitalization and genetic characterization of the FEM grapevine germplasm, one of the largest curated collections in Europe. The publicly released FEMVitisDataset comprises 2,904 accessions from 51 Countries, including cultivated *Vitis vinifera* and wild relatives, interspecific hybrids, and pure wild species, capturing extensive taxonomic and functional diversity.

All accessions were genotyped using nine international reference SSR loci, enabling multilayer True-To-Type validation through comparison with major international databases. The analysis identified 1,937 unique genetic profiles, of which 894 were previously unreported, highlighting the substantial originality and unexplored value of the germplasm. Beyond molecular fingerprinting, the dataset integrates multi-year phenotypic observations—phenology, fertility, ampelography, and biotic stress responses—structured according to MIAPPE standards and semantically harmonized through plant and crop ontologies. The wide phenotypic variability recorded across accessions, including large offsets in phenological timing and reproductive traits, illustrates the adaptive potential retained within the germplasm and its relevance for breeding under climate change scenarios. The standardized data structure provides a transferable framework that can support other germplasm repositories in FAIR digitalization workflows.

The coexistence of historical cultivars, somatic variants and breeding selections provides a unique bridge between conservation and modern genetic improvement pipelines. Approximately one third of the validated profiles correspond to novel genotypes, underscoring the global relevance of this resource for germplasm discovery.

All unique genetic profiles have been genotyped with the High-density Axiom®Vitis22K SNP array, enabling genome-wide association studies, population structure analyses and genomic prediction approaches aimed at accelerating

trait dissection and increasing breeding efficiency. Overall, the FEMVitisDataset represents a quantitatively rich and qualitatively validated resource, demonstrating how curated germplasm banks can evolve into digital infrastructures supporting biodiversity research, data-driven breeding and future viticulture resilience.