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Assessment of diversity and genetic structure is an essential step for effective use of grape germplasm collections

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Abstract: The economic importance of grapevine has driven significant efforts in genomics to accelerate the exploitation of *Vitis* resources for development of new cultivars. However, although a large number of clonally propagated accessions are maintained in grape germplasm collections worldwide, their use for crop improvement is limited by the scarcity of information on genetic diversity, population structure and proper phenotypic assessment. The identification of representative and manageable subset of accessions would facilitate access to the diversity available in large collections. The FEM grape germplasm resources (2273 accessions) were characterised using 22 common microsatellite loci and 384 single nucleotide polymorphisms (SNPs) to examine the structure of genetic diversity and to propose a core set of grape accessions representing the allelic diversity of the whole collection. Retention of the maximum genetic and phenotypic variability was tested for two genetic core collections and one larger core set established based on phenological records. These results can be combined to the definition of inter- and intraspecific levels of germplasm stratification, and make possible to design studies dissecting the genetic basis of **agronomic and domestication-related traits**.

Keywords: Association study, Core collection, Genetic structure, Germplasm, Molecular markers, *Vitis*