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Poster Abstract - C.44

GENETIC VARIATION AT MARKER LOCI IN AN ITALIAN COLLECTION OF WILD AND CULTIVATED GRAPEVINES (*V. VINIFERA* L.)

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Analysis of variants that are found in nature provides an important source of genetic variation that can be used to gain insight into the control of important processes in plants. In many cases, including *Vitis vinifera*, natural variation present among accessions is multigenic, which has historically hampered its analysis.

Phenotypic variation for morphological and physiological traits is abundant in cultivated grapevine and enables almost every *V. vinifera* variety to be distinguished from other varieties. Unfortunately, wild grapevine individuals (*V.v.* ssp. *silvestris*) have been scarcely explored and natural populations are today reduced to a very low size.

In order to improve both management and exploitation of our germplasm collection, we started genotyping every accession of cultivated and wild grapevines at the six most polymorphic and widely used SSR loci. Moreover, suitable map based SSR markers have been included to analyse the allelic variation at certain phenology quantitative trait loci while characterizing the QTLs with candidate genes and experimental segregating populations.

We then investigated the genetic diversity, structure and differentiation within 160 Italian grape cultivars and 210 accessions of wild grapevines collected throughout Italy in the past years.

Since ssp. *silvestris* can principally be distinguished from cultivated grapevine by its dioecism, these accessions were further investigated at the sex-determining locus recently mapped by our group in *Vitis riparia* linkage group 2. The genetic relationship between wild and cultivated grapes and the pattern of variation at four SSR loci linked to the sex gene will be presented.