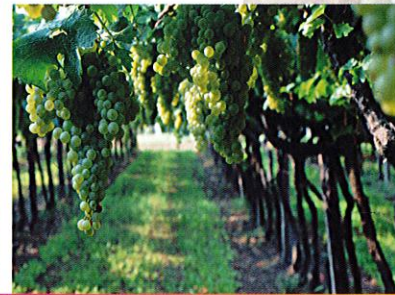
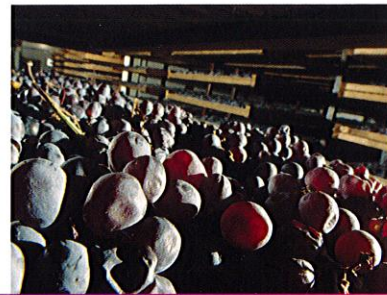




UNIVERSITÀ
di VERONA
Dipartimento
di BIOTECNOLOGIE



X INTERNATIONAL SYMPOSIUM ON GRAPEVINE PHYSIOLOGY AND BIOTECHNOLOGY



BOOK OF ABSTRACTS

June 13th – 18th, 2016
Palazzo della Gran Guardia
Verona, Italy



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Genetic investigation of Caucasian grapevine germplasm with low susceptibility to downy mildew

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According to historical and archeological findings, the South Caucasus is considered the heart of grapevine domestication and this hypothesis makes the germplasm resources of the region particularly fascinating from a genetic point of view. Recently, some grapevine accessions from Georgia have attracted attention because of their low susceptibility to several diseases, including downy mildew (DM) caused by *Plasmopara viticola* (pv). This suggests that there may be potential genetic variation within *Vitis vinifera* to be exploited for sustainable viticulture, in addition to breeding resources from other *Vitis* species.

Here we present the genetic characterization of 25 previously unexplored Caucasian grapevine cultivars aiming to understand the eventual genetic basis of less susceptible phenotypes observed under natural field infection by DM. Our phylogenetic analysis including several hundred grapevine genotypes from across Eurasia, interspecific hybrids and rootstocks, actually placed this germplasm among *V. vinifera* populations. A further screening at major Rpv loci didn't find any SSR marker of the expected size for resistance traits that might have been introgressed from Asian or American resistant grapes. The existence of novel defense factors in the germplasm is being investigated through a combined approach of QTL mapping and bulked transcriptome profiling. Disease severity after preliminary artificial inoculation showed segregation among 157 seedlings obtained by selfing the most promising accession. A genetic map was built essentially with SSR markers and enriched with RAD-derived SNPs chosen to fill in several gaps. Despite the parental plant revealed an exceptionally high level of homozygosity (152 out of 312 SSR loci were monomorphic) all the expected linkage groups were obtained.

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Leaf transcript analysis reveals a distinct regulation of stilbene biosynthesis in diseased and recovered grapevines affected by Flavescence dorée

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Flavescence dorée is an epidemic disease caused by phytoplasma (FDp) infection that still seriously affects European viticulture.

In this work, we analysed gene expression changes following FDp infection in leaves of the highly susceptible *Vitis vinifera* cv Barbera, with particular focus on transcriptional differences occurring in secondary metabolism. Leaf samples were collected in field from healthy (H), infected (FD) and recovered (REC) plants at three time points over the vegetative season. Samples from the second time point (late July), the moment of maximum infection on the basis of molecular diagnosis, were used for RNA extraction,