Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract - C.42

INTEGRATED SNPS-BASED GENETIC MAP OF GRAPEVINE (*VITIS VINIFERA* L.)

M. SALMASO*,**, G. MALACARNE**, M. STEFANINI**, M. S. GRANDO**, R. VELASCO**

*) Department of Environmental Agronomy and Crop Production - Agripolis, University of Padova - marzia.salmaso@unipd.it
**) Istituto Agrario di San Michele all’Adige, San Michele a/A (TN), Italy

functional map, SNPs, grapevine, anthocyanin metabolism, berry colour

Fine mapping is the basic work to develop markers suitable for marker assisted selection programs and map based cloning approaches. To this purpose, several international groups have developed a consistent number of molecular maps in the last few years, mainly based on co-dominant (microsatellites) and dominant (AFLP, RAPDs) markers. SSRs are the essential basis for cross-talk between maps and represent the most useful markers due to multiallelism and reproducibility. A basic number of SSRs used for several referring grapevine maps have been used to build up a framework of co-dominant markers conferring to any growing map an universal value. Dominant markers are useful only when referred to a specific cross but it is difficult to export them to other crossing population analysis. The main objective of the present work was to identify rapid and economical methods to score for co-dominant single nucleotide polymorphimsms (SNPs), possibly applicable to automatic or semi-automatic procedure. As a second goal, the attention has been focussed on SNPs development based on internal or international EST databanks and scored on the crossing population Freiburg 993-60 (complex hybrid between *V. vinifera*, *V. rupestris* and *V. lincecumii*) x *Vitis vinifera* cv. Teroldego. In particular we focalised our attention to the genes belonging to anthocyanin metabolism. We mapped these genes and the transcription factor involved in their expression. The colour of the berry segregates with this gene demonstrating the correlation between MybA and anthocyanin biosynthesis.

Due to the large synteny within Vitis spp., positioning of EST-based SNPs confer to the described data an universal value in grapevine mapping. So this first map based on SSRs and SNPs represents a stimulus to any future mapping work demonstrating the synergy between multiallelic anonymous markers as SSR and biallelic gene-specific markers based on SNPs.