

GRACIOUS

October 29-31, 2014, Sede Boqer, Israel

The Bilateral Israel - Italy Grapevine Symposium Physiology, Genetics & Genomics

Sede Boqer, Israel
2014

BOOK OF ABSTRACTS



Embassy of Italy
Tel Aviv



The Jacob Blaustein Center for
Science Cooperation



French Associates Institute for
Agriculture & Biotechnology of Drylands



The Jacob Blaustein Institutes
for Desert Research



Exploring a large grape germplasm collection for genetic association studies

Grando M.S., Costantini L., Lorenzi S., Moreno-Sanz P., Marrano A., Nwajor C.C., Prazzoli M.L., Yu X., Battilana J., Grzeskowiak L.

Quantitative trait loci (QTL) linkage mapping is an effective tool for the identification of genetic loci underlying natural variation, and several attempts to dissect the architecture of target traits for breeding have been reported in grapevine. Recently, genome-wide association studies (GWAS) have received increased attention for the identification of QTLs in plants as an alternative to, or in combination with linkage mapping. Candidate gene association studies are a complementary extension of GWAS and focus the association analysis exclusively on a selection of genes with known or potential functions in the trait of interest. The candidate gene approach has the potential to narrow down the set of trait associations, and was confirmed to be successful in our experiments to identify the gene and even the individual nucleotides that affect the expression of Muscat flavor in cultivated grapevines.

The objectives of our latest studies were to detect the quantitative trait genes underlying natural variation of key developmental stages (budburst, flowering and the onset of ripening) as well as of anthocyanin content and composition of the berries in *Vitis vinifera*. We used traditional linkage mapping followed by a candidate gene association analysis in panels of multiple grapevine accessions, sorted from a large germplasm collection (2.300 accessions) whose genetic diversity and structure were previously characterized by SSR and SNP markers. Specific genes with proven or suspected activity, for example in flowering time control, are also explored in a broader range of plant materials, to look for variants that may have been selected during domestication.