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**PROGRAM,  
BOOK OF ABSTRACTS,  
AUTHOR INDEX.**

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## Molecular evolution of flowering genes in grapevine

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Flowering is a key adaptive trait important for plant fitness and crop production. Recently, using progenies derived from crosses of different varieties, a new QTL for flowering time was mapped in the grapevine genome. We resequenced candidate floral pathway genes located in this QTL from a collection of multiple grape accessions. These genes cooperate to regulate meristem formation and flowering transition. Two of them, FT and SVP, were suggested as major players in plant thermosensory perception. FT is a floral activator that integrates signal inputs from various pathways and SVP controls flowering time by negatively regulating the expression of FT via direct binding. This interaction is proposed as one of the molecular mechanisms evolved by plants to modulate the timing of the developmental transition to flowering under fluctuating temperature conditions. The pattern of linkage disequilibrium and population differentiation at this locus in grapevine may indicate that these flowering genes are targets of selection. We investigate possible genotype-phenotype relationships for these candidate genes by applying field observations of flowering time in the core collection recorded during several growing seasons. Our long-term objective is to provide information on the genetic variation of phenological traits and to facilitate choice of grapevine varieties adapted to atmospheric conditions of a specific geographic location

## Bacterial community structure changes during summer in high alpine fresh water springs

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Water springs in high elevation environments are one of the most endangered habitats because of their vulnerability to environmental changes. The rapid change of genetic structure of bacterial communities due to little variations of environmental parameters in water systems may reflect evolutionary processes going on throughout the season. Quantitative Amplified Ribosomal Intergenic Sequence Analysis (qARISA) was carried out on environmental DNA extracted from sediments collected in three water spring in the upper Matsch Valley (South Tyrol, Italy.; 2,300 m.a.s.l.) four times during the summer. The fingerprinting matrix was analyzed through canonical correspondence analysis (CCA), and it showed a clustering pattern that reflected a variation of community structure closely linked to the environmental parameters. Shannon ( $H'$ ) diversity index obtained from the fingerprinting matrix was analyzed statistically against the water  $^2\text{H}$  and  $^{18}\text{O}$  isotopic ratios, electric conductivity (EC) and water temperature. The latter features the highest correlation with bacterial diversity ( $r=0.75$ ), followed by EC ( $r=0.58$ ). No significant correlation was detected between diversity and isotopic ratios. Through a multiple regression analysis, bacterial diversity appears to be indeed causally related to EC and water temperature ( $\text{adj-}R^2=0.5$ ,  $p<0.05$ ). Our results suggest that in oligotrophic freshwater environments evolutionary processes may be driven by selective pressures due to water parameter variations.

## Sustainable management for increasing soil microbial diversity in a Mediterranean agro-ecosystem

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Olive can be considered a paradigm species for Mediterranean agro-ecosystems. In conventional olive growing, adopted by the majority of the farmers, frequent soil tillage has reduced soil microbial diversity and microbiota complexity that strongly contribute to the overall soil fertility. Therefore, the conventional agronomic practices should evolve in a more sustainable olive management addressed to improve soil microbial diversity. A better understanding of the ecology of soil microorganisms could lead to identify agricultural management practices that stimulate and select the soil microorganisms having beneficial purposes in agriculture, such those interested in nitrogen cycle. The aim of this study was to evaluate the effects of sustainable practices (grass cover and pruning residues recycling) on soil microbiological quality in a Mediterranean olive orchard. The trials were carried out in a mature olive grove (*Olea europaea* L. – cv