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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 ²H and ¹⁸O 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

Maiatica) located in Basilicata Region (Southern Italy.) and managed for 13 years (medium-term) according to two different soil management systems: the sustainable treatment (ST) and the conventional treatment (CT). Soil microorganisms in the two systems were monitored by both microbiological cultural-dependent and molecular methods, and by microscopy. In the ST olive orchard, soil microbiota showed a higher complexity and metabolic diversity. The adoption of 'innovative', sustainable, agricultural practices had positive effects on soil microbiota and its biodiversity, which in turn can influence soil fertility and plant growth by increasing nutrients availability and turnover. The results of this study encourage the use of sustainable agricultural practices able to enhance physico-chemical and microbial soil fertility and promote good-quality fruit production without detrimental effects on water and soil resources. The role of the identified microorganisms in the soil microbial network is discussed, in order to provide a detailed view of the impact that man-made selection had on soil microorganisms of agricultural relevance in a typical Mediterranean agronomic biosystem.

Insights into *Drosophila*-*Wolbachia* Interactions: Cryptic *Wolbachia* strains in closely related species

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Wolbachia is a widespread group of endosymbiotic bacteria of arthropods that have diverse and complex effects on their host biology. Among them, are the protection against viruses and the mostly known reproductive effects including Cytoplasmic Incompatibility, male-killing, induction of parthenogenesis and feminization. Owing to its effects, *Wolbachia* are considered to be great candidates for their biocontrol potential. Between *Drosophila* species, *Wolbachia* are extremely common and include strains with variable phenotypic effects. Here we report on the genome sequencing of the *Wolbachia* endosymbiont "wSuzi" from the invasive pest *Drosophila suzukii*. The final assembly yielded approximately 1.35 Mbp in 110 contigs, with an average depth of coverage 60X. We found wSuzi to be closely related to the widespread *D. simulans*' wRi strain. The two strains proved to be identical on the basis of the existing typing systems, including Multiple Locus Sequence Typing (MLST) and the most recently Multiple Locus VNTR Analysis (MLVA). However, several structural variations such as InDels and genomic rearrangements were able to discriminate the two strains. Based on the differences between wRi and wSuzi, we identified variable regions that were able to recognize different strains in different populations of *D. suzukii* and in the sister species of *D. suzukii*. Our results show that the currently used marker systems for *Wolbachia* lack the resolution to discriminate and identify potential cryptic strains. This could lead to an underestimation of the true biodiversity of *Wolbachia* bacteria but could also affect the design of applied control strategies and subsequent monitoring procedures.

The influence of fertilization in chlorophyll content of dominant legumes and grasses in a permanent pasture of low hills in Banat (Timis county)

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In this study, the objective was to determine the effects of mineral and organic fertilizers on chlorophyll content of dominant legumes and grasses in a permanent pasture of low hills in Banat (Timis county). The average of the annual air temperature in this region is 10.7°C and the average of the annual rainfall amount is 608 mm. The climate in the studied area is temperate continental with Mediterranean influences. The experimental field was organized by setting 9 fertilisation variants (3 organic, 3 mineral and 3 organic – mineral fertilisation variants) and a control non-fertilised variant. Every studied variant has three replicates. The importance and relevance of fertilizing the grasslands lie in the principle of restoring nutrients exported through the harvested crop, a concept developed by Bossingaul and founded by Justus von Liebig in the 19th century; it refers to the fact that crops consume nutrients from the soil to develop the crop thus depleting the soil from nutrients that are removed with the crop which results in a decrease of soil fertility. Hence the idea of recovering soil nutrients (Sala F, 2008), Chlorophyll content was determined using a portable SPAD. Legumes have a higher content of chlorophyll in all variants compared with grasses. The highest chlorophyll content of legumes case was registered at the organo-mineral variant fertilized with sheep manure 20t/ha + 50kg/ha P₂O₅ + 50kg/ha K₂O (V6). In the case of grasses, the highest chlorophyll content was recorded in chemically variant fertilized with 150 kg/ha N50 kg/ha