Metagenomic analysis of bacterial endophytic communities associated with grapevine (*Vitis vinifera* L.)

P91

S. YOUSAF, M. PANCHER, A. CAMPISANO

Sustainable Agro-ecosystems and Bioresources Department, IASMA Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach 1, 38010 San Michele all'Adige, (TN), Italy

In recent years, interest in endophytic microorganisms has increased, as they play a key role in agricultural environments and are promising because of their potential use in sustainable agriculture. These microorganisms include both commensal species, which have no direct effect on the host plant, and mutualistic symbionts, which could be used in the biological control of pathogens or plant growth promotion. In the present study we investigated how microbial communities in plants from organically managed farms differ from those obtained from integrated pest management (IPM) farms. Microbial DNA isolated from grapevines (*Vitis vinifera* L.) cv Merlot and Chardonnay cultivated in a subalpine area in Northern Italy was PCR amplified to fingerprint endophytic communities, and to assess the distribution of important functional genes in the grapevine microbiome in the studied areas.
Here we report the composition of endophytic microbial communities assessed through a cultivation independent approach: Automated Ribosomal Intergenic Spacer Analysis (ARISA). The changes in community structure and composition are interpreted in the light of the environmental variables considered. Fingerprinting results were validated by multivariate analysis. Other metagenomics approaches are being considered.

Mating type gene search and quantification of *Tuber melanosporum* as tools to evaluate truffle-ground productivity

P92

E. ZAMPIERI[1], R. RIZZELLO[1], P. BONFANTE[1], A. MELLO[2]

[1]Dipartimento di Scienze della Vita e Biologia dei Sistemi dell'Università di Torino, Viale Mattioli 25, 10125 Torino, Italy; [2]Istituto per la Protezione delle Piante del CNR, UOS Torino, Viale Mattioli 25, 10125 Torino, Italy

Among the microbial communities of plant microbiome, mycorrhizal fungi occupy a crucial position. The genome sequencing of the ectomycorrhizal fungus *Tuber melanosporum* has revealed that the fruiting body production depends on the availability in the soil of two mycelia with opposite mating types. This finding has suggested that seedlings produced for truffle-culture programs have to be inoculated with both the mating types. In order to investigate if the productivity is also correlated to a certain amount of *T. melanospoum* in the soil, in addition to the co-presence of mating type genes, we set up a protocol in a model truffle-ground presenting productive and unproductive trees. The quantity of *T. melanosporum* in soil samples was assessed by qPCR on ITS region and its mating types were searched. Results showed that mating type genes were detected in the stand under productive trees when more than 0.3 ng of *T. melanosporum* DNA was present. Up to now the establishment of a *T. melanosporum* plantation has been exclusively based on soil features. Nowadays the proposed analyses can help truffle operators in the management of their plantation by attesting the occurrence of *T. melanosporum*, after seedling inoculation and before the harvest of the fruiting bodies.