

INTERNATIONAL SYMPOSIUM

# MICROBE-ASSISTED CROP PRODUCTION – OPPORTUNITIES, CHALLENGES & NEEDS

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#### **OPPORTUNITIES, CHALLENGES & NEEDS**

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ORGANIZING COMMITTEE: Angela Sessitsch, Alexandra Khassidov, Birgit Mitter

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## PP-PU-17 Role of plant associated microbiota in fruit aroma and plant defense in strawberry and raspberry

Giampaolo Buriani<sup>1</sup>, Brian Farneti<sup>2</sup>, Antonio Cellini<sup>1</sup>, Irene Donati<sup>1</sup>, Lara Giongo<sup>2</sup>, Francesco Spinelli<sup>1</sup>

<sup>1</sup> Agricultural Sciences Dept., University of Bologna, Italy

The study of plant-associated microbiomes is a rapidly growing field of extraordinary interest. In the last few years, an increasing number of functions has been attributed to the microbiome associated to crop plants, including the promotion of host growth, the induction of resistance and the protection against abiotic and biotic stress. Some research has also focused on the contribution of the microbial community to fruit quality. Pioneer studies dealt with the influence of the association between *Methylobacterium* strains and strawberries to the composition of the aroma of fruit.

In this study, the fruit-associated microbiome of different strawberry and raspberry cultivars was characterized by a metagenomic approach, based on the sequencing of the 16S gene on Illumina platform. The profile of volatile organic compounds (VOCs) of the same fruits was previously characterized by PTR-Tof-MS and GC-MS to describe the main chemical components of the berry aroma and the data were correlated to the presence and abundance of microbial species capable of producing VOCs of interest. For the bacterial strains belonging to such species, the growth rates on the fruit and the production of VOCs were measured in order to quantify their contribution to the aroma composition of the fruit.

In addition, the metagenomic exploration highlighted the presence of bacterial species potentially acting as biological control agents (BCAs) or as plant-growth promoting bacteria (PGPB). Their populations were quantified by QPCR in various organs of the plant beside the fruit. Putative BCAs were tested against pathogens, on both plants and fruits in postharvest condition.

The ultimate/last aim of the present work was to identify useful bacteria in the resident microbiome of some valuable crop plants, in order to design a sustainable orchard management strategy, integrating crop associated functional microbes as one of the key components.

### PP-PU-18 Transcriptome analysis sheds light on the *Serendipita indica-*tomato interaction

Fani Ntana<sup>1</sup>, Birgit Jensen<sup>1</sup>, Hans Jørgen Lyngs Jørgensen<sup>1</sup>, David Brian Collinge<sup>1</sup>, Bjørn Hamberger<sup>2</sup>

<sup>1</sup> Plant and environmental sciences, University of Copenhagen, Denmark

Alternative practices are urgently needed to transform current agriculture to more sustainable and environmentally friendly systems. Endophytes, a diverse group of bacteria and fungi growing asymptomatically inside plant tissues, are often associated with enhanced plant growth and tolerance to abiotic and biotic stresses, indicating their potential for improving sustainability in agricultural systems. However, the exact mechanisms and effects of the complicated plant-endophyte interactions remain poorly understood and characterized.

Serendipita indica (syn. Piriformospora indica) is an endophytic fungus with several promising agricultural and biotechnological applications. The fungus can colonize the root cortex of a wide range of plants, enhancing plant growth and modulating plant specialized metabolism. Tomato (Solanum lycopersicum) is an important crop, often challenged by fungal pathogens and insect pests. The wide variety of specialised metabolites produced by the plant, and especially terpenes, plays a crucial role in plant defence, helping in repelling possible enemies.

This project involves establishing a balanced interaction between the fungal *S. indica* and tomato plants, providing a model system for studying general plant-endophyte interactions. However, our main focus is on the mechanisms used by the fungus to induce host specialized metabolism. Preliminary data suggesting that colonization by *S. indica* results in increased production of specific volatile terpenes in fungus-colonised tomato plants encouraged us to study the induction of these metabolites at transcription level. RNAseq analysis on fungus-associated and fungus-free plant tissues is currently ongoing to provide a more-in-depth view on the actual mechanisms underlying the *S. indica*-tomato interaction.

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<sup>&</sup>lt;sup>2</sup> Genetica e miglioramento genetico dei fruttiferi\_fondazione Edmund Mach, S. Michele all'Adige (TN), Italy

<sup>&</sup>lt;sup>2</sup> Department of Biochemistry and Molecular Biology, Michigan State University, Wilson Rd 603, 48824, East Lansing MI, United States of America