

Beneficial microbes application on tomato significantly improve accumulation of metabolites with nutraceutical value

Giuseppina Iacomino¹, Alessia Staropoli^{1,2}, Maria Isabella Prigigallo³, Giovanni Bubici³, Marina Scagliola⁴, Pasquale Salerno⁴, Sergio Bolletti Censi⁵, Giulio Murolo⁵, Francesco Vinale^{1,6}

¹ Institute for Sustainable Plant Protection, National Research Council, 80055 Portici, Italy

² Department of Agricultural Sciences, University of Naples Federico II, 80055 Portici, Italy

³ Institute for Sustainable Plant Protection, National Research Council, 70126 Bari, Italy

⁴ Spagro srl, 76121 Barletta, Italy

⁵ Cosvitech Società Consortile a Responsabilità Limitata, 80142 Naples, Italy

⁶ Department of Veterinary Medicine and Animal Productions, University of Naples Federico II, 80137 Naples, Italy

Tomato (*Solanum lycopersicum*) is an important crop and is consumed worldwide. This vegetable is an excellent source of natural compounds (i.e antioxidants including vitamins C and E, lycopene, β-carotene, lutein and flavonoids) and minerals useful for human health. Several studies have shown the correlation between tomato consumption and the prevention of some types of cancer and chronic cardiovascular diseases. In this study, the improvement of nutritional value of tomato, by using beneficial microorganisms, including selected strains of *Streptomyces*, *Bacillus* and *Trichoderma*, has been investigated. These microbes were applied on tomato plants in a field trial either as single inoculants or as microbial consortia. After the treatments, plants were subjected to a metabolomic analysis by LC-MS qTOF and led to the identification of sixteen metabolites, including tomatine and its derivatives, solafloridine, apo-13-zeaxanthinone, deoxy phytoprostane and L-phenylalanine. Results showed a significant difference in relative abundance of these metabolites among treatments. *Bacillus* application, alone or in combination with T22, induced the production of tomatine, while *Trichoderma* alone or in combination with *Streptomyces* or *Bacillus* and combination between *Streptomyces* and *Bacillus*, induced the production of solafloridine. The combination of *Streptomyces* and *Trichoderma* increased the accumulation of solafloridine, apo-13-zeaxanthinone, deoxy phytoprostane and L-phenylalanine, compared with the single treatments. In conclusion, field applications of *Streptomyces*, *Bacillus* and *Trichoderma* significantly induced metabolic profile change of tomato and the accumulation of metabolites with nutraceutical value.

Keywords: metabolomics; antioxidants; *Streptomyces*; *Bacillus*; *Trichoderma*