

complicates the phylogenetic support of the polyphyletic genus *Pantoea*. The future prospect is therefore an in-depth study of DNA gyrase sequences.

Transcriptome profiling of sanitized artichoke ecotypes and characterization of genes involved in the biosynthesis of secondary metabolites

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Globe artichoke (*Cynara cardunculus* L. var. *scolymus*) is gaining commercial interest for the high content of health-promoting bioactive compounds (BACs) such as inulin, polyphenols and antioxidant molecules. Availability of ecotypes sanitized by viral and fungal infections, characterized by vegetative vigor, productivity and quality has relaunched the crop in the market. We report the effect of sanitation protocol, based on *in vitro* culture and thermotherapy, on BACs accumulation by transcriptomic analysis of two late-flowering artichoke ecotypes Locale di Mola tardivo and Troianella. The analysis highlighted remarkable differences in genetic, environmental information processing and primary cell metabolisms between sanitized and wild-type plants with about 2% of differentially expressed genes (DEGs) mainly involved in biosynthesis of phenylpropanoid, carotenoid and other secondary metabolites. Comparison between the two sanitized ecotypes showed only 75 DEGs, with respect to a higher percentage of DEGs between wild-type ecotypes. This difference could be related to plant response and oxidative burst against pathogen infection in wild-type plants. BACs analysis by HPLC–DAD showed a significant decrease of polyphenols accumulation in sanitized-plants compared to wild-type, speculating a different modulation of the biosynthetic pathway by sanitation protocol. A different response of the two ecotypes was also observed by the analysis of peroxidase activity. A similar approach is being conducted on the early-flowering ecotype Brindisino. This study represents the unique investigation of transcriptome profile and BACs accumulation in artichoke ecotypes exposed to sanitation protocol and aims to promote the soilless cultivation of vigorous and pathogen-free artichokes, even for BACs extraction.

This work was supported by the project ERiCa–6E389E5E funded by Regione Puglia—POR Puglia 2014/2020—Asse X—Azione 10.4.-Research for Innovation – REFIN.

Metabolomics for the selection of beneficial microorganisms and/or their metabolites for a new generation of plant protection products

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Due to an increasing awareness about negative impacts to the environment, there has been a shift from conventional to sustainable agriculture, that has led to a change in regulations and the promotion in the use of microbial-based products as alternatives to synthetic chemical products. Metabolomics is a useful tool to guide the selection of beneficial microbes (single-strain inoculants, synthetic consortia, co-application of two or more microorganisms) and their secondary metabolites as active substances of new bio-formulates, and to evaluate treatment performance. With the aim to discover new formulations for agricultural uses, a metabolomic approach was used to investigate the compatibility of different beneficial microbial strains (i.e., *Trichoderma*, *Streptomyces*, *Azotobacter*) and test selected combinations in applications to different crops (parsley, basil, olive drupes). Moreover, the chelating properties of harzianic acid (a *Trichoderma* siderophore) were studied in order to enhance soil nutrient quality. Results showed that the tested combinations had significant beneficial effects on crops, in terms of pathogen control and improved nutritional value. Statistical analysis of plant extracts revealed a modulation of metabolic profiles depending on the treatment based on beneficial microbe application. It was possible to identify several metabolites (e.g., petroselinic acid, quinic acid, caffeic acid, rosmarinic acid, coumaric acid, oleuropein, luteolin and other phenolic compounds), whose relative abundance was increased in treated samples compared to the water control. Moreover, the analyses of the formulations consisting of harzianic acid and bivalent metal cations (biologically relevant or toxic), highlighted the formation of neutral or charged complexes depending on pH of the solution.

A novel methoxychromone derivative from *Trichoderma harzianum* M10

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