

## CHANGES IN RHIZOSPHERE BACTERIAL COMMUNITY AND PLANT MORPHO-PHYSIOLOGICAL TRAITS AS SIGNATURE OF TOMATO RESPONSE TO RECURRENT DROUGHT STRESS

DE PALMA M.\*, BUBICI G.\*\*, AURILIA V.\*\*\*, DOCIMO T.\*, GUARINO G.\*, RUOCCO M.\*\*\*\*, CELLINI F.\*\*\*\*\*, SUMMERER S.\*\*\*\*\*, PETROZZA A.\*\*\*\*\*

\*) Institute of Biosciences and Bioresources, National Research Council of Italy, Via Università 133, 80055 Portici, Italy

\*\*) Institute for Sustainable Plant Protection, National Research Council of Italy, via Amendola 165/A, 70126 Bari, Italy

\*\*\*) Institute for Agriculture and Forestry Systems in the Mediterranean, National Research Council of Italy, P.le Enrico Fermi 1, 80055 Portici, Italy

\*\*\*\*) Institute for Sustainable Plant Protection, IPSP, National Research Council of Italy, P.le Enrico Fermi 1, 80055 Portici, Italy

\*\*\*\*\*) ALSIA Centro Ricerche Metapontum Agrobios, S.S. Jonica 106, Km 448,2, 75010 Metaponto, Italy

*water scarcity, Solanum lycopersicum, beneficial fungi, microbiomes, high-throughput phenotyping*

Climate change exacerbates the frequency and severity of drought which influences several plant traits, limiting tomato yield. Accordingly, drought stress could impact on composition and activity of rhizosphere microbiomes, which include several microorganisms able to help plant in stress mitigation. Thus, studies on the effects of prolonged drought events on the rhizosphere bacterial community and morpho-physiological traits of plant either alone or supported by root-interacting beneficial fungi could provide new insight underlying stress response in tomato.

Here, we performed a recurrent drought stress trial on cv. “Crovarese” grown in pots with or without pre-treatment (seed coating) with *Trichoderma longibrachiatum* strain Mk1, applying 70% and 80% of water irrigation reduction in two consecutive stress cycles, respectively, each followed by a recovery stage. The complexity of tomato stress response,

also mediated by *Trichoderma*, was assessed through rhizosphere bacteria metagenomic analysis and high-throughput plant phenotyping approach. By sequencing of hypervariable V3-V4 region of 16S rRNA gene, we identified a significant presence of bacteria families in rhizosphere of untreated and Mkl-treated plants before drought stress imposition, compared to bulk soil. In addition, a significant difference in total reads percentage was detected between untreated and Mkl-treated plants. During severe drought stress condition (80% of water reduction), a strong increase of bacteria families (e.g., *Pseudomonadaceae*) having well-known beneficial characteristics for plants was measured in untreated and Mkl-treated plants compared to well-watered plants. Using a Scanalyzer 3D system (LemnaTec GmbH), along the experimental trial, we obtained a digital phenotype based on visible light (RGB) and near-infrared (NIR) images acquisition of untreated and Mkl-treated plants under well-watered and drought stress conditions. We identified several morphometric (e.g., projected shoot area, plant height, etc.) and color-based (e.g., senescence index, green area, etc.) parameters capable of highlighting the detrimental effects on plant growth caused by drought stress. Increased membrane damage, accumulation of proline and photosynthetic pigments in stressed tomato plants further corroborated previous data. Our results provide novel indications on the effects of severe drought stress on tomato and on rhizosphere bacterial community. Interestingly, a synergic effect of tomato-*Trichoderma* interaction was detected in the recruitment of bacteria families. In a future perspective, a detailed characterization of beneficial bacteria composition combined to distinctive phenotypic traits during the two cycles of drought stress and recovery would contribute to a major advance in the early prediction of a water scarcity condition and support sustainable management strategies to limit crop yield loss.