Functional insights into microbiome-driven *Fusarium* suppression in organic matter-enriched tomato rhizospheres

Authors: Cristina Sarmiento[1,2], Francisco M. Cazorla[1,2], José A. Gutierrez-Barranquero[1,2], Victor J. Carrion[1,2,3,4] and Xinya Pan[1,2]

Affiliations:

1. Departamento de Microbiología, Facultad de Ciencias, Campus Universitario de Teatinos s/n, Universidad de Málaga, 29010, Málaga, Spain
2. Departamento de Protección de Cultivos, Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", Campus Universitario de Teatinos, Universidad de Málaga-Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC), 29010, Málaga, Spain
3. Institute of Biology, Leiden University, Sylviusweg 72, 2333 BE, Leiden, The Netherlands
4. Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Droevendaalsesteeg 10, 6708 PB, Wageningen, The Netherlands

Abstract:
Disease-suppressive soils protect plants from root infections caused by soilborne fungal pathogens, primarily through the antagonistic activity of rhizospheric and endophytic microbial communities. However, due to the vast taxonomic and functional complexity of the root microbiome, identifying the key microbial taxa and mechanisms responsible for this phenotype remains challenging. A major contributor to disease suppression is the production of secondary metabolites by soil-associated bacteria, which mediate crucial inter- and intra-species interactions. These bioactive compounds are often synthesized by large enzymatic complexes such as non-ribosomal peptide synthetases (NRPS) and polyketide synthases (PKS), encoded by biosynthetic gene clusters (BGCs) that can exceed 50 kb in length. NRPS and PKS are involved in the synthesis of siderophores, toxins, pigments, and antimicrobial compounds essential for bacterial adaptation and plant protection. Despite their importance, knowledge on the diversity and dynamics of NRPS and PKS in the rhizosphere remains limited, particularly due to the unculturability of many soil microbes.

To address this gap, the microDISCOVER project employs an organic matter-enriched soil—specifically almond shells—as a model for disease suppressiveness in tomato (*Solanum lycopersicum*). Plants were grown in both suppressive and conducive soils under biotic stress induced by *Fusarium oxysporum* f. sp. *Lycopersici* (Fol). Comparative genomics revealed significant differences in the rhizosphere microbiome of both soils. This allowed for the identification of bacterial families potentially involved in antagonistic interactions with Fol. These findings provide valuable insights into the microbial basis of disease suppression in agricultural systems. Future work will focus on deciphering the specific metabolites and enzymatic pathways—particularly NRPS and PKS—underlying the protective interactions.

Keywords:
Suppressive soil, microbiome, fungal antagonism, *Fusarium oxysporum*, NRPS, PKS

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