



## MARIE SKŁODOWSKA-CURIE POSTDOCTORAL FELLOWSHIPS 2022

### EXPRESSION OF INTEREST FOR HOSTING MARIE CURIE FELLOWS

#### HOST INSTITUTION

ITQB NOVA, GREEN-IT Research Unit

#### RESEARCH GROUP AND URL

Plant-microbiome interactions Lab (iPlantMicro Lab)  
<https://www.itqb.unl.pt/labs/plant-microbiome-interactions>

#### SUPERVISOR (NAME AND E-MAIL)

Dr. Juan Ignacio Vílchez  
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#### SHORT CV OF THE SUPERVISOR

Over the last few years, I have developed my career in the field of beneficial plant-microorganism interactions. In this sense, I have been able to approach the area from many points, making very relevant contributions in each of them. Thus, within a leading research group at the University of Granada (Spain), we defined the first index to catalogue microorganisms with biotechnological interest based on their degree of environmental and human biosafety. Our publication in *Frontiers in Microbiology* (Q1), was pioneer in the field, providing insights on the regulation of production and use of biofertilizers. Also, within the same group, and using a multi-omics approach, I could define previously undescribed strategies of plant protection from drought through a beneficial microorganism, yielding 3 publications in *Frontiers of Microbiology* (Q1). In these publications we had the collaboration of groups in Ireland and Germany (IT Carlow and Universität Bielefeld). During the last years, working in the group of Plant Growth Promoting Bacteria at the Shanghai Center for Plant Stress Biology (China), I have been able to go further and define the first direct relationship between epigenetically regulated environmental stress, changes in composition of root exudates and selective attraction of a beneficial bacterial strain, published in *Nature Plants* (Q1). To do this, we followed a very novel approach in the field, using mutants in genes that regulate the methylation status. With this same technique, we could also define changes in natural microbiomes linked to multiple epigenetic regulators (Microbiome, Q1). In this same group and in the context of beneficial interactions, I have collaborated in trials involving the effects of volatile organic components (*EMBO Journal*, Q1), phenols in the rhizosphere and epigenetically regulated late defensive patterns (currently in a second round of review in *Nature Plants*). The experience in this group allowed me to generate a multilevel and interdisciplinary vision of this field of study. In these years, we have also defined the genomes of 7 strains with biotechnological interest and in beneficial interactions with plants. Based on these strains, we could promote 6 international patents (2 of them are pending final validation). Along my research experience, I have been able to present my work at international conferences in Italy, Ireland, China and Uzbekistan. In both Spain and China, I have taught in undergraduate and doctoral courses, and also supervised undergraduate, Master and Doctoral students. Since January 2021, I have obtained a position as Auxiliary Researcher through GREEN-IT research unit, to establish my own group (iPlantMicro) at the António Xavier Institute of Chemical and Biological Technology (ITQB NOVA) where I already started teaching master and doctoral students regarding the progress in microbiome biotechnology for plant improvement. In the coming years, I aim to consolidate a stable group of top-level researchers capable of facing the greatest challenges in microbiome bioengineering, beneficial interactions and technology transference. I also want to contribute for their development as scientists, aware of their responsibilities towards the planet and the society, caring for the environmental sustainability and a healthy economy.

#### 5 SELECTED PUBLICATIONS

- Morcillo, R.J.L., Vílchez, J.I., Zhang, S. Kaushal, R. He, D. Zi, H. Liu, R. Niehaus, K., Handa, A. K.; Zhang, H. (2021). Plant transcriptome reprogramming and bacterial extracellular metabolites underlying tomato drought resistance triggered by a beneficial soil bacteria. *Metabolites* 11(6): 369. <https://doi.org/10.3390/metabo11060369>
- Vílchez, J.I., Yang, Y., He, D., Zi, H., Peng, L., Lv, S., Kaushal, R., Wang, W., Huang, W., Liu, R., Lang, Z., Miki, D., Tang, K., Paré, P.W., Song, C.P., Zhu, J.K. and Zhang, H. (2020) DNA demethylases are required for *myo*-inositol-mediated mutualism between plants and beneficial rhizobacteria. *Nature Plants*, 6, 983–995. <https://doi.org/10.1038/s41477-020-0707-2>

- Vílchez, J.I., García-Fontana, C., Manzanera, M. (2020) Proteome comparison between natural desiccation-tolerant plants and drought-protected *Capsicum annuum* plants by *Microbacterium* sp. 3J1. *Frontiers in Microbiology*. 11, 1537. <https://doi.org/10.3389/fmicb.2020.01537>
- Vílchez, J.I., Niehaus, K., Dowling, D.N., González-López, J., Manzanera, M. (2018) Protection of pepper plants from drought by *Microbacterium* sp. 3J1 by modulation of the plant's glutamine and  $\alpha$ -ketoglutarate content: a comparative metabolomics approach. *Frontiers in Microbiology*. 9,284. <https://doi:10.3389/fmicb.2018.00284>
- Vílchez, J.I., García-Fontana, C., Román-Naranjo, D., González-López, J., Manzanera, M. (2016) Plant drought tolerance enhancement by trehalose production of desiccation tolerant microorganisms. *Frontiers in Microbiology*. 7,1577. <https://doi:10.3389/fmicb.2016.01577>

## PROJECT TITLE AND SHORT DESCRIPTION

### **Mi-Tom-Biome: Use of local microbiota to enhance tomato crops performance: anticipating stress condition by recruiting beneficial bacteria**

Tomato is a major crop in terms of production and industrial uses all along the world. However, its continuity can be jeopardized by soil nutrient deficiencies, spread of pests and pathogens and climate change effects. In this sense, the study of the associated microbiomes would provide solutions at various levels. Previous studies with other plant species have shown that the most vulnerable ecosystems are also those with the least microbial biodiversity. Despite this, it is not yet clear how beneficial interactions are induced by plants in order to face of environmental stresses. Here we propose to examine the hypothesis that certain plant responses are linked to profiles of exudate compounds, capable of influencing on the presence of more favorable microorganisms in their rhizosphere. Our strategy is based on using Portuguese plantations as a study model area, considering previous collaboration and research works. Then, our group proposes to use our experience with root exudate detection and profiling, studies of transcriptomics and beneficial interactions to identify patterns and use them as an effective treatment against tomato plants stresses. Initially, the analysis of the soil microbial populations by metagenomics of the region would help to establish the bases on predominant groups. Likewise, using seedlings from tomato crop varieties, we would evaluate how microbial populations vary under different induced stresses. Individual key compounds will also be tested on the microbiota to assess those results. Complementarily, the analysis changes in the genetic regulation of plants (key gene expression level and full transcriptome analysis) will allow us to correlate exudates composition and genetic response in plants. This will allow us to discern which pathways are behind the changes in root exudate profiles to control beneficial interactions by recruitment in root microbiota. Moreover, we will design compound mixes to anticipately control microbial communities, in order to help plant in facing environmental stresses. With these results, we will enhance beneficial microbiomes in tomato ecosystems through precisely engineered local products. Moreover, in future, this kind of research will ensure a sustainable use of this important natural resource in the medium-long term.

For our project, we have the advice as consultant from highly qualified researchers from international Centers, who agreed to participate in meetings and debates about strategy, presentation of results and discussion of putative issues arising. This will allow us to discern which pathways control beneficial interactions, such as microbial recruitment, as well as those that influence the communities. Mi-TOM-biome will use cutting-edge technology in synthetic exudomes and synthetic communities design. This knowledge will put at our disposal (and of the scientific community) the use of compounds, microbial communities and plant gene regulatory pathways as biotechnological tools. Dissemination of this project will be prepared by participation in international congresses and publications in high impact journals, as well as in commercial applications models and patents. In addition, this project aims to support the training of two MSc students and one PhD student as part of their research career. With the expected results, an important role will be played in enhancing beneficial microbiomes in tomato farmlands through precisely engineering local microbial communities. Moreover, this kind of research will contribute, in the medium-long term, for a sustainable use of this important crops and, will serve as pipeline support for other important crop plants. Finally, due to our institutional links to the "National Operative and Technological Center for Horticulture" (COTHN), we believe that this project will strengthen reciprocal links with local producers and farmers, ensuring a direct and precise transference of knowledge, practices and data.

## SCIENTIFIC AREA WHERE THE PROJECT FITS BEST\*

Life Sciences (LIF)