

# Unlocking the secrets of plant microbiomes

Carrión VJ<sup>1,2,3,4\*</sup>

<sup>1</sup>*Microbiology Department, Sciences Faculty, Malaga University, Málaga, Spain,* <sup>2</sup>*Departamento de Microbiología and crop protection, IHSM-UMA-CSIC, Málaga, Spain,* <sup>3</sup>*Institute of Biology, Leiden University, Leiden, The Netherlands,* <sup>4</sup>*Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands,*

[\\*vcarrion@uma.es](mailto:vcarrion@uma.es)

c

Plant roots are colonized by an astonishing number of microbes, not merely externally (rhizosphere) but also internally (endosphere). In the past years, extensive research has revealed the role of specific members of the plant microbiome to the improvement of plant tolerance to (a)biotic stress factors. However, the molecular mechanisms underlying these functions remain largely elusive. This in turn has raised new questions such as how endophytic bacteria colonize and protect plants against pathogens; and which genes are essential for being pathogenic or beneficial for the plant? In other words, are there genetic markers associated with specific microbial lifestyles?

Here, our newest results are presented to shed light on these outstanding questions. We used in-depth metagenomic sequencing of the endosphere to discover that chitinase and novel NRPS and PKS genes were only activated in endophytic microbes upon pathogen infection. We also developed a new computational tool (MicroLife) to explore large-scale genomic datasets and to identify genes as well as biosynthetic gene clusters (BGCs) associated with specific microbial lifestyles. Using MicroLife, we were able to dig into the microbial dark matter to discover novel genes and BGCs involved in pathogenesis and endophytic lifestyles. Collectively, our results provide new exciting insights into the largely unexplored functional potential of the plant microbiome and the chemical secrets of the endosphere.