

Title: The Hidden World Within Plants: Ecological and Evolutionary Considerations for Defining Functioning of Microbial Endophytes

Authors: Pablo R. Hardoim¹, Leonard S. van Overbeek², Gabriele Berg³, Anna Maria Pirttilä⁴, Stéphane Compant⁵, Andrea Campisano⁶, Matthias Döring⁷, Angela Sessitsch⁵

Institutes: ¹ Univ Fed Rio de Janeiro, Inst Bioquim Med Leopoldo de Meis, Lab Biol Mol Plantas, Rio De Janeiro, RJ, Brazil; ² Plant Research International, Wageningen, The Netherlands; ³ Institute for Environmental Biotechnology, Graz University of Technology, Graz, Austria; ⁴ Department of Biology, University of Oulu, Oulu, Finland; ⁵ Department of Health and Environment, Bioresources Unit, AIT Austrian Institute of Technology GmbH, Tulln, Austria; ⁶ Sustainable Agro-Ecosystems and Bioresources Department, Research and Innovation Centre, Fondazione Edmund Mach, S. Michele all'Adige (TN), Italy; ⁷ Institut für Pflanzenkultur, Schnega, Germany

Summary:

All plants are internally inhabited by diverse microbial communities comprising bacterial, archaeal, fungal, and protistic taxa. These microorganisms showing endophytic lifestyles play a crucial role in plant development, growth, fitness and diversification. We revisit the literature to access the historical evidences reporting endophytes and demonstrate that it is not trivial to clearly distinguish a non-pathogenic endophyte from a pathogen and properties such as pathogenicity or mutualism may depend on many factors. We question the currently applied definition of endophytes and claim that the term “endophyte” should refer to only habitat and not function. The increasing awareness and information on endophytes provides insight into the complexity of the plant microbiome. We use all currently available 16S rRNA gene and full-length ITS region sequences assigned as endophytes to reproduce the endosphere microbiome diversity. Prokaryotic endophytes are diverse, however largely represented by *Proteobacteria* (54%), *Actinobacteria* (20%), *Firmicutes* (16%) and *Bacteroidetes* (6%) encompassing many genera and species. Eukaryotic endophytes mainly belong to *Glomeromycota* (40%), *Ascomycota* (31%), and *Basidiomycota* (20%). Similar to bacterial endophytes, various taxa comprise known phytopathogens and strains without known pathogenic effects. We also elaborate the expected impact of novel technologies on endophyte research. Comparative genomics of bacterial endophytes and others functional groups, such as nodule-forming symbionts, phytopathogens, rhizobacteria and soil bacteria, reveals properties largely discriminative for endophytes (e.g. higher responsiveness to environmental cues, nitrogen fixation, and protection against reactive oxygen and nitrogen species). Endophytes might also exhibit phytopathogenic capabilities and rhizosphere bacteria might also be able to colonize plants internally, suggesting that borders between functional groups are not clear-cut. We intend to address the concept of endophytism considering the latest insights into evolution, plant ecosystem functioning and multipartite interactions. By implementing new technologies and multi-disciplinary approaches, our understanding on endophyte biology and ecology will consistently evolve further, leading to a better knowledge of the plant holobiome.

Key words: Microbiome, Comparative genomics, Phylogenetic analysis, Endosphere, Phytopathogens

Foment agency: EU Cost Action ‘Endophytes in Biotechnology and Agriculture’ (FA1103), the European Community's Seventh Framework Programme (FP7/312117), the Austrian FWF (Science Foundation) and the Portuguese FCT (Foundation for Science and Technology).