DNA BARCODING ANALYSIS OF MICROBIAL COMMUNITY in Olive Orchards : *Olea europaea* L. Bacterial and fungal diversity in Tunisia

Houda Gharsallah¹, Olfa Frikha-Gargouri², Ines Ksentini¹, Karama Hadj Taieb¹, Amel Chatti¹, Christina Schuster^{3,4}, Haifa Ben Gharsa^{3,4}, Mohamed Ali Triki¹, Mohieddine Ksantini¹ & Andreas Leclerque^{3,4}

¹Laboratory of Improvement and Protection of Olive Tree Genetic Resources, Olive Tree Institute, Sfax, Tunisia
²Laboratory of Biopesticides, Centre of Biotechnology of Sfax, University of Sfax, Sfax, Tunisia
³Institute for Microbiology and Biochemistry, Geisenheim University, Germany
⁴Department of Biology, Technische Universität Darmstadt, Germany

hohuda_gharsallah@yahoo.fr

ABSTRACT

Olive production is the main agricultural activity in Tunisia. In this study, we investigated the microbial diversity isolated from soil and one of the major olive tree pests, namely the Olive psyllid, Euphyllura olivina Costa (Homoptera: Psyllidae). We aimed to explore the scarcely known microbiota in Tunisian olive orchards is the first step for elucidating the microbial interactions that meddle the biological control. A total of 215 bacterial and fungal strains were randomly isolated from eight different biotopes situated in Sfax (Tunisia) with different management practices. 16S rRNA and ITS gene sequencing were used to identify the microbial community increasing the board view. The different olive cultivars depicted distinct communities and exhibited dissimilar amounts of bacteria and fungi with distinct ecological functions that coud be considered promising resources in biological control.

Keywords: Biological control, Microbial diversity, Bacteria, Fungi, Olea europaea