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UTILIZATION OF CULTURE-DEPENDENT AND SEQUENING APPROACH FOR STUDYING THE APULIAN OLIVE SAPWOOD ENDOPHYTIC DIVERSITY AND RICHNESS UNDER BIOTIC AND ABIOTIC VARIATION FACTORS

HANANI A.*,**, VALENTINI F.*, CAVALLO G.*, DAVINO S.**, D'ONGIA A.M.*

*) Istituto Agronomico Mediterraneo, (CIHEAM - IAMB), Via Ceglie 9, 70010 Valenzano (Italy)
**) Department of Agricultural, Food and Forest Science, University of Palermo, Palermo (Italy)

Endophytic diversity research has been notably developed through advances in molecular genomics-based techniques, which infer the genetic structure of cultures and the taxonomic composition of endophytic communities. In this sense, culture-dependent methodology and sequencing of 16S rRNA and ITS provide reliable morphological and molecular taxonomic information of endophytes, which has boosted the utilization of beneficial microorganisms for plant disease management and health promotion and the presentation of cultivable microbiome stability and its factorial variation. Our work pursues a study of diversity and occurrence variation of cultivable endophytes in the sapwood of different olive varieties under the effect seasonality, geographical coordinates, and *Xylella fastidiosa* infection status. Briefly, our study confirms the stability of sapwood cultivable endophytic communities in the resistant olive variety, presents the seasonal and geographical fluctuation of olive's sapwood endophytes, describes the diversity and occurrence frequency of fungal and bacterial genera, and finally retrieves some of sapwood-inhabiting fungal and bacterial isolates are known as biocontrol agents of plant pathogens. Thus, the potential role of these bacterial and fungal isolates in conferring olive tree protection against *Xylella fastidiosa* should be further investigated.

Keywords: Olive Sapwood, Endophyte, sequencing, diversity, biocontrol