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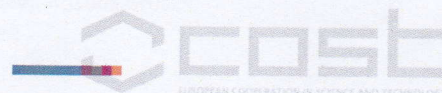
BOOK OF ABSTRACTS



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Effect of host plant and olive leaf spot disease on fungal community assembly in olive tree phyllosphere

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Olive leaf spot (OLS), a disease that usually occurs on the upper surface of the olive leaf, is caused by the fungus *Fusicladium oleagineum* with ability to grow epiphytically and to enter inner leaf tissues. In this work was studied the effect that host plant, at different levels (i.e. at cultivar level, in resistance to the fungal pathogen, and *F. oleagineum* infection), have on the phyllosphere fungal community composition of olive tree. For this, both epiphytic and endophytic fungal community inhabiting OLS-symptomatic and asymptomatic leaves of three co-occurring cultivars with different susceptibilities to OLS were compared, after isolation and identification of species by ITS rDNA sequencing.

The results indicate that the presence of OLS on leaves had a major effect on the fungal community composition than the host plant, either at cultivar level or of their resistance to the fungal pathogen. Both diversity and abundance of epiphytes in asymptomatic leaves were significantly higher (up to 2.0-fold) than in symptomatic leaves. Although less pronounced, this trend was also evident in endophytes of two of the cultivars surveyed. Among the species identified in asymptomatic leaf, *Cladosporium cladosporioides* and *Chromelosporium carneum* were the most frequently isolated within epiphytic and endophytic fungal communities, respectively; whereas in symptomatic leaf, *Cladosporium* sp. and *Pseudocercospora cladosporioides*, were the most frequently isolated within epiphytic and endophytic fungal communities, respectively. Determination of indicator value indices has shown significant preference/specificity of four species with asymptomatic leaves, and of two species with symptomatic leaves. Based on this analysis both *Alternaria* sp. and *Tricharina striispora* seems to be the species with the most potential for OLS disease suppression. Future research needs to decipher these complex and dynamic interaction networks and assess their role in plant health.

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