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SAAF DIPARTIMENTO SCIENZE AGRARIE ALIMENTARI FORESTALI

ABSTRACT FORM

The abstracts must have the following format (see example below):

Margins: 2.5 cm
Language: English
Title: Times New Roman, 12 pt, bold
Authors: Capitalized name initials. Times New Roman 11 pt, bold
Affiliation(s): Times New Roman 10 pt, italics, including the e-mail address of the corresponding author
Text: Times New Roman 11 pt, one paragraph, max 250 words, italicized scientific names, justified
Literature cited: not admitted
Funding information (optional): Times New Roman 10 pt, italics

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Example of abstract

Survey on the persistence of *Plenodomus tracheiphilus* inoculum in of lemon groves during summer

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Plenodomus tracheiphilus is the causal agent of the most destructive lemon disease. The importance and frequency of root infections have been investigated since long time, mostly in growth chamber. By DNA hybridization and later by real-time PCR the fungal inoculum was detected in the soil. The highest fungal DNA concentrations have been detected in March-April, whilst the DNA was nearly undetectable in July and August and increased again in the period September-November. To investigate the actual persistence of the inoculum in the soil during summer a survey was carried out in southern Syracuse, Italy, the most important lemon area of Italy. Soil samples were collected on June-July 2019, in 10 orchards, under the canopy of 53 lemon trees or in the area where the dead trees were grubbed. Lemon trees of different cultivar/rootstock combinations and age were sampled. In each site four subsamples were collected, 232 in total, at 10-20 cm depth where the soil temperature was between 26-32 °C, assembled per tree or site and stored in a refrigerator (4 °C) until analyzed. Total soil genomic DNA was extracted, using the kit DNeasy PowerSoil (QIAGEN). Detection of *P. trachiphilus* by real-time PCR was positive in approximately the 77% of the tests. Variable fungal DNA concentrations were quantified as DNA per gram of soil. Soil aliquots were plated on a semi selective medium to confirm the number of viable propagules. Metabarcoding of fungal communities recognized the presence of the *P. tracheiphilus* in pilot samples.

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