FORMATO ABSTRACT

Gli abstract devono avere il seguente formato (vedi esempio qui sotto):

Margini: 2.5 cm
Lingua: Inglese
Titolo: Times New Roman, 12 pt, grassetto
Autori Iniziali Nome. Cognome, Times New Roman 11 pt, grassetto
Affiliazione(i): Times New Roman 10 pt, corsivo, incluso l'indirizzo e-mail dell'autore corrispondente
Testo: Times New Roman 11 pt, un paragrafo, 250 parole max, nomi scientifici in corsivo, giustificato
Letteratura citata: non ammessa
Informazioni sui finanziamenti (facoltativo): Times New Roman 10 pt, corsivo

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Esempio di 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.

This work was supported by the project S.I.R.P.A. funded by PO FESR 2014-2020 Sicilia action 1.1.5