



Conference Abstract

Biodiversity of soil fungal communities in agro-ecosystems using DNA metabarcoding

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Abstract

Soil fungi are key component of soil biota having an important role in many ecological processes. As pathogens, decomposers and plant mutualists they can affect plant and soil health in agro-ecosystems significantly. The impact of crop management practices on soil fungal communities is diverse and still poorly studied. The lack of knowledge is mainly related to their hidden life mode, high phenotypic diversity, the great heterogeneity of soil microhabitats, difficulty for culturing and species identification. Collecting data with high accuracy to detect effects relevant to ecosystem management is an ongoing challenge for soil ecological studies and biomonitoring. However, the combination of DNA-based identification methods and Next Generation Sequencing technology was recognized as a powerful tool to evaluate biodiversity in environmental samples, especially soil biodiversity. In the frame of the National Research Program "Healthy Foods for a Strong Bio-Economy and Quality of Life", soil microbiome diversity (fungi, prokaryotes and archaea) will be used as indicator for assessing soil and plant health, and ecosystem services in several agricultural ecosystems. Four crop types (apple, lavender, rose and pea) located in

southern Bulgaria, and managed by conventional and organic farming have been selected. Two general objectives related to soil biodiversity study were envisaged:

1. to examine the impact of cropping systems on microbiome structural and functional diversity, and
2. to propose management measures and agronomic practices improving soil and plant health.

Here we present some preliminary results on soil fungal communities evaluated by using amplicon DNA sequencing of the internal transcribed spacer 2 (ITS2) rDNA region. Multiple core soil samples were collected from 18 sampling plots in June 2019. Fungal diversity and community structure were evaluated at different taxonomic levels. The most common and abundant taxa at all sites were *Fusarium* Link 1809, *Solicoccozyma* X.Z.Liu, F.Y.Bai, M.Groenew. & Boekhout 2015, *Cladosporium* Link 1816, *Alternaria* Nees ex Wallroth 1816, and *Mortierella* E.Coemans 1863. The multivariate statistics (PCA) comparing the overall microbial composition revealed loose clusters linked to crops and localities. The study provides a new comprehensive overview of soil fungal communities (composition and diversity) from Bulgarian agro-ecosystems using high-throughput DNA sequencing.

Keywords

conventional agriculture, organic agriculture, *Lavandula officinalis*, *Malus domestica*, *Pisum sativum*, *Rosa damascena*

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