

Soil health management and assessment for agricultural fields

Carolina Córdova¹

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¹ Universidad Estatal de Nebraska-Lincoln,
Departamento de Agronomía y Horticultura.
Nebraska, Lincoln, Estados Unidos de América

* Correspondence: ccordova4@unl.edu

Abstract

Intensive agriculture has led to soil degradation as evidenced by low fertility and productivity. In an attempt to reverse this process, alternative cultivation practices are being sought, aiming to restore soils and recover the microbial populations inhabiting them. In this context, the objective of this research was to evaluate, over the long term, the effect of two tillage systems (conventional and no-till) and the rotation of three plant species (beans, barley and corn) on the physical, chemical and biological properties of the soil (here in focusing on the abundance and diversity of fungi and bacteria in the fourth crop cycle). The study was conducted at the Experimental Station «La Tola» of the Faculty of Agricultural Sciences at the Central University of Ecuador, located in Tumbaco. A split-plot design with three replications was applied; rotations were placed in the large plot and tillage systems in the small plot. At harvest, soil samples were taken from each experimental unit, which were then pooled to obtain a single sample per treatment. DNA was extracted using the Purelink microbiome DNA purification kit from Invitrogen, following the manufacturer's instructions. The rest of the DNA analysis was performed by AZENTA of the United States. Amplification of the V3 and V4 regions of the 16S gene from bacteria and the ITS of the 18S gene from fungi was performed with AZENTA's own primers. The Illumina 2xP250bp platform was used for parallel sequencing of the amplicons, which was performed after construction and quality control of the libraries. For the bioinformatics analysis, Qiime software was used to clean the sequences, assign OTUS with 97% identity and determine the taxonomy using the Bayesian RDP algorithm and the Greengenes and UNITE databases for bacteria and fungi, respectively. The results, in the fourth cycle, showed differences in the abundance of bacteria and fungi among tillage systems and among rotations, at various taxonomic levels. At the genus level, in no-till [NT] compared to conventional tillage [CT] and in rotation 1 [R1] (beans-corn-beans-corn) compared to the other rotations, the bacterial genera with the highest presence were: *Rhodoplanes* (phototrophic), *Nitrospira* (nitrifying), *Bradyrhizobium* (N fixer), and *Pedomicrobium* (bioremediation). Fungal genera predominantly included organic matter decomposers (*Penicillium*, *Clonostachys*, *Chrysosporium*, and *Mucor*), and an entomopathogen (*Metarhizium*). The Chao1 (6784 species), Shannon (10,77), and Simp-

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son (0,99) indices indicated, respectively, high species richness, high diversity, and high dominance in all treatments. It is concluded that NT and R1 appear favorable for the accumulation of bacterial and fungal genera with beneficial functions for crops. Confirmation of this will depend on further research over a longer period of time.

Keywords: 16S, ITS, Crop rotation, Parallel sequencing, No-till