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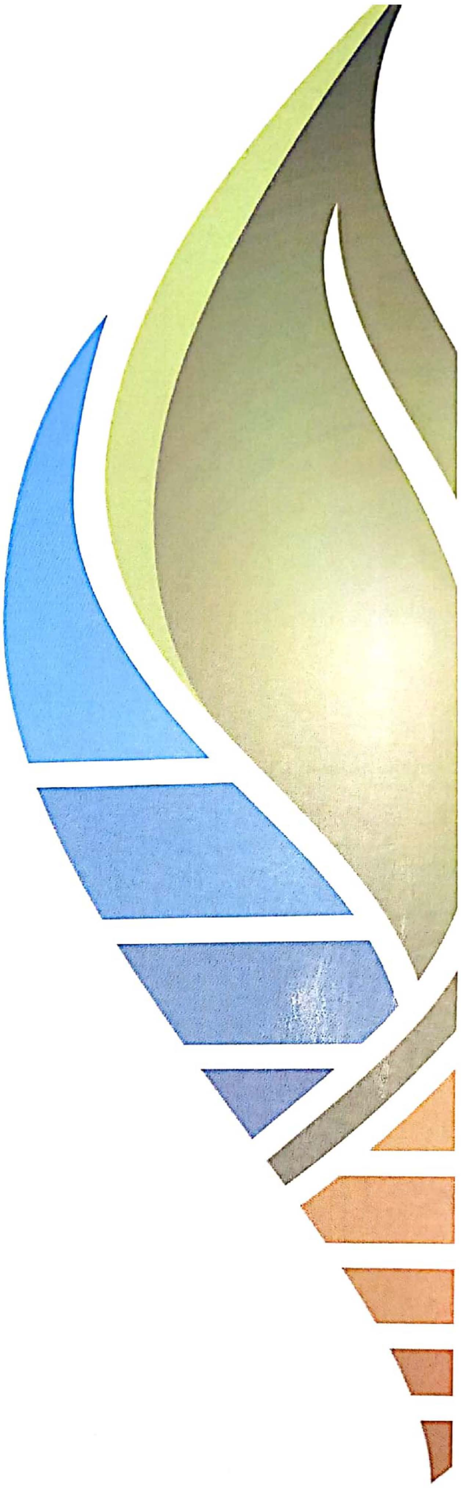
- Abstracts -



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Effects of conventional agricultural practices on soil fungal and bacterial communities

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Agricultural intensification has been facilitated by application of agrochemicals and soil tillage, causing environmental and soil health problems such as loss of soil fertility and biodiversity. Since soil microorganisms are the key players of many ecosystem processes, the objective of this study was to compare the fungal and bacterial communities in soils under different long-term agricultural management. To achieve this goal, bulk soils from two different tillage systems (Cultivator Tillage [CT] vs Mouldboard Plough [MP]) with two fertilization levels (Standard N fertilization [INT] vs 50% less N fertilization [EXT]) were compared after harvest of winter wheat. The soils originated from a long-term field experiment established in 1992 with maize/wheat/barley/rapeseed/wheat rotation in Bernburg (Germany). Analysis of microbial community composition based on 16S rRNA genes or internal transcribed spacer (ITS) fragments, for bacteria or fungi, resp., amplified from total community-DNA, were analyzed by Denaturing gradient gel electrophoresis (DGGE). The fingerprints showed that soil microbial communities were affected by tillage system and fertilization level. To analyze in more detail the effect of agricultural management on the community structure of both microbial groups, Illumina Miseq amplicon Sequencing was performed. Similar to DGGE, the PERMANOVA analysis showed a significant effect of the tillage, the fertilization and the interaction between these factors for both fungi and bacteria, but effects were stronger for bacteria and no clear differences between treatments were observed for fungi. Alpha-diversity indices (richness, Shannon and Chao-1´s diversity, Pielou´s evenness) indicated that bacterial communities in CT soils were less diverse, but more evenly distributed compared to MP. In the case of fungi, no significant differences in terms of alpha-diversity were observed between treatments, but CT-EXT tended to have higher diversity and less dominant species. This suggests that soil bacterial communities seem to be more sensitive to agricultural management than fungi. Regarding taxonomy, 36 phyla were found for bacteria, with Proteobacteria, Actinobacteria and Acidobacteria being most abundant. Fungal ITS sequences were affiliated to seven different phyla, being Ascomycota and Basidiomycota the predominant ones. Finally, management-depending responders analysis is still in process for a better understanding about the complex interactions in this agroecosystem. Future work will aim to deepen the identification of microbial taxa that may serve as possible biological indicators for a sustainable crop production management.