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INFLUENCE OF EXOGENOUS ORGANIC MATTER ON PROKARYOTIC AND EUKARYOTIC MICROBIOTA IN AN AGRICULTURAL SOIL

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The soil is a complex, dynamic and heterogeneous habitat harbouring metabolically active prokaryotic and eukaryotic communities. In order to improve soil fertility, i.e. ameliorate soil structure, enhance soil organic matter (SOM) content and N and P availability, as well as to increase soil whole biological activity, organic amendments are commonly used. Moreover, the application of organic amendments to soils (pig slurry, sewage sludge and compost) can play an important role in soil fertility by enhancing C stock and by affecting the microbial structure and activity.

A multidisciplinary study was carried out to test the effect of the amendment by anaerobically digested pig slurry on bacterial, yeasts and fungal populations. The application of fresh digestate, affected the short-term dynamics of microbial community, as reflected by the high amount of CO2 released immediately after the amendment.

Moreover, a next-generation sequencing approach was employed to investigate the effect of the digestate on the dynamics of prokaryotic and eukaryotic microbiota (bacteria, yeasts and filamentous fungi). A total of 56,650 16S bacterial and 5550 ITS fungal raw pyrotag reads were obtained from 8 DNA soil samples (4 control and 4 DG-amended soil samples taken at 4 time points: from 0.5 to 90 days after amendments). Bacterial OTUs were affiliated to 25 phyla including Proteobacteria (30.5%), Acidobacteria (24.6%), Actinobacteria (16.5%) and Bacteroidetes (14.9%) while the overall yeast + fungal community was dominated by Ascomycota (48.8) and Basidiomycota (16.5%).

Generalized Linear Models (GLMs) were used to compare DG-amended soil and CT in terms of bacterial community dynamics based on the proportion of sequences found for each phylum out of the total number of sequences. Interestingly, data reveal statistically significant differences for bacterial communities within the first five days after amendment, while at 12 and 90 days after amendment no significant differences were detected.

Moreover, the observed richness in DG-amended soil vs CT was 228:199 for bacteria and 111:112 for yeasts + fungi, respectively.

Finally, we found some bacterial contaminants (Enterococcaceae) in DG-amended soils until 12 days after amendments. This fact could represent a relevant issue with regards to the food safety. Indeed, if these bacteria persist for several days in the soil amended with pig slurry (or other animal–derived waste material), they could contaminate the crops through the soil particles adhering to the edible tissues (roots, leaves, whole plant). These and other results will be presented and discussed.