Spatio-temporal variations in 16S rDNA bacterial profilings and sanitary state of permanent grassland soil: Assessment of sustainable utilization of digestate

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Résumé

Soil microbial diversity contributes greatly to multiple ecosystem functions that are key for the sustainability of agroecosystems. However, soil microbial communities are currently threatened by land-use intensification, and understanding of how microbial soil in permanent grassland faces stressors including seasonal variations and repeated use of a biofertilizer is still unresolved. The main objective of this study was thus to determine the short (24 hours and 3 weeks after seasonal amendment) and the long-term (2017-2021) impacts of agricultural digestate on the permanent grassland soil microbial diversity and abundance. Bacterial community structures were investigated using 16S rDNA V4 ASV analyses. Soil sanitary state was investigated based on the occurrence of 38 sanitary indicators including pathogenic bacteria, virulence factors, mobile genetic elements, and antibiotic resistance genes as well as 7 heavy metals and 19 polycyclic aromatic hydrocarbons. The effects of two doses of digestate named D230 and D350 (equivalent 230 and 350 kg nitrogen/hectare/year) in comparison to fertilizer free control and slurry amended soil (S230) have been analyzed in real pedological condition. We focused on the topsoil, targeted two layers 0-15 cm and 15-30 cm during two sampling seasons (autumn 2021 and spring 2022). NMDS ordination based on Bray-Curtis dissimilarity computed from the 16S rDNA V4 ASV profiles of the soil samples indicated that bacteria communities were clustered according to the season and depth but also related to the amendment type. Following 4 years of treatment, bacteria communities of digestate-amended soils were different from those of control and S230 amended soils at both depths. The observed richness of bacterial communities at 0-15 cm decreased in D350 and D230 amended soils compared to control and S230 amended soils. Interestingly, significant relationships

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*Intervenant

between 16S rDNA V4 ASV ordination patterns and concentrations in arsenic, nickel, zinc, and benzo(k)fluoranthene were highlighted. Bacterial DNA sequences at genus level found in high abundance in the digestate were found at high abundance in the soil (0-15 cm) after 24 h and 3 weeks of treatment but failed to establish for a long time. Whereas, in S230 and control soils several shared genera decreased at 0-15 cm after 24 h and 3 weeks of treatment. However, these evolutions observed at 0-15 cm and during autumnal amendment were less significant at 15-30 cm or during spring amendment. Concerning the health indicators, the difference depended on whether the biofertilizer was used or not rather than its type. Finally, the destabilization of microbial communities by digestate application could lead to a lower resistance to environment disturbances and influence soil multifunctionality.

Mots-Clés: Spatio, temporal variations, Bacterial community, Grassland soil, Sanitary state, Digestate