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BOOK OF ABSTRACTS

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P-232 - ASSESSMENT OF THE IMPACT SYNTHETIC FE(III)-CHELATES AMENDMENT ON SOIL MICROBIAL COMMUNITY DYNAMICS

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Background

Iron has a crucial role in plant nutrition, being an essential element for plant growth. However, one-third of the Earth soil is iron deficient, resulting in iron deficiency chlorosis (IDC) growth of several crops worldwide, including staple foods. The use of synthetic Fe(III)-chelates is one of the most effective measures to correct IDC in plants, but their environmental impact must be mastered. Therefore, the search for more effective Fe-chelates remains an important issue. Previously [1], a 3,4-HPO Fe-chelate was proposed as a novel-fertilizing agent. Since the increase of nutrients availability in soil is thought to have an impact on the microbial composition, this question needs to be addressed. Therefore, the aim of the study was to investigate the effect of iron complexes of the 3,4-HPO class of ligands on soil bacterial dynamics to better understand their pathways.

Method

Laboratory scale soil columns (LSSC) were set up, with different soils origin and characteristics (Agricultural, Forestry and Urban), and exposed to two iron-chelates using rain simulations. The structure and abundance of the bacterial community was evaluated by automated ribosomal intergenic spacer analysis (ARISA) and qPCR (*rpoB*) approaches.

Results & Conclusions

Cluster analysis of ARISA profiles revealed that the soil characteristics were the major driving selection for the microbial community composition, with the samples from the same soil type clustering together, disregarding the amendment performed. Also, it emerged that the microbial community of forestry and agricultural soils were more similar (46%) than the one present in urban soil, as expected due to the plant influence. Considering each soil type individually, it was possible to observe a clear response to Fe(III) amendment on the microbial assemblage. Additionally, it seems that one of the compounds, the Fe-chelate derived from the ligand Deferiprone, induced greater and/or faster changes, and that the forestry soil was more prone to the microbial shift. These changes can underline a selection for bacteria that can use Fe(III) in its metabolism, or more tolerant to its presence, that needs to be better understood.

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[1] Santos CS et al. (2016) Plant Physiology et Biochemistry 106, 91-100. https://doi.org/10.1016/j.plaphy.2016.04.050

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