FEMS7-2232
Environmental Microbiology/Microbial Ecology /Microbial Communities - Part II

IMPACT OF IRON AMENDMENT ON SOIL BACTERIAL ABUNDANCE AND DIVERSITY

A. Machado[1,2], R.B.R. Mesquita[1,3], J.F.C. Vieira[3], M. Rangel[4], A.O.S.S. Rangel[3], A.A. Bordalo[1,2]
[1]ICBAS-UP - Institute of Biomedical Sciences Abel Salazar- University of Porto, Hidrobiology and Ecology Laboratory, Porto, Portugal
[2]CIIMAR/CIMAR - Centro Interdisciplinar de Investigação Marinha e Ambiental, Hidrobiology and Ecology Laboratory, Porto, Portugal
[3]Universidade Católica Portuguesa- CBQF - Centro de Biotecnologia e Química Fina – Laboratório Associado- Escola Superior de Biotecnologia, ., Porto, Portugal
[4]REQUIMTE-UCIBIO- Instituto de Ciências Biomédicas de Abel Salazar- Universidade do Porto, ., Porto, Portugal

Backgrounds

According to the World Health Organization, two billion people suffer iron deficiency, and the consumption of iron-rich plants can be a way of tackle the problem. Iron has also a crucial role in plant nutrition being an essential element for plant growth, yet one-third of earth soil is iron deficient. The use of synthetic Fe(III)-chelates remains one of the most effective measures to solve this iron deficiency in plants, but their environmental impact must be mastered, since they are highly stable in soils. The search for efficient and sustainable Fe-chelates is, therefore, pressing.

Objectives

The aim of the study was to investigated the effect of iron complexes (synthetic Fe(III)-chelates), on soil bacterial dynamics to better understand their mode of action.

Methods

Soil pots with and without strawberry plants (*Fragaria* sp.), were exposed to different ferrous iron treatments (Fe(III) solution as weak complexes with hydroxide ions, FeEDDHA iron-chelate present in commercially fertilizers, and $Fe(dmpp)_3$ as new alternative iron-chelate). The abundance and diversity of the bacterial community was evaluated by PCR-DGGE and qPCR (*rpoB)* approaches.

Conclusions

No major differences were found in the abundance between soil treatments. Cluster analysis of DGGE profiles revealed that the presence of the plant by itself was not enough to cause a significant change in the bacterial composition. However, the microbial composition seems to shift as a response to Fe(III) amendment and bioavailability. These changes can underline a selection for bacteria that can use Fe(III) in its metabolism, or are more tolerant to its presence, that need to be understood