

# Soil microbiota benefits from phytoremediation coupled to metal-resistant rhizobacteria



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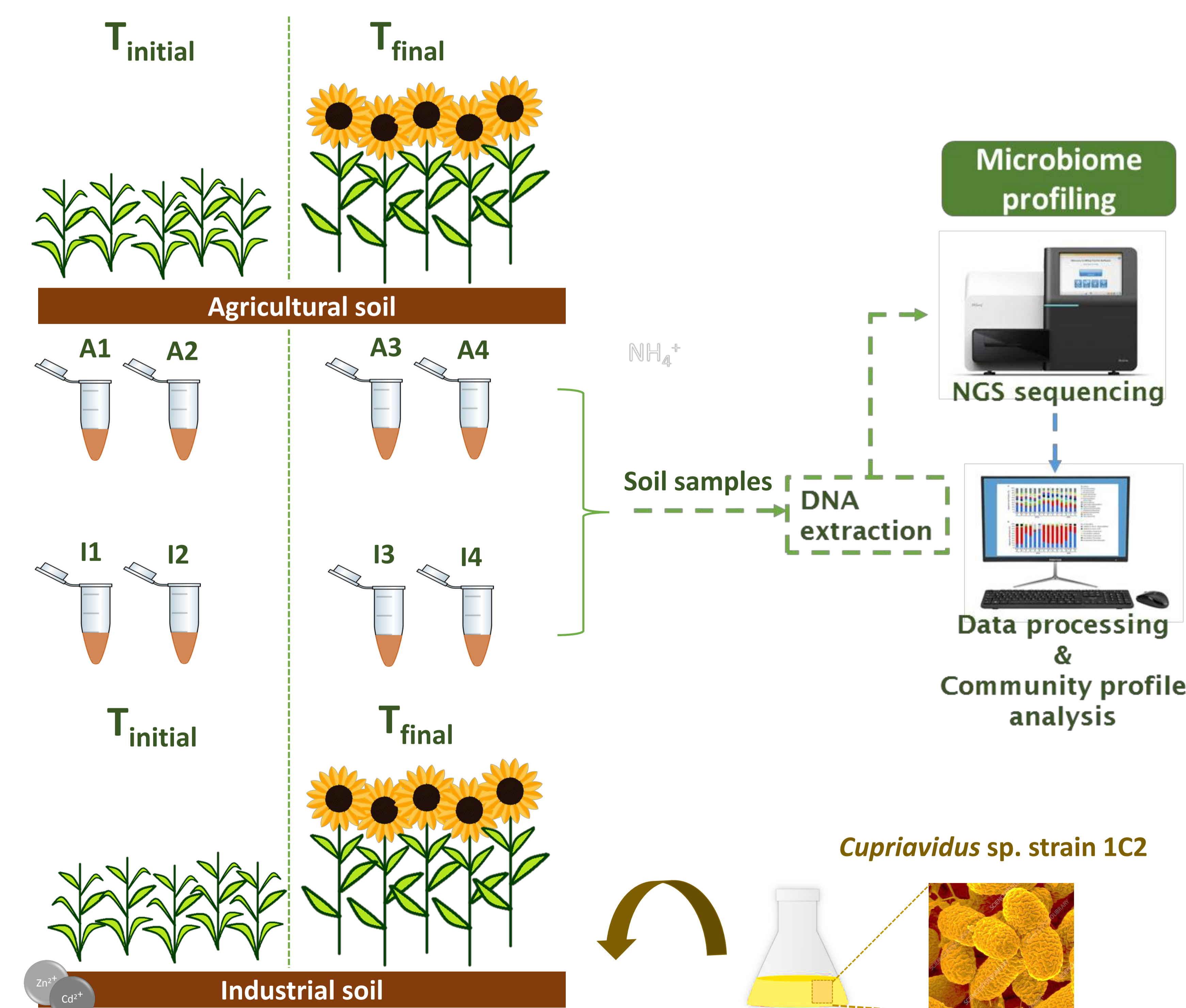
Ana M. S. Paulo<sup>1</sup>, Paula M. L. Castro<sup>1</sup> and Ana P.G.C. Marques<sup>1</sup>

<sup>1</sup>Universidade Católica Portuguesa, CBQF - Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Rua de Diogo Botelho, 1327, 4169-005 Porto, Portugal

## Introduction

**Phytoremediation** is used for requalifying soils contaminated with **heavy metals (HM)**. Sunflower (*Helianthus annuus L.*) is one of the most studied species for the remediation of HM-contaminated soils. To increase the bioavailability of nutrients and of metals in soils, **metal-resistant plant growth promoting rhizobacteria (PGPR)** can be associated to phytoremediation strategies. **Soil microbiota** can benefit from this association due to the reduced exposure to HMs toxic effect. In this study, **next-generation sequencing (NGS)** was applied for investigating shifts in microbial communities of an industrial soil, inoculated with *Cupriavidus sp. strain 1C2*, before and after HMs remediation using sunflowers. A non-contaminated soil (agricultural) was used as control. The main objective of this study was to investigate the relationship between soil microbiota and phytoremediation strategies achievements.

## Methods



## Results

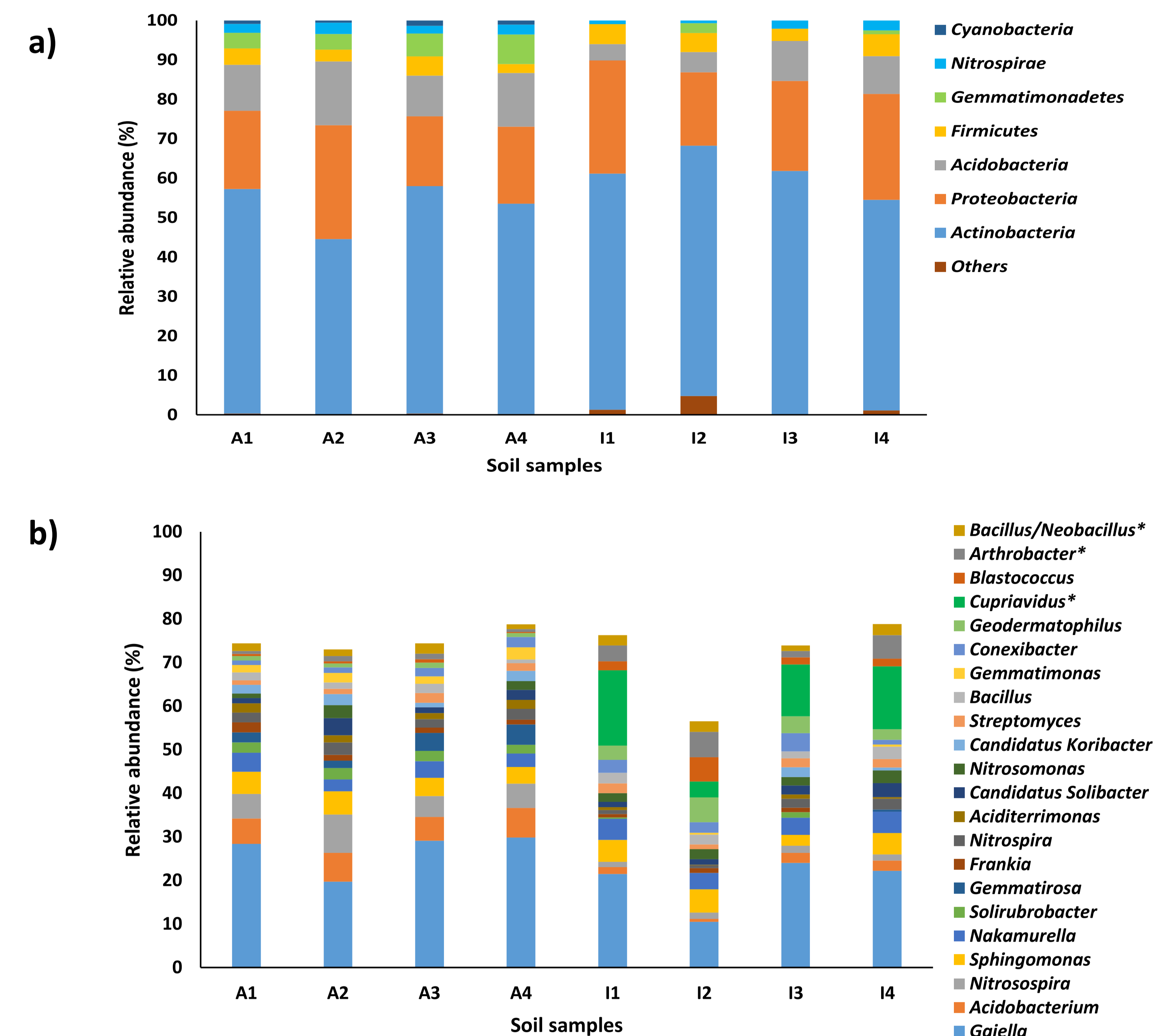


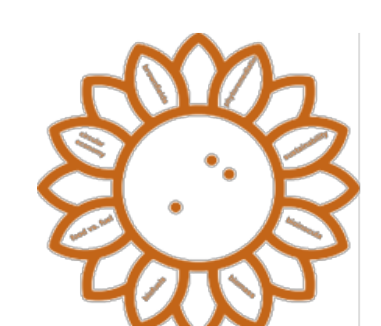
Figure 1 – Relative abundance of bacterial phyla (a) and top 10 bacterial genera (b) presenting the highest relative abundances in the soil samples at the beginning and end of plant growth; \*Bacterial genera identified using BLAST from NCBI.

## Conclusions

- *Actinobacteria* were dominant while *Proteobacteria* was the second most abundant phylum in both soils;
- *Acidobacteria* and *Nitrospirae* were present in higher relative abundance in the control soil;
- *Cupriavidus sp. strain 1C2* remained in the contaminated soil until the end of plant growth;
- Phytoremediation associated to PGPR induced changes in the contaminated soil microbial community: *Acidobacterium* (*Acidobacteria* phylum) and *Nitrospira* (*Nitrospirae* phylum) bacterial genera increased their abundance at the end of plant growth, in the industrial soil, possibly resulting in the improvement of the microbial diversity in this contaminated soil.

## Acknowledgements

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