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Effect of sustainable fertilizations on PGP microbial communities in rice paddy fields: a focus on phosphate

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BACKGROUND

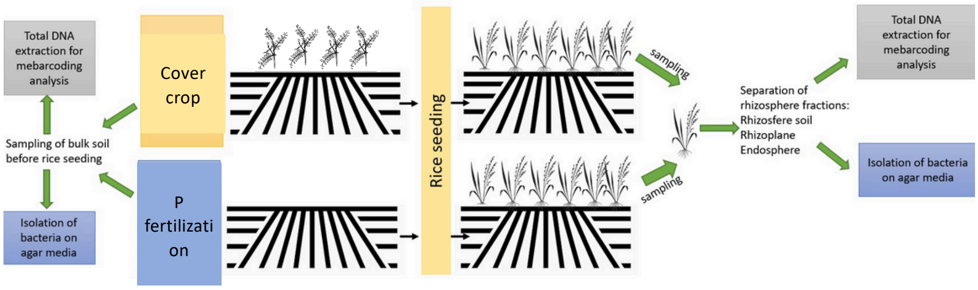
Phosphorous (P) is abundant in soils, although only a very small percentage of it (about 1%) is available for plant uptake, where it is absorbed P as $H_2PO_4^-$ and HPO_4^-. P is usually found within the soil in mineral or organic forms. Mineral P, such as apatite, hydroxyapatite or oxyapatite, is poorly soluble in soil. On the other hand, organic P, such as phosphodiesters, phospholipids and nucleic acids, tends to co-precipitate with a variety of metals (Aluminum, Calcium and Iron), becoming unavailable for plants. Many strategies have been developed by plant and microorganism for solubilizing mineral and organic forms of P.

Because of the scarce availability of P in soils, and the significant yield losses that a P deficiency can lead to, abundant phosphoric fertilization is often adopted. Nevertheless, P becomes quickly unavailable within the soil, precipitating with other elements and becoming insoluble. This practice, besides increasing the cost of agricultural production, has negative effects on the environment, playing a major role in the eutrophication of surface water that could lead to algal blooms and it causes a reduction of soil fertility. Agronomic practices have a huge impact on the cycle and availability of nutrient elements in the soil. Other macro-elements such ad N and K received many attentions, especially in the distinctive flooded water regime present in rice paddies. However, little is known regarding how P is affected by agronomic practices.

METHODS

The microbiome of rice plants (*Oryza sativa*) was explored in light of different agronomic practices: presence (+CC) and absence (-CC) of a cover crop (i.e, hairy vetch, *Vicia villosa*) and supplement (+P) of P fertilizer compared to a lack of P addition (-P).

Rice plants were sampled from Italian rice paddies located in Castello D'agogna (PV) and Nicorvo (PV) at the booting stage. The cover crop was also sampled before the ploughing in preparation of rice seeding.



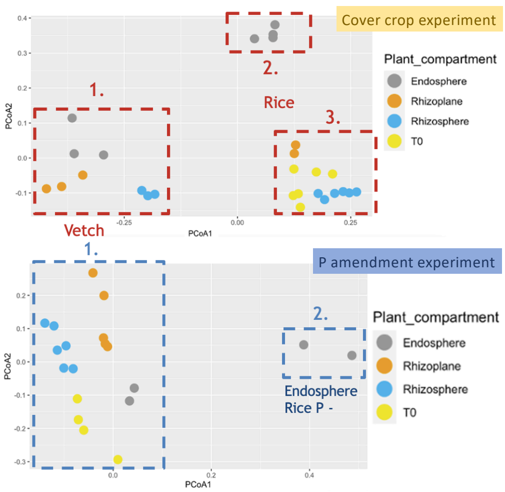
Illumina amplicon sequencing of:

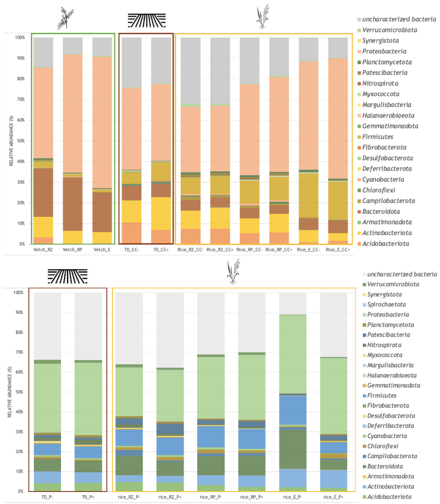
- V3-V4 region of bacterial and archaeal 16S rRNA gene
- fungal ITS

Screening for PGP activities:

- tricalcium phosphate TCP
- monocalcium phosphate MCP
- phytate solubilization
- nitrogen fixation
- Indole-3-acetic acid (IAA)
- ACC deaminase production

METAXONOMIC CHARACTERIZATION OF THE MICROBIAL COMMUNITIES IN THE DIFFERENT COMPARTMENTS



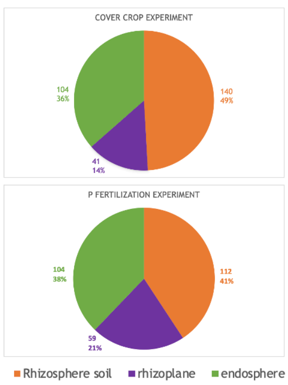


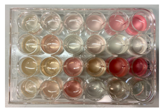
The rice and vetch microbiomes were significantly different in all compartments.

In the P fertilization experiment, both the compartment and the fertilization led to significant differences in the microbial communities.

In all samples, 7 dominant families belonging to the Proteobacteria were present.

CULTUROMICS





In total, 560 bacterial strains were isolated from all plant compartments. After a first de-replication, 219 strains were screened for their PGP activities in 24-well plates.

- The capacity of solubilizing organic phosphate was the most widespread in the culture collection (78%), followed by TCP (26%) and MCP (7%).
- Both cover crop and P fertilization promoted the ability to solubilize TCP.
- Cover crop promoted the presence of bacterial strains able to solubilize phytate in the rhizosphere soil.
- Phosphate fertilization increased the number of N_2-fixing and IAA-producing bacteria.

CONCLUSIONS AND PERSPECTIVES

The outputs of this project will help to understand the role of P-solubilizing bacteria in rice nutrition under different agronomic settlements and develop biofertilizers able to enhance the uptake of soil endogenous phosphate.

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