

TITLE: INFLUENCE OF MICROBIAL DIVERSITY ON PHOSPHORUS AVAILABILITY

AUTHORS: RODRIGUEZ, Y.F., CAPOZZI, J.F., DIAS, A.C.F., ANDREOTE, F.F., COTTA, S.R.

INSTITUTION: ESCOLA SUPERIOR DE AGRICULTURA “LUIZ DE QUEIROZ” – ESALQ-USP (AVENIDA PÁDUA DIAS 11, PIRACICABA, SÃO PAULO, BRAZIL)

Global food demands is increasing rapidly, as are the environmental impacts of agricultural expansion. However, the agriculture paradigm changed on the last years with adds of sustainability concept as the core strategy for its development. Microorganisms showed a high potential to be use on sustainable agriculture due its important role for growth and health of their hosts. However, the fully understand of the ecology of plant-associated microbes linked with microbial assembly and plant performance still lacking. The influence of microbial assembly will be essential for any attempt to manage agricultural microorganisms, and to develop an effective microbiome inoculation strategy for agriculture. Based on this premise, we hypothesized that high microbial diversity on a soil environment promote a more effective phosphorus disponibilization to plant. To test this hypothesis, we developed a gradient of soil microbial diversity where this diversity was manipulated by dilution extinction approach. This manipulated microbial community was inoculated on a microscop with three phosphorus sources (Calcium phytate, Araxá rock phosphate and Super Triple phosphate) and maize seed. The experiment was incubated on vegetation House for 30 days. After 30 days, it was observed differences on a growth rate of maize. On a Calcium phytate and Super triple phosphate was observed a gradient of growth, where plants growth more on a higher microbial diversity. On Araxá rock phosphate the plants showed a low growth, similar to control plants. A similar pattern was observed when acid phosphate was evaluated. Higher microbial diversity led to increase enzyme production. Analyzes associated with independent methods of cultivation are in progress. Total microbial communities (bacteria and fungi) and phosphorus solubilizers are being analyzed by PCR-DGGE and qPCR. This work intend to link microbial diversity and its functionality with plant development to shed light on rhizosphere ecology to provide accurate information for a future microbiome manipulation project.

Keywords: microbiome manipulation; maize; rhizosphere; phosphorus solubilization; phosphorus mineralization

Development agency: CNPq, CAPES, FAPESP