



Does the rice crop rotation stage influence the composition and activity of cultivable microbial populations of bulk soil from organically farmed rice fields?

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This study aimed at comparing the composition and activity of cultivable microbial populations of bulk soil of two adjacent organically farmed rice paddies (A and B) differing in the stage of the rice crop rotation. The crop rotation was: alfafa (2 years) and rice (2 years) and the paddies studied were in the first (A) and second year (B) of rice crop. Triplicate composite soil samples were collected in both paddies at 3 different stages of rice culture: before seeding (April), maximum tillering (July), and after harvesting (September).

All soil samples were characterized regarding some physicochemical (pH in H₂O and KCl; moisture; redox potential; total C and N; labile C; organic and inorganic labile P; NH₄⁺-N; NO₃-N;), biochemical (activities of several hydrolytic enzymes of the N cycle, N mineralization capacity and microbiological properties (MPN of (an)aerobic heterotrophs, diazotrophs, ammonifiers, denitrifiers; and anaerobic ammonia oxidizers–anammox bacteria and Community Level Physiological Profiles (CLLP)). Canonical correspondence analysis was carried out in order to assess the influence of the physicochemical and biochemical parameters on the variance of the microbial community composition (MPN data) and functional activity (CLPP data).

In both soils, the composition of the microbial community was distinct at different sampling dates, evidencing a pattern of variation over the rice cycle. The heterotrophs and diazotrophs were the microbial populations that contributed most to the observed variations. The variables that mainly explained these variations were casein-protease activity and soil redox potential. In July, in both paddies, the functional activity differed from the other sampling periods. Changes in the abundance of organisms growing at expenses of putrescine, β -phenylethylamine, cellobiose, o-hydroxybenzoic and galacturonic acid, and glycogen contributed to the observed variation, and were explained by the water content of soils.

The microbial communities of soils A and B, differed at each sampling time. The higher abundance of anammox population in soil A than in soil B contributed most to these variations, which were explained mainly by the labile inorganic P content of soils. The most important differences in the functional activity of soils A and B were observed in July. The abundance of organisms growing on keto-butiric, malonic, malic and o-hydroxybenzoic were responsible for the differentiation of both paddies and the labile C was the variable that contributed most to explain the variance observed

In summary, it was observed that microbial composition and functional activity of bulk soil vary over the rice cycle, independently of the rice crop rotation stage. Nevertheless, rice crop rotation was observed to have also a significant influence, mainly in July, when rice plants were actively growing towards maturation.