

## **Zoom in new insights of potential microbial control of N and CH<sub>4</sub> gaseous losses induced by different agricultural practices in temperate paddy soils**

Maria Alexandra Cucu (1,2), Laura Bardi (2), Daniel Said-Pullicino (1), Dario Sacco (1), Luisella Celi (1), and Roberta Gorra (1)

(1) Rice Agro-ecosystem and Environmental Research Group, Department of Agricultural, Forest and Food Sciences, University of Turin, Italy, (mariaalexandra.cucu@unito.it), (2) Agricultural Research Council, Turin, Italy

Rice is the world's single most important food crop and a primary food source for more than a third of the world's population. Usually, rice is grown in flooded paddies that result in anoxic soil conditions throughout a major part of the cropping period. Redox processes in wetland ecosystems combined with crop residue incorporation play an important role in element cycling and ecological functions of rice ecosystems. Microbial communities are at the basis of the functioning of wetlands and the ecosystem services they provide. Agronomic management practices adopted in rice paddies may have important effects on microbial biomass functionality and interactions, but these are largely unknown *in situ*. They mediate important processes such as nitrification, anaerobic ammonia oxidation (Anammox), denitrification, and methanogenesis that regulate ecosystem functioning and control greenhouse gases (GHG) emissions. Therefore, it is crucial to comprehend the microbial control of these processes as a function of different crop residue and water management practices.

Here we highlight recent findings based on the exploration of microbial functional genes as biogeochemical indicators. Through both lab and field experiments and by linking to GHG emissions and soil chemistry, we evaluated niche differentiation between microbial communities and the crucial role of agronomic management in regulating their potential functionality.

Recent studies showed a high abundance of both 16S communities, bacteria and archaea, confirming the high relevance of archaeal mediated processes in rice ecosystems. Our results unravel the complete denitrification as key player in regulating major nitrogen (N) fluxes in fertilized paddies. In a laboratory experiment this process was shown to be driven by both archaea and bacteria harboring *nosZ* gene, but especially by archaea in the absence of straw. In addition, part of the immobilized N was attributed to nitrous oxide (N<sub>2</sub>O) reducing archaea, suggesting that the assimilation of N contributes to the last step of archaeal denitrification. In a field experiment a high abundance of aerobic ammonia oxidizers suggested nitrification as proxy for complete denitrification, highlighting the importance of the latter in mitigating N<sub>2</sub>O emission from rice ecosystem. As a new insight for temperate rice paddies, our data indicated a high abundance of Anammox bacteria, suggesting this process to be very important in controlling N losses independently of water and rice straw management. Characteristic treatment interactions and cooperation were shown between aerobic and anaerobic ammonia oxidizers. Rice straw incorporation and the increased rice biomass due to N fertilization supported the methanogenesis. In this regard, a high abundance of *mcrA* gene was shown *in situ* level.

Our findings highlighted the possibility of microorganisms niche differentiation not only driven by differential responses to NH<sub>4</sub><sup>+</sup> concentration, but also through different organic C substrates derived from more or less labile pools, and the contrasting straw C/N ratios in different treatments.

The results provide novel insights into the influence of paddy soil management on microbial communities dynamics, with important implications on their potential functionality. These studies are a step forward in understanding the overall microbial control in N and CH<sub>4</sub> gaseous losses mitigation from rice fields.