

Background: Arsenic content in rice grains is limited by European Union directives. In rice paddies, continuous flooding leads to the dissolution of iron (oxyhydr)oxides and release of arsenic from soil minerals with subsequent uptake by rice plant and translocation to the grains. Sulfate fertilization was suggested to reduce arsenic accumulation in rice grains. While direct and indirect microbial arsenic transformations have been widely studied over the last years in rice paddies, the dynamics involving thioarsenates are poorly characterized.

Objectives: Composition and activities of the rhizospheric microbial communities were investigated in relation to carbon content, sulfur fertilization, thioarsenates occurrence in pore-water and arsenic speciation in rice.

Methods: Rice was cultivated in soils with different carbon content and sulfate fertilization in mesocosms placed in the open air. The main physico-chemical parameters were monitored in the pore-water and related to arsenic accumulation in rice grains. Microbial communities were screened by 16S rRNA genes Illumina sequencing in rhizosphere soil and pore water at different time points. Genes related to sulfur and arsenic metabolism were quantified by real-time quantitative PCR.

Results: During rice growing season, sulfate addition led to a higher proportion of thioarsenates and methylated arsenic in the pore-water. In rice grains, total arsenic decreased while the proportion of methylated arsenic increased. Illumina libraries revealed that in rhizosphere soil and in pore-water sulfate-reducing microorganisms were promoted, probably linked to higher arsenic thiolation. In the pore-water of sulfate-fertilized mesocosms, arsenic-methylating microorganisms were more abundant, possibly explaining the higher proportion of methylated arsenic in rice grains.