## The diversity and abundance of As(III) oxidizers on root iron plaque is critical for arsenic bioavailability to rice

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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. Among agricultural crops, rice is the major route of exposure for the uptake of inorganic arsenic (As) through food. As toxicity in rice is manifested as reduced growth and sterility and poses potential risks for human exposure through the food chain. Thus, As uptake by rice threatens food security by impacting both the quantity (yield) and quality (toxicity) of rice and represents a serious environmental issue for human health and ecosystem function. Iron plaque is a strong adsorbent on rice roots, acting as a barrier to prevent metal uptake by rice. However, the role of root iron plaque microbes in governing metal redox cycling and metal bioavailability is unknown. In this study, the microbial community structure on the iron plaque of rice roots from an arsenic-contaminated paddy soil was explored using high-throughput next-generation sequencing. The microbial composition and diversity of the root iron plaque were significantly different from those of the bulk and rhizosphere soils. Using the aoxB gene as an identifying marker, we determined that the arsenite-oxidizing microbiota on the iron plaque was dominated by Acidovorax and *Hydrogenophaga*-affiliated bacteria. More importantly, the abundance of arsenite-oxidizing bacteria (AsOB) on the root iron plaque was significantly negatively correlated with the arsenic concentration in the rice root, straw and grain, indicating that the microbes on the iron plaque, particularly the AsOB, were actively catalyzing arsenic transformation and greatly influencing metal uptake by rice. This exploratory research represents a preliminary examination of the microbial community structure of the root iron plaque formed under arsenic pollution and emphasizes the importance of the root iron plaque environment in arsenic biogeochemical cycling compared with the soil-rhizosphere biotope.