

## **Silicon as a driver of rice paddy microbial arsenic methylater communities**

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Rice is a staple food for half the world's population and is prone to arsenic (As) uptake. Nearly half of total daily As ingestion for people in As contaminated regions is due to cooked rice consumption. Arsenic is taken up by paddy rice due to chemical similarities between reduced As (arsenite) and silicon (Si); the latter being a quasi-essential nutrient for rice. Organic forms of As are also transported along the Si uptake pathway. Rice is efficient in uptake of Si—and therefore As—into roots.

Addition of Si to soils is an emerging and effective strategy to decrease As uptake and grain accumulation without compromising yield. However, Si addition to soils has also been shown to alter the speciation of As in grain, shifting to higher concentrations of organic As forms. These organic As species are microbially derived and are less toxic to humans than inorganic As species. The mechanism(s) for why and how Si addition shifts As speciation to organic As forms is not well resolved.

We hypothesize that Si addition increases inorganic arsenic desorption, due to competition for binding sites. This desorbed inorganic arsenic then triggers an increase in microbially-mediated arsenic methylation, shaping the microbial community of arsenic methylaters. We sequenced an arsenic methylater functional marker gene and chemically characterized rice paddy mesocosms treated with three silicon amendments. We found that the communities of arsenic methylaters separated by treatment, and inorganic porewater arsenic and porewater silicon were significant factors in driving divergence between treatments. These findings support our hypothesis and open questions about how silicon amendments influence the entire community of microbes in paddy soil.