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Mapping interactions among anaerobic arsenic-transforming soil microorganisms

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Arsenic (As) is a toxic contaminant that is prevalent in the environment. In soils, it is most commonly found in its inorganic forms, either as arsenate (As(V)) in oxic environments or as the more mobile arsenite (As(III)) in anoxic environments. By establishing reducing conditions, the practice of flooding in rice paddy fields mobilizes As into the soil solution. Microbial communities inhabiting arsenic-rich soils can perform diverse arsenic biotransformations, including changes in methylation state (methylation, demethylation) and oxidation state (oxidation and reduction). These microbial transformations induce changes in the toxicity, mobility, and bioavailability of As in soils, which, in the context of rice cultivation, may have consequences on crop growth (straighthead disease) and on food safety (contaminated rice grains). Here, we focus on the transformations that methylate or demethylate arsenic. Although they have been described extensively in aerobes, there remain large gaps in the collective knowledge of which anaerobes are able to mediate the same processes. In particular, further understanding has been limited by the difficulty of isolating anaerobic microorganisms with specific phenotypes of interest.

The present work explores a novel high-throughput isolation approach consisting of single-microbe encapsulation into picoliter capsules, selective in-capsule growth, and fluorescent-activated cell sorting (FACS). At this stage, soil anaerobes have been shown to grow within capsules from single cells to microcolonies, and FACS-selected capsules could be individually dispensed into microplates, producing pure cultures in each well. The approach is being tested to isolate arsenic-resistant microbial species from a paddy soil. Ultimately, isolates will be co-cultured to investigate the role of interspecific interactions in arsenic biotransformations.