

Response of soil microbial communities to elevated antimony and arsenic contamination indicates the relationship between the innate microbiota and contaminant fractions

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Mining of sulfide ore deposits containing metalloids, such as antimony and arsenic, has introduced serious soil contamination around the world, posing severe threats to food safety and human health. Hence, it is important to understand the behavior and composition of the microbial communities that control the mobilization or sequestration of these metal(loid)s. Here, we selected two sites in Southwest China with different levels of Sb and As contamination to study interactions among various Sb and As fractions and the soil microbiota, with a focus on the microbial response to metalloid contamination. Comprehensive geochemical analyses and 16S rRNA gene amplicon sequencing demonstrated distinct soil taxonomic inventories depending on Sb and As contamination levels. Stochastic gradient boosting indicated that citric acid extractable Sb(V) and As(V) contributed 5% and 15%, respectively, to influencing the community diversity. Random forest predicted that low concentrations of Sb(V) and As(V) could enhance the community diversity but generally, the Sb and As contamination impairs microbial diversity. Co-occurrence network analysis indicated a strong correlation between the indigenous microbial communities and various Sb and As fractions. A number of taxa were identified as core genera due to their elevated abundances and positive correlation with contaminant fractions (total Sb and As concentrations, bioavailable Sb and As extractable fractions, and Sb and As redox species). Shotgun metagenomics indicated that Sb and As biogeochemical redox reactions may exist in contaminated soils. These observations collectively hold the potential to provide fundamental knowledge for implementing an in situ bioremediation strategy.

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