

Linkage of organic molecules and microbes in arsenic-prone groundwater

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High arsenic groundwater had been widely observed throughout the world, posing health risks to hundreds of millions of people [1]. Reductive dissolution of Fe(III) oxides has been accepted to be the key processes of arsenic mobilization triggered by dissolved organic matter and indigenous microbes [2-5]. However, linkage of organic molecules and microbes and its role in arsenic mobilization are unclear. Groundwater samples were taken approximately along a flow path to analyze molecular characteristics and microbial properties. Potential reaction analysis of molecular formulas indicated that organic matter mineralization to ammonium (deamination) was critical to enrichment of groundwater ammonium along the groundwater flow path. Abundance of the metagenomic assembled genomes (MAGs) was widely correlated with the abundance of N-containing formula. MAGs of marked genes related to the organic matter mineralization to ammonium (*ureABC* and *gdh2*) were positively correlated with N-containing formula. However, no *ureABC* and *gdh2* was encoded in MAGs marked iron reduction proteins and As(V)-detoxifying reduction genes, indicating that they did not participate in the organic matter mineralization to ammonium. The study suggested that the As-mobilizing microorganisms were under C and N limited conditions.

References

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