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Methylmercury production and degradation by soil microbial communities

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Rice consumption is now recognized as an important pathway of human exposure to the neurotoxin methylmercury (MeHg), particularly in countries where rice is a staple food. Although the discovery of a two-gene cluster *hgcAB* has linked Hg methylation to several phylogenetically diverse groups of anaerobic microorganisms converting inorganic mercury (Hg) to MeHg, the prevalence and diversity of microbial communities associated with MeHg production and degradation in paddy soils remain unclear. Both Illumina and PacBio sequencing analyses revealed that Hg methylating communities were dominated by iron-reducing bacteria (i.e., *Geobacter*) and methanogens, with a relatively low abundance of *hgcA*⁺ sulfate-reducing bacteria in the soil. A positive correlation was observed between the MeHg content in soil and the relative abundance of *Geobacter* carrying the *hgcA* gene. Our structure equation modeling suggested a much stronger link between bacterial community composition and %MeHg, compared to the abundance of methylating gene (*hgcA*) and edaphic properties. More importantly, random forest models suggested a more important role of non-Hg methylators than Hg methylators in predicting variations of soil %MeHg.

Microbial demethylation was demonstrated by significantly more degradation of MeHg in the unsterilized soils than the sterilized controls, although more degradation was observed in water-saturated soils than the unsaturated soil. 16S rRNA Illumina sequencing and metatranscriptomic analyses consistently revealed that *Catenulisporaceae*, *Frankiaceae*, *Mycobacteriaceae*, and *Thermomonosporaceae* were among the most likely microbial taxa in influencing MeHg. These findings provide new insights into microbial communities associated with MeHg accumulation in paddy soils, with important implications in mitigating the net production and bioaccumulation of MeHg in rice worldwide.