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Evolutionary Coupling of Arsenic Resistance and Mercury Methylation: Meta-omic Insights from Legacy Gold-Mining Soils

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Microbial methylation of mercury (Hg) to neurotoxic methylmercury (MeHg) represents a key biogeochemical transformation controlling Hg mobility, bioaccumulation, and ecological risk. Although the genetic basis of Hg methylation (*hgcAB*) is now well established [1], the environmental and evolutionary drivers that regulate this process remain poorly understood. Laboratory evidence from sulfate-reducing bacteria has shown that arsenic (As) can regulate *hgcAB* transcription through cross-talk with As-responsive resistance systems (*ars*), suggesting that As may be an unrecognised control on Hg methylation in contaminated environments [2]. However, it is unknown whether such regulatory coupling occurs in natural ecosystems or reflects an evolutionary association shaped by long-term metal(loid) stress. To address this, we conducted an integrated meta-omic and geochemical study across legacy gold-mining sediments in Victoria (Australia), selecting floodplain sites identified as arsenic- and mercury-enriched [3] from archaeological mining reconstructions [4] and verified by in-situ pXRF measurements (As: <10–3324 ppm; Hg: non-detect to 12 ppm). DNA was extracted from soils and 16S rRNA and *hgcAB* amplicon profiling guided high-throughput metagenomic sequencing of targeted samples. We recovered metagenome-assembled genomes (MAGs) of putative Hg-methylating taxa and quantified *ars–hgcAB* co-occurrence, genomic neighbourhood structure, and shared regulatory motifs across contamination gradients. Early analysis of one representative site shows a marked reduction in microbial community complexity in high-As sediments, consistent with arsenic-mediated selection. Ongoing comparative and phylogenomic analyses will determine whether these patterns reflect deeper evolutionary associations between *ars* resistance systems and *hgcAB*. Together, these insights will help define the environmental controls on microbial mercury methylation and improve our ability to predict methylmercury production in arsenic- and mercury-impacted ecosystems.

[1] Parks, J. M. *et al.* (2013), *Science* 339, 1332-1335. doi: 10.1126/science.1230667

[2] Gionfriddo, C. M. *et al.* (2023), *Applied and Environmental Microbiology* 89, e01768-01722. doi:10.1128/aem.01768-22

[3] Colombi, F. *et al.* (2024), *Environmental Geochemistry and Health* 46, 247. doi:10.1007/s10653-024-02003-5

[4] Lawrence, S. *et al.* (2023), *Geoarchaeology* 38, 389-405. doi:10.1002/gea.21958