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merAB-DB: A consensus database for a standardised detection of methylmercury demethylation and mercury reduction genes

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The global fate of mercury (Hg) is largely shaped by microbial activity. Through specialized metabolic pathways, microorganisms can control both the formation of the neurotoxic compound methylmercury (MeHg) and its breakdown via demethylation and reduction to volatile Hg species. Reflecting the importance of these processes, a consensus reference database has recently been developed for the Hg-methylating genes *hgcAB*. However, an analogous consensus database is still lacking for MeHg demethylation (*merB*) and mercury reduction (*merA*) genes. Building on pre-existing knowledge from culture-dependent and culture-independent approaches, our collaborative effort aims to: (1) define true (functional) *merA* and *merB* genes, (2) retrieve previously unrecognised or uncatalogued *merA/B* genes from publicly available databases (i.e. genomes, genes, and nucleic acid sequences), and (3) create user-friendly bioinformatic tools to retrieve and taxonomically identify *merA* and *merB* genes from newly generated (meta)genomic data. Altogether, we aim to provide a standardized framework for the identification of Hg-detoxifiers in the environment, facilitating inter-study comparisons and providing a tool to deepen our understanding of Hg microbial transformations across diverse ecosystems.