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Evolutionary Diversification of Toxic Metal Resistance Genes Along a Climate-Driven Runoff Gradient in Arctic Lake Hazen

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Rapid Arctic warming is intensifying hydrological connectivity in polar watersheds, reshaping microbial communities and altering the transport and remobilization of toxic metals from thawing soils into lake sediments. However, the evolutionary consequences of these climate-driven hydrological changes for microbial functional genes remain poorly understood. Here, we investigated the phylogenetic diversity and evolutionary structuring of multiple microbial metal-resistance gene families along a runoff gradient in the Lake Hazen watershed (Nunavut, Canada), where increased runoff represents a direct consequence of glacier melt and permafrost thaw. Using metagenomic assemblies generated with MegaGTA and a standardized bioinformatic workflow, we reconstructed hundreds of unique variants of key detoxification genes, including mercury reductase (*merA*), cadmium efflux ATPase (*cadA*), arsenate reductase (*arsC*), and chromate reductase (*chrR*), from sediment and soil samples collected at control, low-runoff, and high-runoff sites. Codon-aware alignments and maximum-likelihood phylogenies were used to quantify nucleotide diversity, Faith's phylogenetic diversity, Tajima's D, and episodic positive selection across hydrological regimes. High-runoff environments consistently exhibited greater nucleotide and phylogenetic diversity of metal-resistance genes than control and low-runoff sites, indicating enhanced evolutionary diversification under increased hydrological connectivity. Codon-based analyses detected episodic positive selection in several gene families, suggesting adaptive responses to changing redox conditions and metal availability. Tajima's D values revealed contrasting evolutionary signatures among regimes, consistent with demographic expansion or purifying selection in some environments and balancing or diversifying selection in others. Together, these results demonstrate that climate-driven runoff in Arctic watersheds influences not only microbial community composition but also the evolutionary trajectories of metal-detoxification pathways. Increased hydrological connectivity associated with Arctic warming may accelerate diversification of resistance genes, potentially altering metal cycling and microbial resilience in polar freshwater ecosystems. Our study highlights the importance of integrating phylogenetic diversity, population genetics, and selection analyses to understand how environmental change drives functional evolution in microbial communities.