

Metal tolerant bacteria in Arctic ecosystems – Hidden treasures to uncovering the genomic mysteries of pollution

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In the light of enhanced warming conditions in the Arctic and the reports on the long-range transport of metal pollutants via atmospheric and oceanic circulation along with the localized inputs, it is imperative to understand the trace metal distribution in various Arctic ecosystems and how they are impacting the microbiota of the system. The present study revealed the background trace element concentration from a glacio-marine system in Arctic along with the assessment of metal-tolerant bacterial fraction through enrichment studies (with metals such as Hg, Pb, Cd, Ni, Co, Zn, Mn) and a genome centric approach. Higher trace metal concentrations were noted in the sediments as compared to the water samples from terrestrial and fjord systems. The decreasing order of toxicity of metals based on the viable counts from each of the amendments for the different glacio-marine samples was in the order Hg > Zn > Co > Cd > Pb > Mn > Ni. The dominant metal-tolerant bacterial fraction belonged to the class γ -proteobacteria (45%), α -proteobacteria (19.8%), and Actinobacteria (15.8%).

Screening of the metal-tolerant bacterial fraction lead to the identification of three potential bacterial species - closely related to *Psychrobacter glaciei*, (99.72%), *Halomonas neptunia* (99.57%), and HM12, and *Planococcus halocryophilus* (100%), exhibiting the highest MIC levels towards different metals tested. The selected bacterial isolates could efficiently accumulate the different metals tested with significantly higher Pb removal efficiency. Further, it was noted that the metals had an impact on the bacterial enzyme production and antibiotic resistance properties. The genome-based study revealed the presence of metal-resistant genetic elements- *merA*, *merR*, *czcD*, and *arsC* involved in the regulation and detoxification of metals in all the three bacterial genomes. The presence of different efflux pump mediated multi-drug-resistant genes belonging to resistance-nodulation-division (RND) family transporters was observed indicating a common strategy in Arctic bacteria to export metals, antibiotics and other noxious substances across the cell surface to reduce their intracellular load. Thus, this work demonstrated the role of Arctic bacteria for bioremediation applications in Polar Regions, which is a potentially transformative solution for ecosystem restoration.

