INVESTIGATION OF MECHANISMS FOR METHYLMERCURY BIOREMEDIATION BY INDIGENOUS BACTERIAL STRAIN IN COMPARISON WITH NON-INDIGENOUS METAL RESISTANT STRAIN OF BACILLUS THROUGH PROTEOMICS STUDIES

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Methylmercury (MeHg) is highly toxic and poses a severe threat to biota worldwide. Theseriousness of toxicity of this neurotoxin is characterized by its ability to augment food chains. The general population is primarily exposed to MeHg through the consumption of contaminated fish and marine mammals. Still, recent studies have reported high levels of MeHg in rice and confirmed that in China, human exposure to MeHg is related to frequent rice consumption in mercury (Hg) polluted areas. Several remediation approaches have been implemented to rehabilitate MeHg contaminated sites. Bioremediation is considered a cheaper and greener technology than conventional physicochemical means. Therefore, the main objective of this studyis to investigate the mechanisms for MeHg bioremediation by indigenous bacterial strain in comparison with non-indigenous metal resistant *Bacillus* strain (MRS-1) bacteria through proteomics studies. Since MeHg resistant bacteria could be used for remediation of MeHg in contaminated water and soils, the evaluation of the molecular and cellular mechanisms underpinning MeHg resistance can pave the way to improve the bioremediation process.

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