

Molecular Characterization of Mercury Resistant Bacteria Isolated from Tannery Wastewater

ABSTRACT

Mercury resistant (HgR) bacteria were isolated from heavy metal polluted wastewater and soil, collected from the proximity of some tanneries from Kasur, Pakistan. Three out of 30 bacterial strains were screened out on the basis of resistance level against various concentrations of HgCl₂. Bacterial isolates AZ-1, AZ-2 and AZ-3 showed resistance up to 40 µg/mL of HgCl₂ and mercury sensitive (HgS) isolate ZA-15 was taken as a negative control. 16S rDNA ribotyping and phylogenetic analysis were performed for the characterization of isolates as *Bacillus* sp. AZ-1 (KT270477), *B. cereus* AZ-2 (KT270478), *B. cereus* AZ-3 (KT270479) and *Enterobacter cloacae* ZA-15 (KJ728671). Phylogenetic relationship on the basis of *merA* nucleotide sequence confirmed 51-100% homology with the corresponding region of the *merA* gene of already reported mercury resistant Gram-positive bacteria. Restriction fragment length polymorphism (RFLP) analysis was applied to the amplification products of 16S rRNA and *merA* genes and a specific restriction patterns was successfully obtained after treatment with different endonucleases. A small-scale reservoir of Luria Bertani (LB) medium supplemented with 30 µg/mL of HgCl₂ was designed to check the detoxification ability of the selected strains. The results demonstrated 83% detoxification of mercury by both *B. cereus* AZ-2 and *B. cereus* AZ-3, and 76% detoxification by *Bacillus* sp. AZ-1 ($p < 0.05$).