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Molecular characterization of metal–resistant bacteria isolated from contaminated industrial effluent in Sri Lanka

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Removal of heavy metals from contaminated effluents has gained much attention during the recent past due to increasing contamination by industrial processes. The use of bacteria for heavy metal bioremediation has become popular, as it is cost effective and more eco-friendly than conventional methods.

The aim of this research was the molecular characterization of bacterial strains isolated from effluent samples collected from the textile dyeing industry. Towards this, a few endogenous bacteria that were isolated previously were used. The metal remediation efficiency of the isolates for metals Cu^{2+}, Zn^{2+}, Cd^{2+} and Pb^{2+} was determined using Atomic Absorption Spectrophotometry. Two methods were used for isolation of bacterial genomic DNA and included the modified Guanidine Thiocyanate (GES) method and a commercially available kit (Wizard® Genomic DNA purification Kit - Promega). To molecularly characterize the isolates 16S ribosomal DNA sequences of the isolated bacteria were amplified using universal primers (fD1 and rD1) and the resulting sequences were subjected to homology comparison. Sequences were analyzed using BLAST and BioEdit software v7.1.11. A Phylogenetic tree was constructed using MEGA 5.1 software.

The isolated bacterial strains when tested for heavy metal reduction activity showed significant remediation ability for the metal ions listed above. Strains designated D5 and D7 removed all the Pb^{2+} and Cd^{2+} ions (1 mg dm^{-3}) respectively, in culture on the 7th day of the inoculation. Strain G removed 74% of Zn^{2+} ions (1 $mgdm^{-3}$) on the 7th day.

BLASTn analysis of the B4 strain showed a high degree of homology (100%) to *Bacillus cereus* (Accession number: NR_074540.1). Strain O1 showed a high degree of similarity (99%) to *Paracoccus pantotrophus* (Accession number: NR_026457.1) and B1 and B2 strains showed 99% homology to *Bacillus flexus* (Accession number: NR_024691.1). Strains O5, O6, O8 and O10 showed highest similarity (99%) to *Staphylococcus epidermidis* (Accession number: NR_036904.1).

Keywords: 16S rDNA, bioremediation, dyeing industry, heavy metals, industrial effluents

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