ISSN: 1391-8796
Proceedings of
5th Ruhuna International Science & Technology Conference
University of Ruhuna, Matara, Sri Lanka
February 15, 2018

Identification of metallothionein gene in *Staphylococcus warneri* strain G isolated from industrial effluent in Sri Lanka

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Controlling pollutants has become a crucial requirement with the world's population increase and urbanization. Studies on bacteria with metal tolerance capabilities have revealed the presence of heavy metal tolerant mechanisms and their potential use in bioremediation. Identification and isolation of genes that confer metal resistance in bacterial isolates is important as they can be used to modify organisms using genetic engineering to enhance bioremediation abilities. Metallothionein is an intracellular protein found in both prokaryotes and eukaryotes that has the ability to bind heavy metals *via* thiolate bonds and thereby reduce the toxic effects of heavy metal ions to living organisms.

Heavy metal tolerance analysis showed that *Staphylococcus warneri* strain G, which has been previously_isolated from a textile dyeing industry has metal tolerance ability in the order of Pb^{2+} (1000 ppm) > Cd^{2+} (100ppm) > Cu^{2+} (25ppm). Although metallothionein gene is known to present in *S. epidermidis* genome, it has not yet been assigned in any of the *S. warneri* genomes. Primers were designed exploiting the *S. epidermidis* gene sequences to amplify a region of 295 bp flanking the complete metallothionein gene and to amplify a region of 628 bp which included the complete sequence of the possible regulator gene along with the complete metallothionein gene of *Staphylococcus spp*. Both Polymerase Chain Reaction amplifications resulted bands of expected sizes for *S. warneri* strain G where the nucleotide sequencing of the two amplicons showed a similarity of 98% for the complete metallothionein gene and for the complete regulator gene present in *S. epidermidis* 949_S8. It was concluded from the above study that *S.warneri* strain G has the potential to synthesize metallothionein which can contribute in the heavy metal tolerance of *S.warneri* strain G.

Keywords: Metallothionein, *Staphylococcus warneri*, Genetic engineering, Bioremediation

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