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Molecular identification of bacteria in wastewater collected from Pannala industrial zone using 16S ribosomal RNA genes

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Water pollution is a burning issue all round the world. Bioremediation of wastewater is a popular emerging remedy to clean water due to its environmental soundness and low cost. Bioremediation uses naturally occurring microorganisms or their enzymes to degrade various types of wastes. This study was done to detect the naturally available bacteria in wastewater collected from the Pannala industrial zone in the Kurunagala District with the general objective of isolating biodegradable bacteria from waste environments. Molecular detection by using primers amplifying consensus sequence of 16S ribosomal RNA genes was done by using extracted DNA from isolated bacterial colonies. Amplified products of Polymerase Chain Reactions (PCR) were sequenced. Then homology search was performed for every sequence by using the Basic Local Alignment Search Tool (BLAST). The bacterial species *Acinetobacter baumannii* strain BM0067, *Staplylococcus spp.* and *Staphylococcus sciuri* strain M-2 were identified. These bacteria have proved successful in bioremediation processes in the recent past. *Acinetobacter baumannii* was observed to degrade oil and waste containing chromium. *Staplylococcus spp.* was shown in treating wastewater contaminated with heavy metal and hydrocarbons where *Staphylococcus sciuri* was shown in treating xenobiotics like phenol and chlorophenol. So this study opens up a pathway to investigate the bacteria capable of degrading water contaminants and their mechanisms. Identifying bacteria involved in the biodegradation and use of naturally occurring bacterial consortia for treating wastewater will be a good solution to the wastewater issue.

Keywords: 16S ribosomal RNA genes, bioremediation, wastewater