



King Abdulaziz University
Faculty of Science
Department of Biological Sciences



IDENTIFICATION OF BACTERIAL STRAINS ISOLATED FROM GOLD MINES

(1)RzazAbdulrazaqKashmeri,(1)Nidal MohammedZabermawi,(2)SalahMohammedAbo Abo

(1) Department of Biological Sciences, Faculty of Sciences, King Abdulaziz University, Jeddah 21589, Saudi Arabia.

Email: rkashmeri@kau.edu.sa , Phone: +966594147090

Email: nzabermawi@Kau.edu.sa , Phone: + +966505658458

(2) Department of Microbial Biotechnology, College of Biotechnology, Misr University of Science and Technology, Giza, P.O. Box, 77 Egypt

Email: salah_aboaba@yahoo.com , Phone: +966556049954

ABSTRACT

- **Problem statement:** Soil represents one of the most complex and diverse microbial habitats on Earth, hosting a wide range of bacteria that play critical roles in nutrient cycling and ecosystem stability. Understanding the taxonomic composition and genetic diversity of soil bacteria, particularly in mining environments, is essential for identifying strains with potential applications in biotechnology such as gold bioleaching.

- **Methods:** Soil samples were collected from mining environments, and bacterial isolates were obtained and purified. Partial 16S rRNA gene sequences of the isolates were generated and analyzed using bioinformatics tools. Identification was performed through BLASTn searches, while comparative analyses of sequence characteristics, including length and GC content, were conducted for genomic profiling. Phylogenetic relationships among isolates were reconstructed using the Neighbor-Joining method with bootstrap analysis to ensure reliability.

- **Results:** The molecular analysis successfully identified the taxonomic positions of the bacterial isolates, revealing diversity among the recovered strains. Sequence comparisons and phylogenetic reconstruction demonstrated clear evolutionary relationships between isolates and closely related reference species. Variations in GC content and sequence length provided additional insights into genomic diversity. The findings enabled the selection of the most suitable bacterial strain with promising characteristics for further applications in gold bioleaching and genetic improvement studies.

- **Conclusion:** The use of 16S rRNA gene sequencing combined with bioinformatics analysis is an effective approach for the identification and characterization of soil bacterial isolates. This study

highlights the potential of mining-associated bacteria for biotechnological applications, particularly in bioleaching processes, and provides a foundation for future genetic enhancement of selected strains.

Key Words: Soil Bacteria, 16S rRNA, Bioinformatics, Phylogenetic Analysis, Bioleaching, Mining Soil, Genetic Diversity