Metagenomic Approaches to Isolation of Extremophiles: Emphasizing the Isolation of Bacterial Diversity from Himalayan Pink Salt

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ABSTRACT

Extremophilic microorganisms, thriving in extreme environments, hold immense potential for biotechnological applications. Metagenomics provides transformative methodologies for isolating and characterizing these microbes without the need for traditional culturing. Advanced sequencing technologies, such as 16S rRNA gene sequencing, shotgun metagenomics, and single-cell genomics, enable comprehensive profiling of microbial diversity and functional potential in extreme habitats. Metagenomic assembly and binning allow the reconstruction of near-complete genomes from complex microbial communities, facilitating the identification of extremophiles. Functional gene annotation aids in pinpointing genes responsible for stress tolerance, such as osmotic regulation, high salinity adaptation, and enzymatic stability at extreme temperatures. Integrating long-read sequencing technologies, such as Nanopore and PacBio, enhances genome resolution, particularly for organisms with large or complex genomes. The use of transcriptomics and metaproteomics in conjunction with metagenomics provides insights into active metabolic pathways and adaptive strategies, linking microbial functions to environmental conditions. Bioinformatics tools further enable comparative analysis of extremophile genomes, revealing novel metabolic pathways and stress tolerance mechanisms. By applying these approaches, extremophilic microorganisms with unique traits can be effectively isolated, opening avenues for innovations in biotechnological fields such as enzyme production, bioremediation, and drug discovery. This comprehensive toolkit of metagenomics promises unprecedented opportunities for exploring microbial diversity in extreme environments, paving the way for sustainable solutions and industrial advancements.

Keywords: Extremophiles, Metagenomic approach, Diversity study, Functional dissection

How to Cite

Imran Sheikh, “Metagenomic Approaches to Isolation of Extremophiles: Emphasizing the Isolation of Bacterial Diversity from Himalayan Pink Salt”, *AIJR Abstracts*, p. 4, Mar. 2025.

Published by AIJR Publisher in “Abstracts of International Conference on Current Perspectives on Extremophiles and Their Biomolecules” (CUPEB 2025), 24-26 March 2025. Organized by Sarojini Naidu Government Girls PG (Autonomous) College, Bhopal-462012 (MP), India.

DOI: 10.21467/abstracts.177 ISBN: 978-81-984081-3-6 (eBook), 978-81-984081-9-8 (Paperback)