

Prevalence of Antimicrobial resistant genes in the Arctic – Study from Arctic glacier foreland and migratory birds

T. Jabir^{1*}, S. Venkatachalam¹, P.V. Vipindas¹, P. Akhil Prakash², A. A. Mohamed Hatha² and Archana Singh¹

¹National Centre for Polar and Ocean Research, Ministry of Earth Sciences (Government of India), Headland Sada, Vasco-da-Gama, Goa 403 804, India

²Department of Marine Biology, Microbiology, Biochemistry, School of Marine Sciences, Cochin University of Science and Technology (CUSAT), Kochi 682 016, India

*Corresponding Author: Thajudeen Jabir

Abstract

Antibiotic resistance poses a critical threat to human health, with melting glaciers and permafrost being potential contributors to the dissemination of Antibiotic Resistance Genes (ARGs) in the Arctic. While antibiotic resistance has been detected in permafrost and glacier samples dating back millions of years, the mechanisms and patterns of ARG release into the Arctic environment are not fully understood. Our study focuses on elucidating the sources of antibiotic resistance in the Arctic, encompassing both natural resistances arising from thawing permafrost and glaciers, as well as anthropogenic sources, including the transmission of resistant strains by migratory birds. Metagenomics survey's on the foreland soil of Arctic glaciers, including Midtre Lovrenbreen in Svalbard, Russell Glacier in Greenland, and Storglaciären glacier in Sweden, revealed the presence of 713 ARGs. Bacitracin-resistant genes were found to be dominant in the samples, followed by multidrug, rifamycin, fosfomycin, novobiocin, vancomycin, tetracycline, and beta-lactam resistant genes. Additionally, our findings highlight the substantial role of migratory birds in the dissemination of Antibiotic-Resistant Bacteria (ARB) in the Arctic. Migratory birds, such as the Arctic tern known for extensive migration, were found to harbour 105 ARGs, particularly towards multidrug, polymyxin, beta-lactam, and bacitracin antibiotics. This study provides valuable baseline data on Antimicrobial Resistance (AMR) in various Arctic sources, shedding light on the potential risks associated with changing Arctic conditions driven by climate change. The insights gained contribute to a better understanding of the complex dynamics of antibiotic resistance in the Arctic ecosystem, emphasizing the need for proactive measures to mitigate the impact on human health and the environment.

Key words: Arctic, Antibiotic-Resistant Bacteria, Antimicrobial Resistance gene, Climate change