

Microbiome and Resistome of Migratory Birds from the Arctic, Antarctic and Tropical Regions

Akhil Prakash E^{1*}, Tereza Hromádková², Maarten J.J.E. Loonen³, Jabir T.⁴, Farsana A.¹, Mohamed Hatha A. A.^{1,5}

¹ Department of Marine Biology, Microbiology, and Biochemistry, School of Marine Sciences, Cochin University of Science and Technology (CUSAT), Kochi 682 016, India

² Department of Zoology, Faculty of Science, University of South Bohemia, 370 05 České Budějovice, Czech Republic

³ Arctic Centre, University of Groningen, Groningen, the Netherlands

⁴ National Centre for Polar and Ocean Research, Ministry of Earth Sciences (Government of India), Headland Sada, Vasco-da-Gama, Goa 403 804, India

⁵ CUSAT-NCPOR Centre for Polar Sciences, Cochin University of Science and Technology (CUSAT), Kochi 682 016, India

Corresponding author: Akhil Prakash E (akhilprakash24@gmail.com)

Abstract

Antibiotic resistance poses a substantial threat to human health, stemming from the widespread use and misuse of antimicrobial drugs in both human healthcare and livestock management. Migratory birds are implicated in the dissemination of antibiotic resistance, as recent studies highlight their gut microbiota as a reservoir of antibiotic resistance genes (ARGs). This research focuses on faecal samples from three migratory bird species: Arctic terns (*Sterna paradisaea*) from the Arctic, Brown Headed Gulls (*Chroicocephalus brunnicephalus*) from tropical regions, and South Polar Skuas (*Stercorarius maccormicki*) from Antarctica. Analysis of faecal metagenomes of these birds identified a total of 3,278 distinct genera of bacteria among the faecal samples of these birds, with Firmicutes dominating across all species. In Arctic tern samples, 760 genera were identified, with *Arthrobacter*, *Clostridium*, *Carnobacterium*, and *Yersinia* as the most prevalent. Gull samples displayed the highest genus diversity (1782 genera), primarily *Vagococcus* and *Enterococcus*. South Polar Skua samples contained 736 genera, with *Bacillus*, *Escherichia*, and *Clostridium* as predominant. A total of 124 ARGs were identified, with Arctic terns exhibiting occurrences of highly diverse ARG's, particularly those involved in multidrug resistance, polymyxin, MLS, beta-lactam, and bacitracin antibiotics. *E. coli* from the faecal samples of South Polar Skua showed relatively high degree of resistance, notably multidrug, polymyxin, MLS, tetracycline, bacitracin, and beta-lactam antibiotics. The primary resistance mechanisms observed were efflux pumps for multidrug resistance, followed by MLS and polymyxin resistance in gulls

and the highest resistance showed by *E. coli*. These findings emphasize the role of migratory birds in carrying antibiotic-resistant bacteria, contributing to the spread of ARGs across diverse environments, including polar regions.

Keywords: migratory birds, arctic, antarctic, microbiome, antibiotic resistant gene, resistome

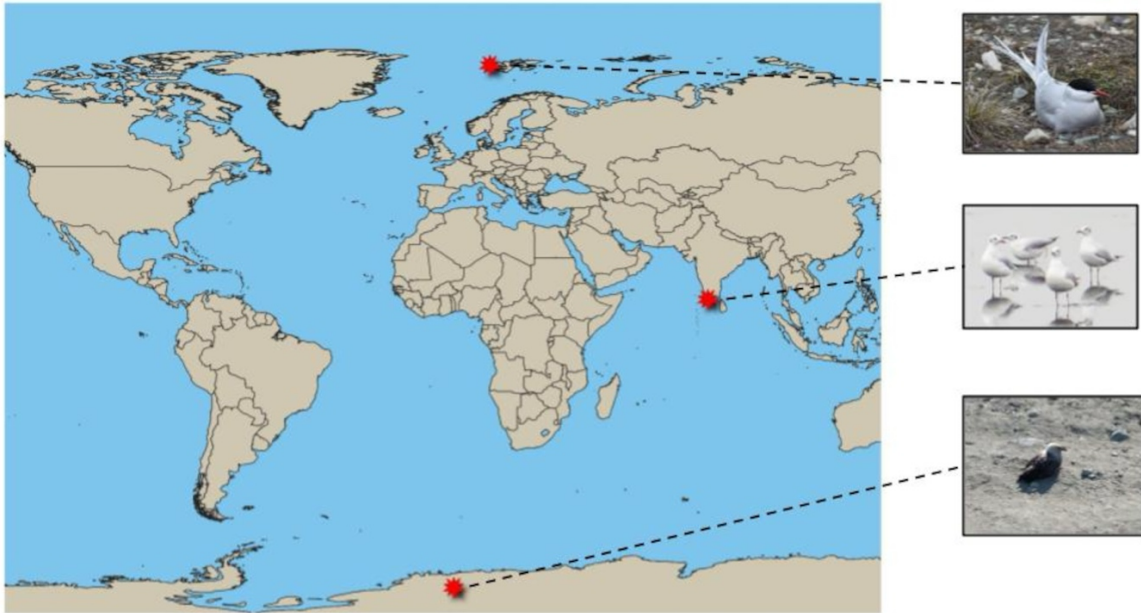


Fig.1. Locations where the study species were sampled: Arctic tern samples from Ny-Alesund, Svalbard; Brown Headed Gull samples from Chanagaram Wetlands, Kerala; and South Polar Skua Samples from Antarctica.

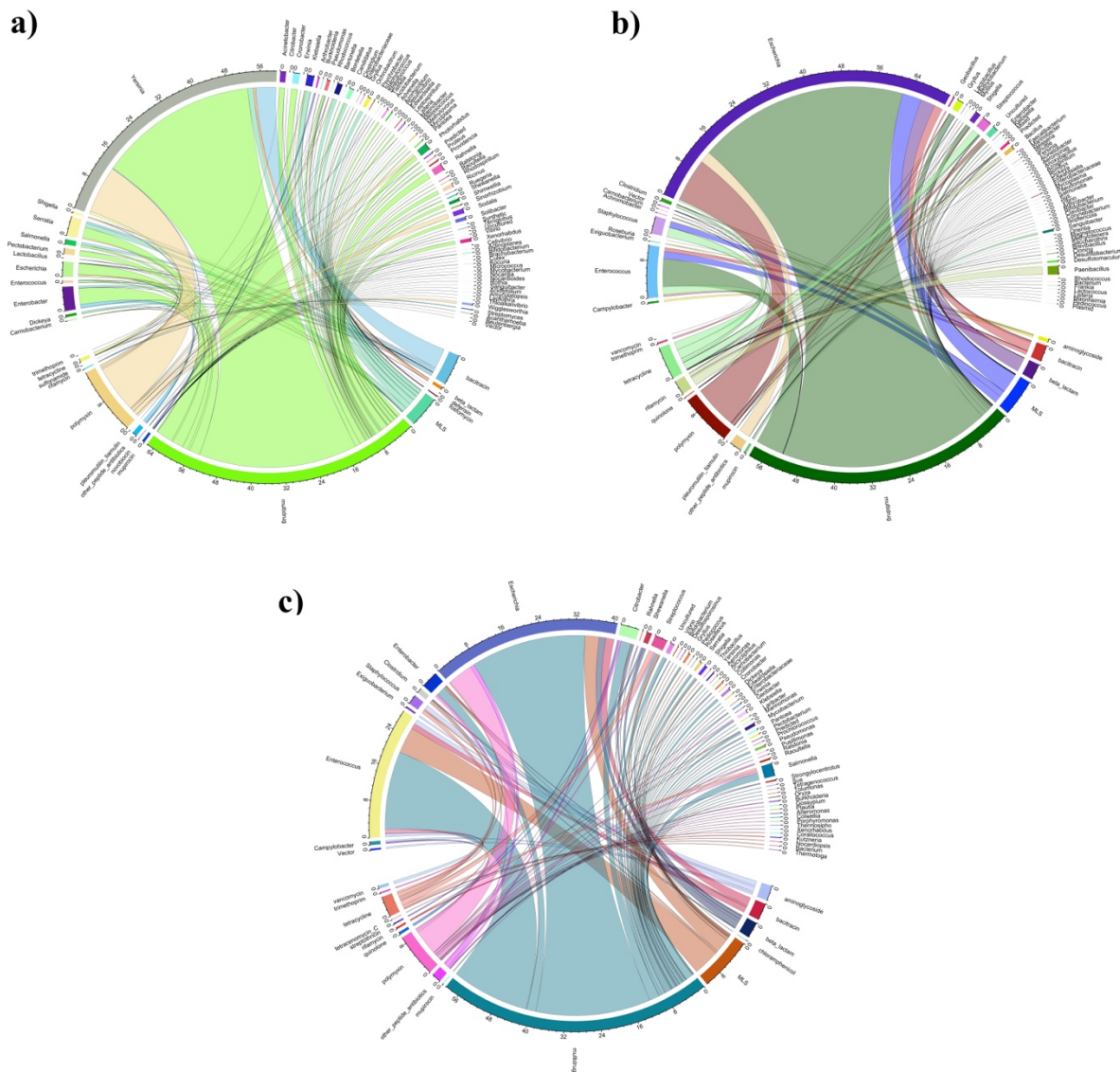


Fig.2. Correlation of AMR type and bacterial genera in a) Arctic Tern, b) South Polar Skua and c) Brown Headed Gull.

Reference

1. Prakash, E. A., Hromádková, T., Jabir, T., Vipindas, P. V., Krishnan, K. P., Hatha, A. M., & Briedis, M. (2022). Dissemination of multidrug resistant bacteria to the polar environment-Role of the longest migratory bird Arctic tern (*Sterna paradisaea*). *Science of The Total Environment*, 815, 152727.
2. Cao, J., Hu, Y., Liu, F., Wang, Y., Bi, Y., Lv, N., & Gao, G. F. (2020). Metagenomic analysis reveals the microbiome and resistome in migratory birds. *Microbiome*, 8, 1-18.
3. Hromádková, T., Pavel, V., Flousek, J., & Briedis, M. (2020). Seasonally specific responses to wind patterns and ocean productivity facilitate the longest animal migration on Earth. *Marine Ecology Progress Series*, 638, 1-12.