

Letter to the Editor

Critical-priority resistant bacteria hidden in ship ballast water: A challenge for global epidemiological surveillance

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Dear Editor,

In the era of unprecedented global connectivity, the phenomenon of globalization has transcended borders, fostering the exchange of cultures and economies across continents. While this interconnectedness has brought numerous benefits, it has also given rise to unintended negative consequences, such as the transboundary dissemination of antimicrobial resistance (AMR) [1]. Among the various vectors facilitating the spread of AMR, transoceanic shipping activities have emerged as novel transmission pathways, highlighting the complex interplay between international trade and the dissemination of superbugs [2].

The ocean waters held in the ballast tanks and cargo holds of ships are known as ballast water (BW), being used for stability and balance. International vessels may carry a mix of BW collected during navigation to different ports. In this context, it is often collected in one location and discharged in another, leading to concerns about the potential spread of various invasive aquatic organisms (e.g., crustaceans, bivalves, and fishes) that could compete with native fauna and cause environmental imbalances. Indeed, the introduction of new organisms to native ecosystems was recognized as one of the four greatest threats to the world's oceans by the International Maritime Organization (<https://www.imo.org/en/OurWork/Environment/Pages/BWMConventionandGuidelines.aspx>). Therefore, it is plausible that clinically relevant bacterial pathogens and their genetic determinants, emerging in a specific country, could be also silently introduced to other countries through this transoceanic pathway (Fig. 1).

A prime example of this epidemiological event could be the report of international high-risk clone of the extended-spectrum- β -lactamase (CTX-M-27)-producing clade C1 of *Escherichia coli* sequence type 131 arriving in Brazil, in 2016 [3]. Classified as critical priority pathogens by the World Health Organization (WHO), strains of this lineage have been increasingly detected across Europe and Asia, being early identified in Brazil in bivalves used as marine sentinels of anthropogenic pollution of ecosystems associated with the largest international Latin America seaport. Noteworthy, only after this environmental report, the first cases of human infections [4] and fresh vegetable contamination [5] by this

lineage were described in Brazil. While the epidemiological link of this phenomenon could be speculative, the introduction of novel AMR pathogens into seaport areas, with subsequent spread to other sources, could be presumed as demonstrated in the movement of imported food and travelers across borders [1].

Although the role of BW in the spread of AMR has been recently recognized as a transnational and intercontinental issue by the UN Environment Programme (<https://www.unep.org/resources/superbugs/environmental-action>), this problem remains inadequately investigated. We systematically evaluated the global scientific literature reporting the occurrence of AMR in BW. In the last two decades, only nine studies have addressed this issue. These studies have been performed in Asian (China, India, Malaysia, Singapore, and Türkiye), African (South Africa), and American (United States) countries and most of them have focused on *Vibrio* species that are not usually carriers of clinically important antimicrobial determinants. Furthermore, no study has so far identified WHO critical priority bacteria in BW. Another important issue is the lack of studies using the newest DNA-based technologies, including whole-genome sequence-based analysis, which can predict the transmission routes of superbugs and the factual impact of BW in AMR evolution (Table S1). Hence, it seems that there are many epidemiological gaps regarding the international exchange of WHO critical priority bacteria through BW, and the neglect of their transboundary spread via this vehicle is evident.

In summary, we draw attention to the need for epidemiological genomic investigation for tracking WHO critical priority bacteria in BW. The main obstacles that hinder the development of robust studies on this topic are the complex nature of shipping and obtaining permissions for collecting and processing BW samples. Therefore, the global scientific community and environmental authorities should work towards developing strategies to monitor and strengthen the surveillance of AMR through transoceanic activities.

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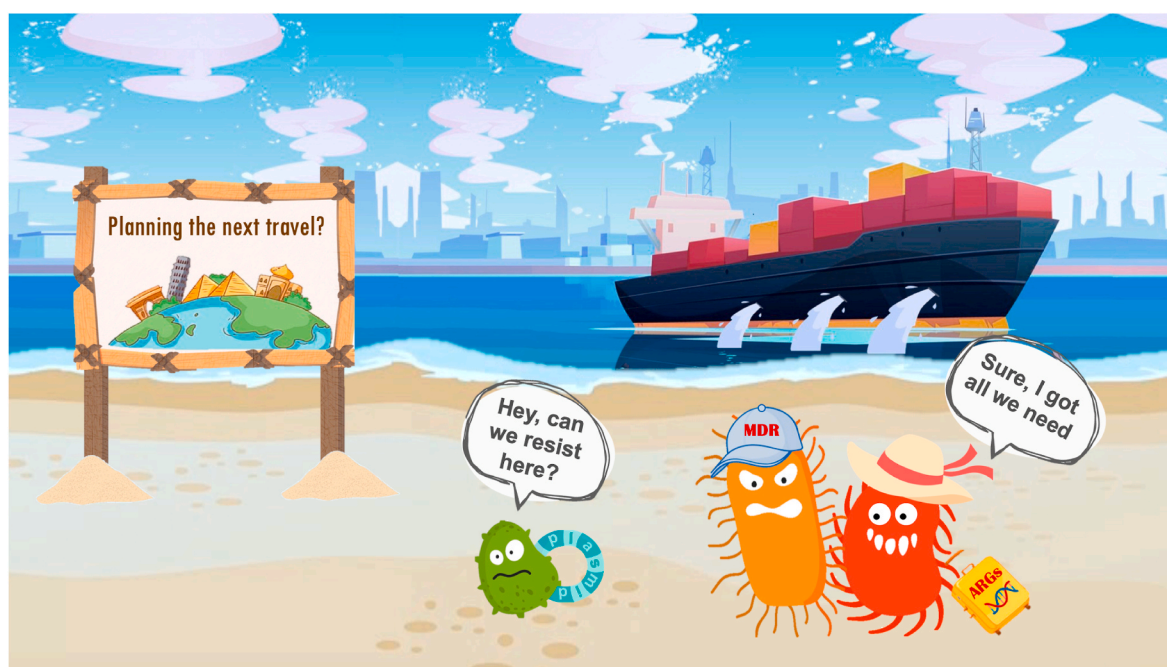


Fig. 1. This cartoon aims to illustrate the international transmission of AMR through ballast water as follows: i) multidrug-resistant (MDR) bacteria and antimicrobial resistance genes (ARGs) are captured in one country and transported via maritime traffic to other countries; ii) MDR bacteria and ARGs initially enter seaport areas; iii) MDR bacteria interact with the resident microbiota and exchange genetic information; iv) MDR bacteria and ARGs are introduced into their new environment and spread to other sources.

CRediT authorship contribution statement

Fábio Parra Sellera: Conceptualization, Data curation, Writing – original draft, Writing – review & editing. **Nilton Lincopan:** Conceptualization, Data curation, Writing – original draft, Writing – review & editing. **Elia Guedes Stehling:** Conceptualization, Data curation, Writing – original draft, Writing – review & editing. **João Pedro Rueda Furlan:** Conceptualization, Data curation, Writing – original draft, Writing – review & editing.

Declaration of competing interest

None declared.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.nmni.2024.101236>.

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