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Letter to the Editor

Sand as a vehicle for exposing of humans and animals to WHO priority pathogens: A public health issue hidden in the ground

Dear Editor,

Antimicrobial resistance (AMR) poses a serious global public health threat that demands strategies for improving community awareness and continuous surveillance to determine the prevalence, risk factors, and vehicles of transmission of antimicrobial-resistant bacteria [1]. Although the environment is dominant in the evolution and dissemination of AMR, the role of sand in the dissemination of AMR and pathogens is rarely addressed [2].

Beach and river sands are important for the development of coastal and urban areas, especially those used for recreation, tourism, and sports. The quality of sand is closely related to the quality of water, which increases the risk of contamination of multidrug-resistant pathogens mainly by sewage discharged into water ecosystems [3]. Another potential route includes sand contamination by animal feces [4]. Consequently, humans and animals may be directly and indirectly exposed to contaminated sands, increasing the risk of colonization and/or infections. Indeed, for sensitive populations, the risk for long-term effects is recognized [5].

Microbial indicators of fecal pollution have been the most frequently studied in sand samples [6]; however, there are gaps regarding the occurrence of WHO priority bacterial pathogens [7] in this sector. Reviewing the global scientific literature, we identified 15 studies documenting the occurrence of these pathogens in the Americas, Africa, and Asia. Methicillin-resistant *Staphylococcus aureus* (MRSA) is the most prevalent WHO priority bacteria isolated from sand samples, being described in the United States (Fig. 1), South Africa (Eastern Cape), and Turkey (Northern Cyprus). Additional reports include the presence of vancomycin-resistant enterococci and carbapenem-resistant *Pseudomonas aeruginosa* strains in Malaysia (Selangor) and Brazil (São Paulo), respectively (Table S1). Due to the prevalence of studies in the United States, our discussion has been limited.

Most of the bacteria were obtained from sand of public beaches; however, there is a report on a beach club. It is noteworthy to remark that there was an increase of sports and training practiced in sands in the last decade, which contribute to sand-to-human transmissions. The identification of MRSA belonging to the sequence type (ST) 8 on the sand of a marine rehabilitation center with subsequent animal infection by the same clone [8] underlines the role of sand in the environmental transmission of WHO priority bacteria. A great diversity of MRSA clones commonly reported in hospital- and community-acquired human infections [9] were identified in sand samples from the United States. Worryingly, ST8-SCC*mec* IV, known as USA300 North American epidemic clone [10], was prevalent in sands (Table S1), evidencing its survival in this environment and a possible risk of transmission to humans and animals.

In summary, we present global data of WHO priority bacteria recovered from sand samples and recognize that the prevalence of these pathogens in this sector is underestimated. Environmental contamination might result in cross-transmissions to humans and animals that can act as asymptomatic carriers of these potential pathogens. This can also contribute to the spread within the household environment. In light of this, we call attention to this matter and encourage epidemiological surveillance studies for mapping the incidence, AMR patterns, and genomic data of these pathogens that seem to be hidden from the view of public health authorities.

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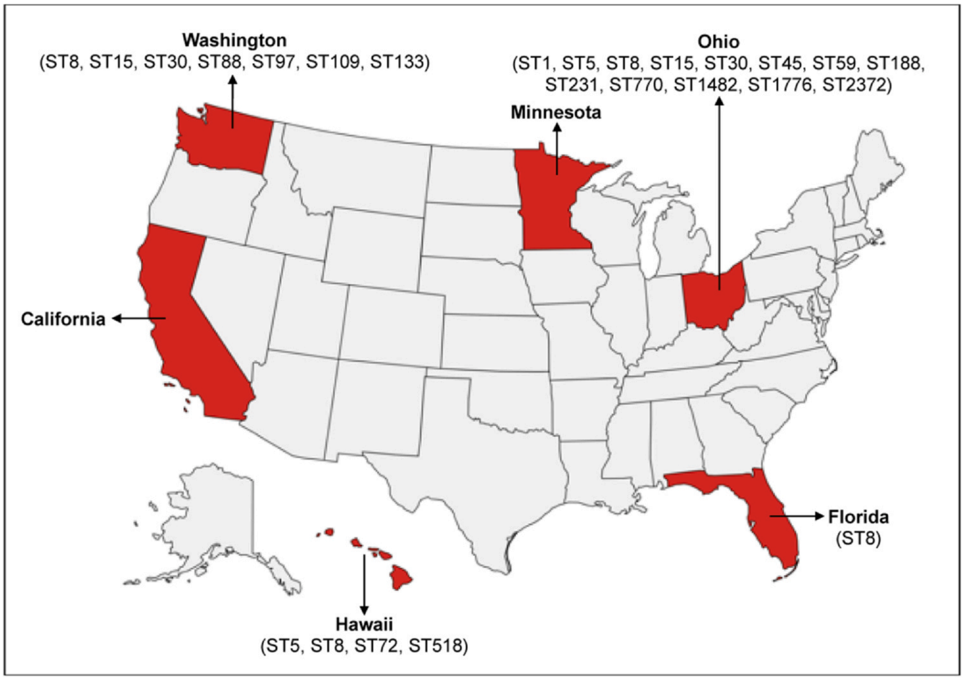

Fig. 1. Distribution of MRSA belonging to different STs recovered from sand samples in the United States. Data were retrieved from PubMed database via the National Center for Biotechnology Information (NCBI) interface (accessed on May 30, 2023).

Ethical approval

Not required.

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Declaration of Competing Interest

The authors have no conflict of interest to declare.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.jiph.2023.10.015.

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