Unifying genomic datasets: Leveraging metadata standardization for AMR interpretation in a One-Health context

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Abstract

Antimicrobial resistance (AMR) is a global health concern necessitating a holistic approach, integrating data across human, animal, and environmental health domains, known as the One-Health perspective. The advent of high-throughput genomics technologies has revolutionized the study of AMR, generating vast amounts of data that would provide the highest practicable level of structural detail on the individuating traits of an organism. In our comprehensive global study, genomic datasets of ESKAPE pathogens available from different continents were analyzed using different bioinformatics tools to identify AMR genetic traits and understand the global and region-wise spatiotemporal trends in antimicrobial resistance. The genomic data will also be correlated with other collected metadata and antibiotic consumption data to enable an important contribution to disease control and prevention, particularly in designing diagnostics and effective intervention strategies for controlling ESKAPE pathogens. A notable challenge was identified throughout our study—the lack of unified metadata in genomic datasets across public databases—which impedes the effective utilization of invaluable genomic information. During the presentation in this conclave, we will explore the critical role of metadata standardization in unifying genomic datasets and its leverage in maximizing AMR insights within the One-Health perspective. Researchers can enhance data interoperability, facilitate meaningful comparisons, and derive comprehensive insights into AMR dynamics across various sectors by employing consistent metadata standards. Such a unified approach should emphasize the necessity of a standardized metadata framework for effectively utilizing genomic data, advancing our understanding of AMR within the broader One-Health perspective.

Keywords: One-Health, ESKAPE pathogens, Antimicrobial resistance, Metadata