

Development of a metagenomics assisted tool for AMR surveillance

Abstract

Environmental antimicrobial resistance (AMR) is a major public health concern, yet surveillance across interconnected environmental sectors remains limited. This study investigated AMR across six environmental sectors in India using integrated microbiological, molecular, physicochemical, and metagenomic approaches. Wastewater-associated environments exhibited greater resistance burdens than agricultural and surface water samples. Correlation analysis and Elastic Net modelling identified associations between resistance determinants, microbial taxa, and environmental pollutants. *Acinetobacter*, *Polynucleobacter*, conductivity, chloride, and cobalt emerged as potential predictors of AMR. The findings highlight the multifactorial nature of AMR and the potential of metagenomics-assisted predictive modelling for environmental surveillance, warranting validation using larger, independent datasets.