Scenario of antibiotic resistance in Pakistan: A systematic review

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Abstract

Background: During the last six decades, extensive use of antibiotics has selected resistant strains, increasing the rate of fatal infectious diseases, and exerting an economic burden on society. This situation is widely accepted as a global problem, yet its degree is not well elucidated in many regions of the world. Untill now, no systemic analysis of antimicrobial resistance (AMR) in Pakistan has been published. The current study aims to describe the antibiotic-resistance scenario of Pakistan from human samples of the last ten years, to find the gaps in surveillances and methodology and recommendations for researchers and prescribers founded on these outcomes.

Method: Original research articles analyzed the pattern of antibiotic resistance of any World Health Organization (WHO) enlisted priority pathogens in Pakistan (published onward 2009 till March 2020), were collected from PubMed, Google scholar, and PakMedi Net search engines. These articles were selected based on predefined inclusion and exclusion criteria. Data about the study characteristics and antibiotic-resistance for a given bacterium were excluded from literature. Antibiotic resistance to a particular bacterium was calculated as a median resistance with 95% confidence interval (CI).

Results: Studies published in the last ten years showed that urinary tract infection (UTI) is the most reported clinical diagnosis (16.1%) in Pakistan. E. coli were reported in 28 (30.11%) studies showing high resistance to antibiotics' first line. Methicillin resistant staphylococcus aureus (MRSA) was found in 49% of S. aureus' total reported cases. Phenotypic resistance pattern has mostly been evaluated by disk diffusion method (DDM) (82.8%), taken clinical laboratory standards institute (CLSI) as a breakpoint reference guideline (in 79.6% studies). Only 28 (30.11%) studies have made molecular identification of the resistance gene. blaTEM (78.94% in Shigella spp) and blaNDM-1 (32.75% in Klebsiella spp) are the prominent reported resistant genes followed by VanA (45.53% in Enterococcus spp), mcr-1 (1.61% in Acinetobacter spp), and blaKPC-2 (31.67% in E. coli). Most of the studies were from Sindh (40.86%), followed by Punjab (35.48%), while Baluchistan's AMR data was not available.

Conclusion: Outcomes of our study emphasize that most of the pathogens show high resistance to commonly used antibiotics; also, we find gaps in surveillances and breaches in methodological data. Based on these findings, we recommend the regularization of surveillance practice and precise actions to combat the region's AMR.

Biography

Hazrat Bilal is from Pakistan, currently doing a PhD (Microbiology 3rd year) at the Institute of Health Sciences, Anhui University. He did his bachelor's and master from Hazara University and Khyber Medical University, Pakistan, respectively. Due to his good academic carrier, he was two time awarded gold medals from respective universities at Pakistan. His research focus is antibiotic resistance bacteria, especially mcr-1 blaKPC-2, and blaNDM-1 harboring E. coli and K. pneumoniae.

Publications

Antibiotic resistance in Pakistan: a systematic review of past decade

Detection of mcr-1 gene in extended-spectrum β-Lactamase-Producing Klebsiella pneumoniae from human urine samples in Pakistan

Detection of MCR-1 Gene in Multiple Drug Resistant Escherichia coli and Klebsiella pneumoniae in Human Clinical Samples from Peshawar, Pakistan

Plasmid-mediated mcr-1 gene in Acinetobacter baumannii and Pseudomonas aeruginosa: first report from Pakistan