

Antibiotyping and Genotyping of Extensively Drug-Resistant (XDR) *Salmonella* Sp. Isolated from Clinical Samples of Lahore, Pakistan

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ABSTRACT

Background: The rise of extensively drug-resistant (XDR) *Salmonella* strains is a critical global health challenge, particularly in developing countries like Pakistan, where antimicrobial resistance has surged in recent years. In 2016, Pakistan witnessed its first outbreak of XDR *Salmonella* Typhi, characterized by resistance to nearly all first- and second-line antibiotics, significantly complicating treatment protocols. The global dissemination of XDR strains, facilitated by international travel, continues to be a major public health concern. This study aims to evaluate the prevalence and resistance patterns of XDR *Salmonella* in Lahore, a region that has been heavily affected by these strains.

Objective: The primary aim of this study was to evaluate the prevalence of XDR *Salmonella* among the local population of Lahore, Pakistan, and to investigate the genotypic characteristics of the isolated strains to better understand the mechanisms driving antibiotic resistance.

Methods: A total of 200 blood samples were collected from patients suspected of typhoid fever. Bacterial identification was conducted using biochemical, serological, and molecular techniques, with antibiogram analysis performed to classify the isolates as multidrug-resistant (MDR) or XDR. Genetic analysis was also conducted to detect antibiotic resistance genes, such as *ampC* and *gyrA*.

Result: Of the 200 samples, 157 isolates were identified as *Salmonella* Typhi and 23 as *Salmonella* Paratyphi. The antibiogram revealed that 67.2% of the isolates were MDR, while 34.4% were XDR. Key antibiotic resistance genes, including *ampC* and *gyrA*, were found to contribute to resistance against first-line antibiotics and third-generation cephalosporins.

Conclusion: The study highlights the alarming prevalence of XDR *Salmonella* strains in Lahore, underscoring the urgent need for targeted therapies and improved surveillance systems. The detection of significant resistance genes in the isolates calls for enhanced antimicrobial stewardship to mitigate the growing public health threat posed by these resistant pathogens.

Significance: This research adds to the expanding body of evidence on the spread and evolution of XDR *Salmonella* strains. It advocates for a global response to antimicrobial resistance, particularly in regions with limited healthcare infrastructure, where resistant strains are likely to proliferate without adequate interventions.

Keywords: XDR *Salmonella* Typhi, MDR *Salmonella*, *ampC* and *gyrA* Resistance, Cephalosporin Resistance, Antimicrobial Resistance.