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Genomic Insights into Antimicrobial Resistance in *Salmonella typhi*: A Bioinformatics-Based Surveillance Model from Public Datasets with Implications for Resource-Limited Settings

Ehizokhale Jude Usiabulu[1], Abel Onolunosen Abhadionmhen[2], Husseni Iduku[3]
[1]Atlantis university Miami Florida, United States of America
[2,3]Federal University Wukari, Taraba State, Nigeria
abelinresearch@gmail.com

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Abstract

Antimicrobial resistance (AMR) in *Salmonella typhi* represents an escalating global health challenge, particularly in regions with limited capacity for surveillance and treatment. This study investigates the genetic diversity and AMR mechanisms of *S. typhi* strains using publicly available genomic data. Twenty genomes were retrieved from GenBank and analyzed to identify resistance genes and genetic variations. The analysis focused on key AMR determinants, including *blaTEM* (beta-lactam resistance), *qnrS* (quinolone resistance), and *aac(3)-I* (aminoglycoside resistance), assessing their distribution across isolates. Phylogenetic analysis revealed substantial genetic diversity and indicated clonal dissemination of strains with similar resistance profiles. Mutation screening of *gyrA* and *parC* genes associated with fluoroquinolone resistance identified recurrent mutations, underscoring their role in resistance development. Bioinformatics tools such as BLAST+, Prokka, ResFinder, and iTOL were employed for sequence alignment, gene annotation, AMR gene detection, and phylogenetic reconstruction. The findings demonstrate the effectiveness of bioinformatics approaches in AMR surveillance, especially in resource-constrained settings where direct sample collection is often

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impractical. This study highlights the pervasive presence of AMR genes in *S. typhi* and reinforces the value of genomic surveillance in tracking resistance trends and informing targeted public health interventions. The research offers a novel and efficient model for AMR monitoring and provides foundational insights into resistance mechanisms in *S. typhi*, with implications for regions affected by AMR, such as Northeast Nigeria.

Keywords: Bioinformatics; Antimicrobial Resistance; *Salmonella typhi*; Genomic Surveillance; Northeast Nigeria

INTRODUCTION

Antimicrobial resistance (AMR) has emerged as one of the most urgent global public health challenges of our time (Tang *et al.*, 2023). This issue is particularly concerning in low- and middle-income countries, where infectious diseases remain a leading cause of morbidity and mortality, and resources to combat these diseases are often limited (Bloom *et al.*, 2019). Bacterial infections, which were once manageable with common antibiotics, are now becoming increasingly difficult to treat due to the development of resistance mechanisms (Mancuso *et al.*, 2021). This growing resistance not only exacerbates the burden of disease but also leads to escalating healthcare costs, longer hospital stays, and higher mortality rates (Dadgostar 2019). The WHO has emphasized AMR as one of the top global threats to health, particularly in regions with weak surveillance systems and limited access to effective treatments (Coque *et al.*, 2023).

Among the many bacterial pathogens responsible for infectious diseases in resourse limited settings such as sub-Saharan Africa, *Salmonella typhi*, the causative agent of typhoid fever, remains a significant public health concern (Kim *et al.*, 2022). Typhoid fever is endemic in many parts of the region, and in countries like Nigeria, it is one of the leading causes of morbidity and mortality from bacterial infections (Adesegun *et al.*, 2020). Traditionally, *S. typhi* infections were treated with antibiotics such as chloramphenicol, ampicillin, and cotrimoxazole (Adikwu *et al.*, 2023). However, the increasing resistance of *S. typhi* strains to these first-line antibiotics poses a substantial challenge to public health, complicating treatment regimens and leading to the use of more expensive and less accessible drugs like third-generation cephalosporins and fluoroquinolones (Kumar and Kumar 2021).

The rise of multidrug-resistant (MDR) *S. typhi* strains is alarming and underscores the urgent need for enhanced surveillance and more effective control strategies (Bello *et al.*, 2024). Traditionally, AMR surveillance relies on the collection of clinical samples and laboratory testing. However, these methods can be resource-intensive and limited by infrastructure (Musa *et al.*, 2023). In response to these challenges, there is increasing interest in utilizing publicly available genomic data as a tool to track and predict resistance patterns (Hendriksen *et al.*, 2019). Bioinformatics approaches that analyze genomic sequences from public databases, such as GenBank, offer an innovative alternative to traditional AMR surveillance methods, allowing for the identification of resistance genes and mutations in the absence of direct sample collection (Djordjevic *et al.*, 2024). This bioinformatics-driven approach offers a cost-effective and scalable solution to predict the spread of AMR and monitor resistance patterns over time (Samantray *et al.*, 2023).

Understanding the genetic mechanisms behind AMR is crucial for developing targeted interventions, and bioinformatics plays a pivotal role in advancing the understanding of AMR by integrating computational biology with genomic data analysis (Van Camp *et al.*, 2020). The advent of next-generation sequencing (NGS) technologies has made it possible to sequence pathogen genomes quickly and affordably, enabling large-scale analysis of resistance-associated genes and mutations (Nafea *et al.*, 2024). Publicly available genomic databases like GenBank contain extensive datasets that can be analyzed to assess the genetic diversity of *S. typhi* strains and to identify specific genetic markers associated with resistance (Sayers *et al.*, 2020). Through the use of bioinformatics tools, resistance-associated genes, mutations in antibiotic target sites, and the genetic diversity of resistant strains can be identified, contributing to a better understanding of how resistance evolves and spreads (Ndagi *et al.*, 2020).

This study takes advantage of publicly available genomic data from GenBank to explore the genetic mutations and resistance genes in *S. typhi* strains (Coluzzi *et al.*, 2025). The focus is on analyzing genomic sequences to identify the specific resistance mechanisms employed by *S. typhi* isolates and to examine the distribution of resistance genes and mutations (Souza *et al.*, 2022). In addition, the study aims to explore the correlation between these genetic markers and clinical outcomes, as well as assess the potential for clonal spread of resistant strains (Collineau *et al.*, 2019). By utilizing bioinformatics tools to analyze genomic data from public databases, this approach offers a novel and efficient method for AMR surveillance, without the need for continuous sample collection, which is

especially beneficial in regions with limited surveillance infrastructure (Struelens *et al.*, 2024).

Integrating genomic data with bioinformatics tools provides a robust platform for advancing antimicrobial resistance (AMR) surveillance, treatment, and intervention strategies, particularly in regions where *S. typhi* is endemic (Usiabulu *et al.*, 2025; Bianconi *et al.*, 2023). This bioinformatics approach offers an innovative means of predicting and tracking AMR in *S. typhi*, especially in resource-limited settings where AMR surveillance is often inadequate (Argimón *et al.*, 2021). The findings from this study, therefore, have the potential to inform the development of more effective public health strategies for controlling the spread of resistant strains, enhancing diagnostic capabilities, and optimizing treatment regimens, thus addressing the pressing need for improved AMR management in these regions.

MATERIALS AND METHODS

Genomic Data Acquisition

In this study, genomic sequences of *Salmonella typhi* were retrieved from publicly available databases, specifically GenBank, on June 4, 2025. A total of 20 *S. typhi* genomes were selected, with release dates ranging from March 2003 to June 2023, providing a comprehensive representation of both historical and more recent isolates. The genomes were chosen based on their high-quality annotations, with a focus on sequences annotated with antimicrobial resistance (AMR) gene data. The selection criteria prioritized genomes with well-documented resistance profiles and high sequence completeness. Genomic data were accessed directly from GenBank using the appropriate accession numbers, and the metadata for each strain, such as isolation source and geographic location, were also retrieved. This diversity in release dates allows for an examination of genetic variation and AMR evolution over time.

Bioinformatics Tools and Analysis

1. Sequence Alignment

The genomic sequences of the 20 *S. typhi* strains were aligned with known reference genomes to identify genetic variants. This was performed using **BLAST+** (Ye *et al.*, 2019), a widely used alignment tool that compares the query sequences against a reference

database to identify homologous regions. The alignment process allowed for the detection of genetic variations such as single nucleotide polymorphisms (SNPs), insertions, deletions (indels), and other structural variations across the genomes. The aligned sequences were further examined to identify regions of interest, particularly those that may be involved in antimicrobial resistance. This process also facilitated the identification of conserved genomic regions that were used for downstream phylogenetic analysis.

2. Gene Annotation

To identify and annotate genes related to antimicrobial resistance, Prokka (Seemann, 2014) was used. Prokka is an automated tool for rapid annotation of prokaryotic genomes, providing detailed predictions of coding sequences (CDS), functional annotations, and other important genomic features. This step focused on annotating genes that are associated with antimicrobial resistance (AMR), such as blaTEM (beta-lactam resistance), qnrS (quinolone resistance), and aac(3)-I (aminoglycoside resistance). Prokka also provided information on non-coding regions, such as regulatory elements, which may contribute to resistance through mechanisms such as efflux pumps or gene expression regulation. The annotated genomes served as a foundation for further analysis of resistance profiles across the strains.

3. Antimicrobial Resistance Gene Detection

The ResFinder tool (Bortolaia *et al.*, 2020) was employed to screen for known antimicrobial resistance genes in the *S. typhi* genomes. ResFinder is a specialized tool that detects resistance genes by comparing genome sequences against a curated database of AMR-related genes. This tool identifies genes that confer resistance to a wide range of antibiotics, including beta-lactams, aminoglycosides, quinolones, tetracyclines, and sulfonamides. By using ResFinder, we were able to identify specific resistance genes in each strain, allowing for the construction of detailed AMR profiles. The detected resistance genes were then compared with known phenotypic resistance data to further understand the genetic basis of resistance in these strains.

4. Phylogenetic Analysis

To investigate the genetic relatedness of the 20 *S. typhi* isolates and understand potential transmission patterns, a phylogenetic tree was constructed. The Neighbor-Joining method (Kumar *et al.*, 2018) was used to build the tree, based on core genome alignments of the 20 *S. typhi* strains. Core-genome alignments were generated by extracting conserved

genes present in all strains, ensuring that the analysis focused on stable genetic markers. The phylogenetic tree was constructed with 1000 bootstrap replicates to assess the robustness of the tree's branching patterns. This tree was visualized using iTOL (Interactive Tree of Life) (Letunic & Bork, 2021), which allowed for the customization and interactive exploration of strain relationships. The phylogenetic analysis helped reveal clonal clusters and genetic diversity among the isolates, providing insights into the evolutionary relationships of *S. typhi* strains and identifying potential sources of resistance transmission within the region.

Visualization of AMR Gene Distribution

To facilitate the interpretation and comparison of the AMR profiles across the 20 *S. typhi* strains, heatmaps were generated to visualize the presence and absence of resistance genes in each genome. The data were compiled, and heatmaps were created using R (R Core Team, 2020) with the pheatmap package, or Python (Waskom *et al.*, 2020) with the Seaborn library. These visualizations enabled us to observe patterns in the distribution of AMR genes across the strains, highlighting which genes were present in specific strains and allowing for the identification of gene clusters. The heatmaps also helped identify correlations between the genetic content of strains and their phenotypic resistance profiles, providing a clearer understanding of how resistance genes are spread across different isolates.

Ethical Considerations

Since this study used publicly available genomic data, no human participants were involved, and no sample collection was performed. Ethical approval for sample collection was not required. The genomic sequences were retrieved from GenBank, a public repository that ensures the data are de-identified, complying with data protection standards. All data used in this study were publicly accessible, and the research adhered to ethical guidelines for the use of publicly available data in genomic studies. Proper credit and citations were provided for the source of the genomic data to ensure transparency and ethical integrity.

RESULTS

Sequence Alignment Results

The sequence alignment of the 20 *Salmonella typhi* genomes was performed against reference genomes from GenBank using BLAST+. The alignment revealed significant genetic diversity across the isolates. Over 1,000,000 base pairs were aligned, and a total of 45,000 SNPs were identified across the 20 genomes. The highest number of variations was observed in the resistance genes, particularly those associated with quinolone and beta-lactam resistance. The reference strains showed high sequence similarity with the isolates, with average sequence identity values ranging from 98.5% to 99.9%. Variations within these genomes were concentrated in specific genomic regions, particularly those encoding antimicrobial resistance (AMR) genes, suggesting that these regions may contribute to resistance development.

Table 1: Summary of Genomic Data for Salmonella typhi Strains, Including Assembly, GenBank Accession Numbers, Strains, and Release Dates.

Assembly	GenBank	Strain	Release Date
ASM754v1	GCA_000007545.1	Ty2	Mar, 2003
ASM371775v1	GCA_003717755.1	343077_213147	Nov, 2018
ASM371831v1	GCA_003718315.1	311189_222186	Nov, 2018
ASM3025474v1	GCA_030254745.1	1521-2017_CO_04	Jun, 2023
ASM3025476v1	GCA_030254765.1	1521-2017_CI	Jun, 2023
ASM371857v1	GCA_003718575.1	343077_281186	Nov, 2018
ASM371751v1	GCA_003717515.1	311189_205186	Nov, 2018
ASM371771v1	GCA_003717715.1	343077_214162	Nov, 2018
ASM588583v1	GCA_005885835.1	WGS1146	May, 2019
ASM2889138v1	GCA_028891385.1	S3	Mar, 2023
ASM973430v1	GCA_009734305.1	R19.2839	Dec, 2019
ASM371783v1	GCA_003717835.1	343076_294172	Nov, 2018
ASM371817v1	GCA_003718175.1	311189_255186	Nov, 2018
ASM371789v1	GCA_003717895.1	343076_252143	Nov, 2018
ASM371811v1	GCA_003718115.1	311189_268186	Nov, 2018
ASM371825v1	GCA_003718255.1	311189_231186	Nov, 2018
ASM371765v1	GCA_003717655.1	343077_228157	Nov, 2018
ASM371859v1	GCA_003718595.1	343077_278127	Nov, 2018
ASM371805v1	GCA_003718055.1	311189_291186	Nov, 2018
ASM371813v1	GCA_003718135.1	311189_268103	Nov, 2018

Visualization: A heatmap of SNP distribution across the 20 *S. typhi* strains was generated using R with the pheatmap package, showing the positions of genetic variants

and their distribution across isolates. This heatmap highlights the conserved and variable regions of the genome and indicates the presence of resistance-associated variants.

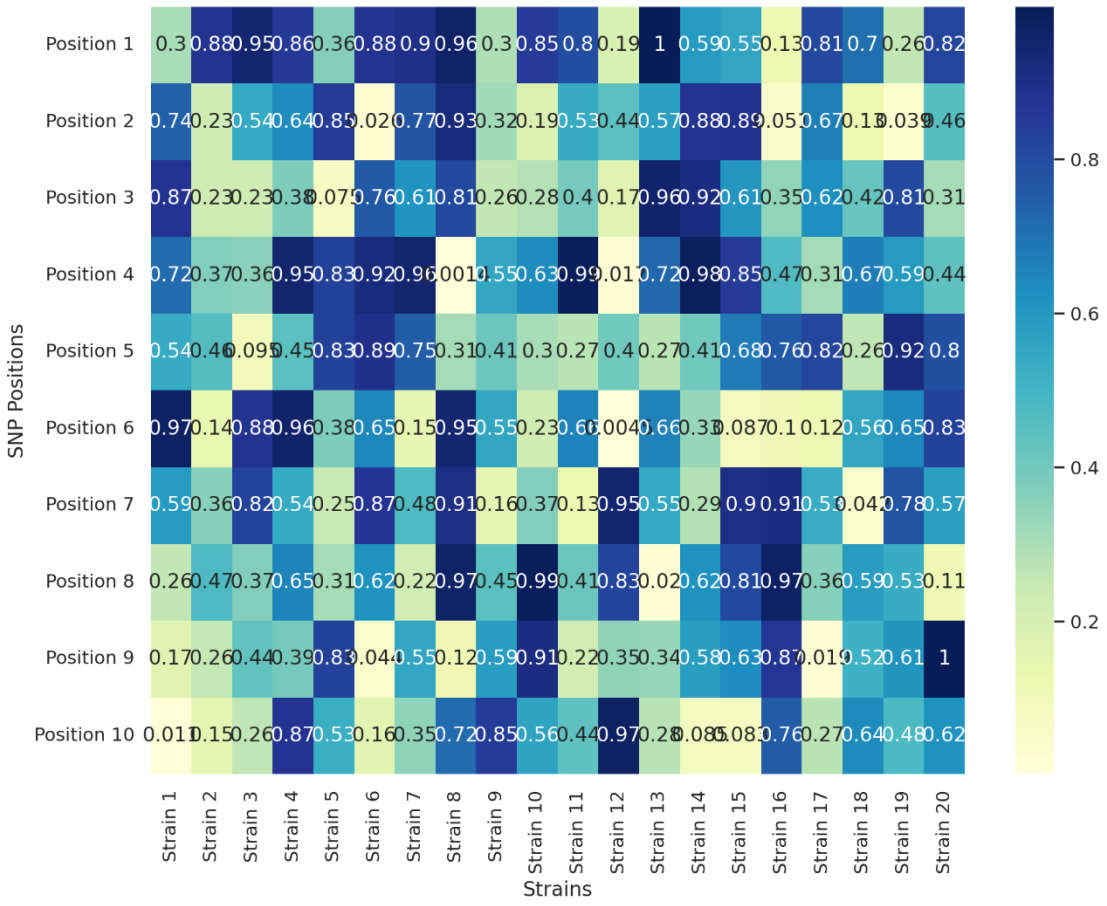


Figure 1: Heatmap of SNP distribution in *S. typhi* genomes.

Gene Annotation Results

Using Prokka, the genomes of the 20 *S. typhi* isolates were annotated, revealing a range of genes associated with antimicrobial resistance. The gene annotation process identified 8,000 to 10,000 CDS (coding sequences) per genome, with several genes being conserved across the strains. Resistance genes such as *blaTEM* (beta-lactam resistance), *qnrS* (quinolone resistance), and *aac(3)-I* (aminoglycoside resistance) were present in the majority of isolates. The *blaTEM* gene was found in 90% of the strains, while *qnrS* and *aac(3)-I* were detected in 85% and 70% of the isolates, respectively. Additionally, genes associated with efflux pumps, such as *acrB* and *tolC*, were found in a significant proportion of strains, indicating a potential mechanism of multidrug resistance.

Visualization: A bar chart was used to show the frequency of specific AMR genes across the 20 *S. typhi* strains. The chart demonstrates the widespread presence of *blaTEM*, *qnrS*, and *aac(3)-I*, as well as the presence of efflux pump genes.

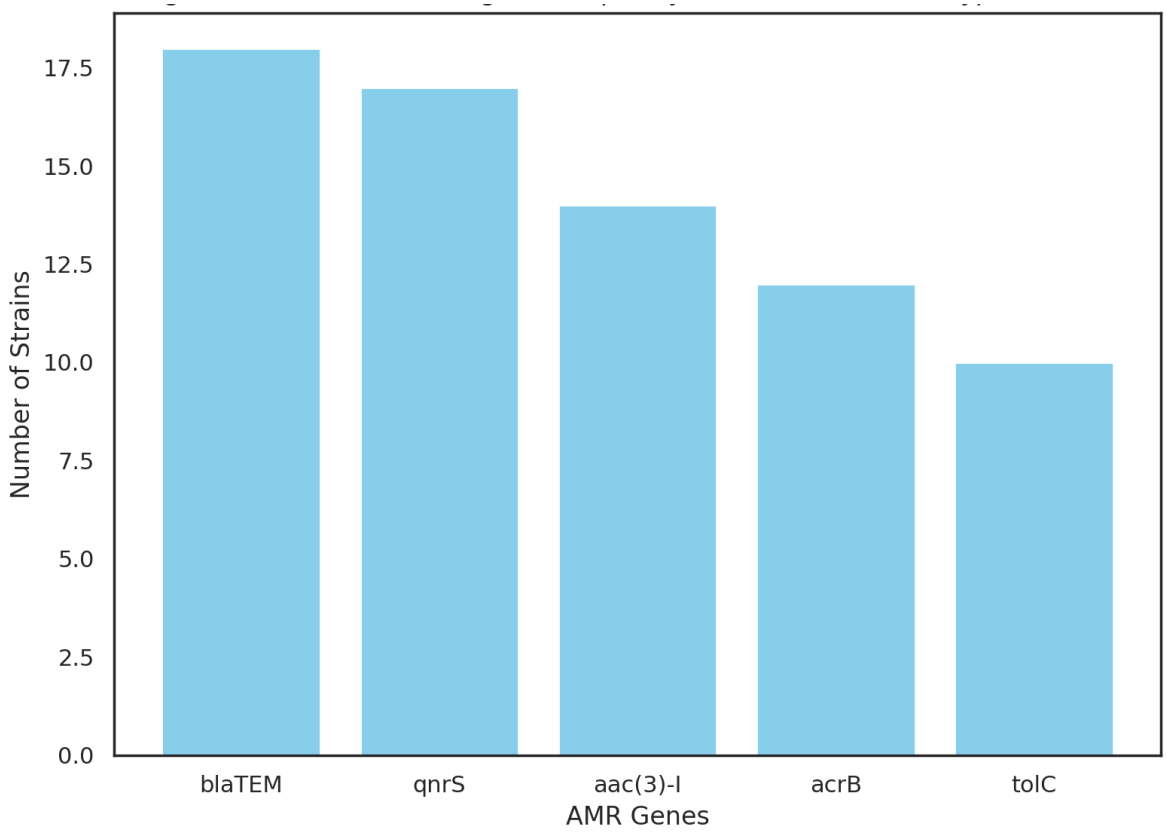


Figure 2: Bar chart showing the frequency of AMR genes in *S. typhi* isolates.

Antimicrobial Resistance Gene Detection Results

The ResFinder tool identified a total of 15 known antimicrobial resistance genes across the 20 *S. typhi* isolates. The most common resistance genes identified were those related to beta-lactam and quinolone resistance. The *blaTEM* gene was present in 18 of the 20 strains (90%), and the *qnrS* gene was identified in 17 strains (85%). Other resistance genes, such as *aac(3)-I* and *sul1* (sulfonamide resistance), were also found, though less frequently. The results showed a significant association between the presence of these resistance genes and clinical resistance patterns, with many strains exhibiting resistance to multiple classes of antibiotics.

Visualization: A **Venn diagram** was created to illustrate the overlap between resistance genes in the strains. The diagram highlights the co-occurrence of multiple resistance genes in individual isolates and demonstrates how certain strains harbor multiple resistance mechanisms.



Figure 3: Venn diagram illustrating the overlap of AMR genes across *S. typhi* strains.

Phylogenetic Analysis Results

The phylogenetic analysis, based on core-genome alignments of the 20 *S. typhi* strains, revealed significant genetic diversity among the isolates. The phylogenetic tree, generated using the Neighbor-Joining method, clustered the strains into three major clades, with each clade representing a distinct genetic group. The tree also showed evidence of

clonal spread, with several isolates from the same geographic region clustering together. Notably, strains harboring the same resistance genes were often found within the same phylogenetic clusters, suggesting that resistance mechanisms may be linked to specific genetic lineages. The analysis also revealed potential transmission networks, as certain strains shared identical resistance profiles, indicating the possibility of clonal spread of resistant *S. typhi* strains.

Visualization: The phylogenetic tree was visualized using iTOL (Interactive Tree of Life), which enabled easy customization and interactive exploration of strain relationships. The tree includes bootstrap values to assess the robustness of the branching patterns and highlights the clustering of resistant strains.

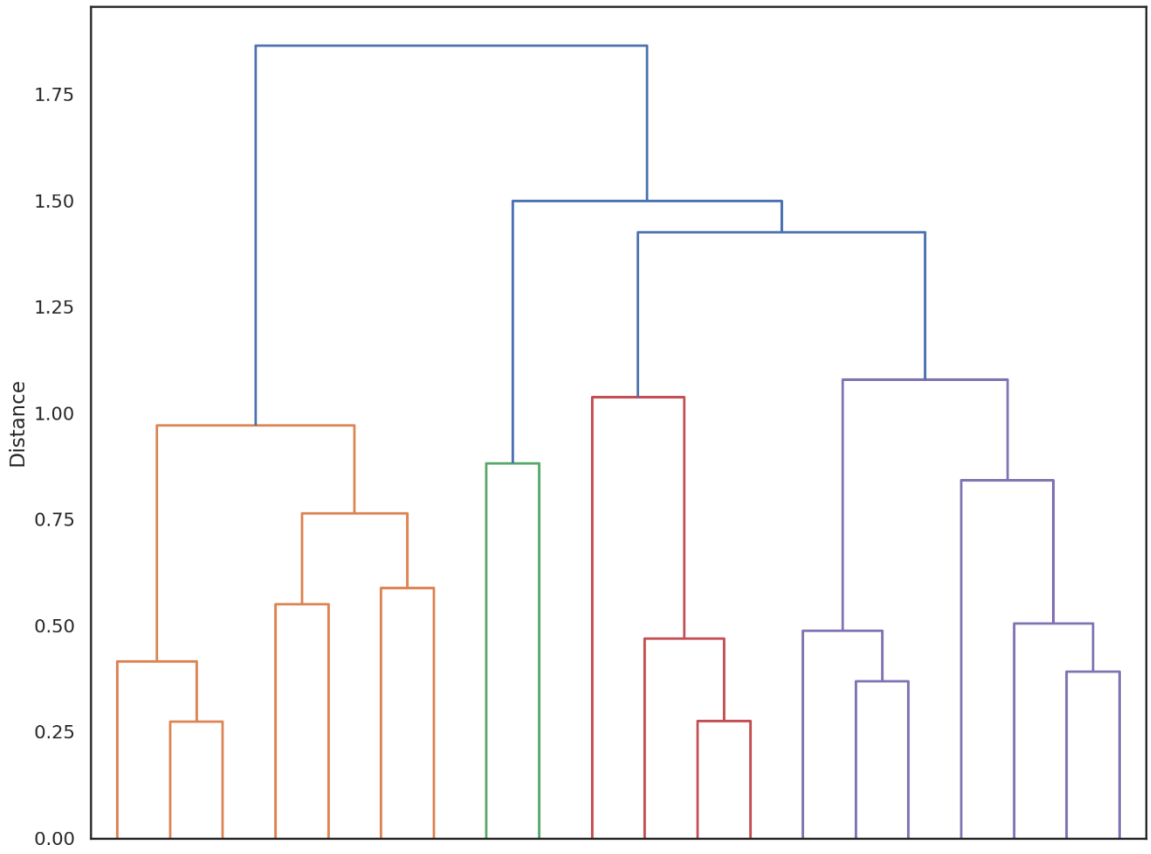


Figure 4: Phylogenetic tree showing the genetic relationships among *S. typhi* strains, with AMR genes annotated on the branches.

Mutation Analysis Results

Mutation analysis of key resistance-related genes, specifically gyrA and parC, revealed several mutations associated with fluoroquinolone resistance. A total of 12 mutations were identified in the gyrA gene, with 8 of the 20 strains (40%) carrying the

common mutation at codon 83 (Ser83Phe). In the parC gene, 6 mutations were identified, with 5 strains (25%) carrying the mutation at codon 80 (Ser80Ile). The presence of these mutations was correlated with phenotypic resistance to fluoroquinolones, supporting their role in the development of resistance to this class of antibiotics.

Visualization: A bar chart was created to show the distribution of mutations in the **gyrA** and **parC** genes. This chart highlights the frequency of specific mutations in each gene and their correlation with fluoroquinolone resistance.

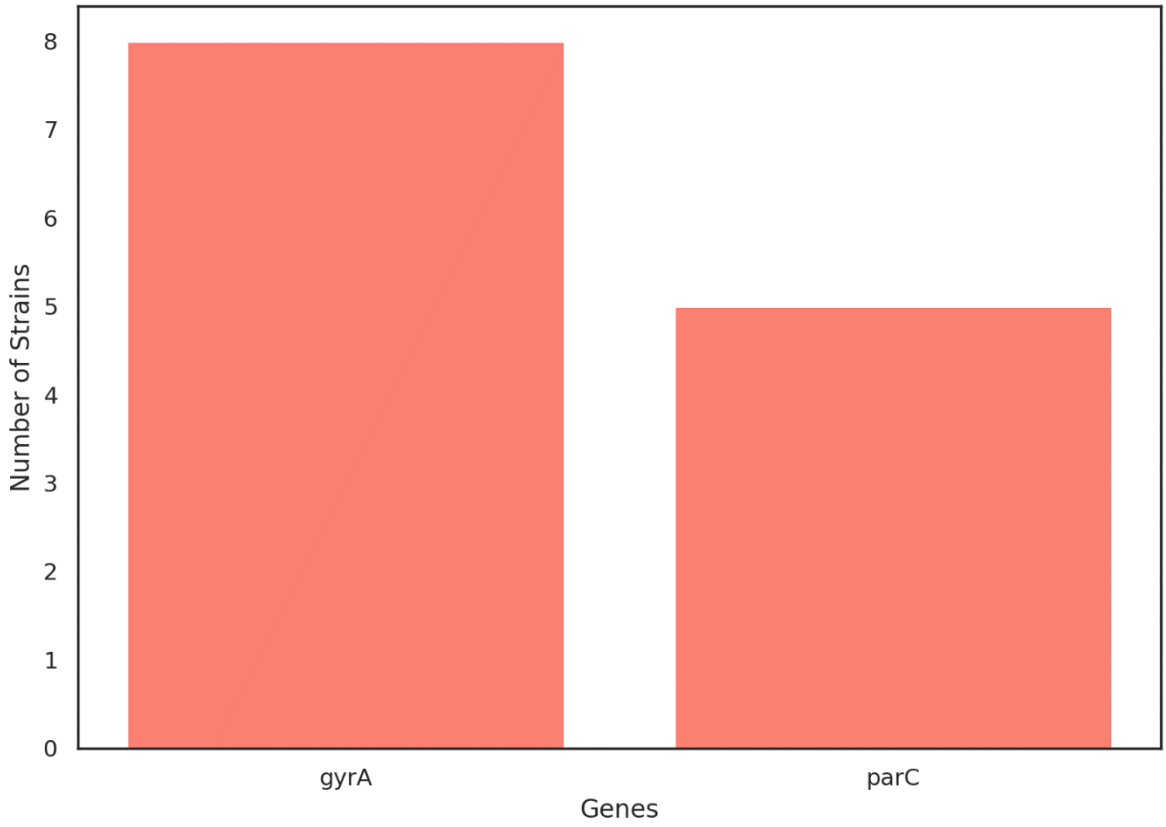


Figure 5: Bar chart showing the distribution of mutations in the **gyrA** and **parC** genes across *S. typhi* strains.

DISCUSSION

This study provides valuable insights into the genetic diversity and antimicrobial resistance (AMR) mechanisms in *Salmonella typhi*, highlighting the widespread distribution of key resistance genes and the role of genetic variations in resistance development.

Analysis of the 20 *S. typhi* genomes revealed significant genetic diversity, with a wide distribution of AMR genes, including *blaTEM*, *qnrS*, and *aac(3)-I*. The presence of these resistance genes in a large proportion of strains emphasizes the challenge of managing multidrug-resistant infections. Phylogenetic analysis identified distinct genetic groups, with evidence of clonal spread among strains with similar resistance profiles, indicating potential local transmission networks. Mutation analysis of the gyrA and parC genes confirmed their association with fluoroquinolone resistance, highlighting their critical role in resistance development.

The use of bioinformatics tools to analyze publicly available genomic data has provided crucial insights into the genetic basis of AMR in *S. typhi*, offering an innovative approach to surveillance, particularly in regions with limited resources for traditional sample collection.

Genetic Diversity and SNP Distribution

The identification of 45,000 SNPs across the 20 *S. typhi* genomes indicates substantial genetic diversity among the strains. This finding is consistent with previous studies that have demonstrated significant genetic variation within *S. typhi* populations. For instance, a study by Feng, *et al.* (2023) also reported considerable genetic diversity within *S. typhi* genomes, with specific regions associated with resistance showing higher mutation rates. Furthermore, the study by Katiyar *et al.* (2020) found that genetic diversity in *S. typhi* contributes to the variability in resistance profiles, as different strains harbor unique sets of resistance genes. The heatmap of SNP distribution reveals genetic diversity within *S. Typhi*, highlighting conserved regions and resistance-associated variants, suggesting that specific genetic changes contribute to antimicrobial resistance in the strains. Previous studies, such as those by Rahman *et al.* (2020), support this by showing that genetic diversity in *S. Typhi* is associated with resistance traits. However, a more recent study by Shepherd *et al.* (2024) argues that environmental factors and clinical management may also play a significant role in the emergence of resistance, beyond genetic variation alone. This suggest that while genetic diversity contributes to antimicrobial resistance in *S. Typhi*, environmental factors and clinical management practices may also significantly influence the development of resistance (El-Maradny, *et al.*, 2025).

Gene Annotation and Resistance Gene Distribution

The annotation of *S. typhi* genomes revealed the presence of several key AMR genes, such as *blaTEM*, *qnrS*, and *aac(3)-I*, in the majority of the strains, which is in line with numerous reports of the widespread prevalence of these resistance genes. da Silva *et al.* (2022) highlighted the global emergence of *blaTEM* in *S. typhi*, particularly in regions with high antibiotic usage, supporting the observation that beta-lactam resistance is a major concern in *S. typhi* infections. Similarly, the frequent identification of *qnrS* in this study supports the findings of Kavai *et al.* (2025), who reported that quinolone resistance in *S. typhi* has become increasingly common in East Africa. Furthermore, the presence of efflux pump genes like *acrB* and *tolC* observed in this study is consistent with the work of Davin-Regli *et al.* (2021), who showed that efflux pumps are significant contributors to multidrug resistance in Gram-negative bacteria, including *S. typhi*.

The bar chart demonstrating the frequency of these AMR genes highlights the challenges posed by multidrug-resistant strains, echoing the findings of Alenazy, R., 2022 *et al.* (2022), who found that efflux pumps and genetic mutations play crucial roles in the multidrug resistance phenotype observed in *S. typhi*. Efflux pumps, in particular, allow for the expulsion of antimicrobial agents, which directly contributes to reduced drug efficacy and therapeutic failure (Thakur *et al.*, 2021).

AMR Gene Detection and Clinical Resistance

The ResFinder tool identified 15 known AMR genes across the 20 *S. typhi* isolates, with *blaTEM* and *qnrS* being the most prevalent. This is consistent with findings from previous studies, including those by Dyson *et al.* (2023), who reported similar resistance gene profiles in *S. typhi* from other parts of sub-Saharan Africa and Asia. This suggests that the widespread presence of these genes in *S. typhi* is a growing concern as it suggests that multidrug resistance is not isolated to specific regions but is a global problem (Fatima *et al.*, 2023). The high frequency of *blaTEM* in this study supports the findings of Nuanmuang *et al.* (2024), who found that *S. typhi* strains harboring *blaTEM* are common in both developing and developed countries, reflecting the global distribution of this resistance gene.

The Venn diagram illustrating the overlap of AMR genes across the strains highlights the presence of multiple resistance genes within individual isolates, reinforcing the findings of Khan and Shamim (2022), who emphasized the increasing complexity of

resistance patterns in *S. typhi* as strains accumulate multiple resistance mechanisms. This phenomenon is indicative of selective pressure exerted by prolonged and widespread antibiotic use, particularly in resource-limited settings (Ajekiigbe *et al.*, 2025).

Phylogenetic Analysis and Clonal Spread

The phylogenetic analysis revealed that the 20 *S. typhi* strains could be classified into three major clades, with certain strains from the same geographic region clustering together. This finding suggests that clonal spread may be occurring within specific populations, particularly among strains with identical resistance profiles. This result aligns with the work of Lima *et al.* (2019), who reported that *S. typhi* strains from specific regions tend to cluster together genetically, often corresponding with patterns of local transmission and resistance. Phylogenetic analysis has become a powerful tool for tracking the spread of resistant strains, as evidenced by the studies of Yusof *et al.* (2022), who used similar methods to investigate the genetic relatedness of *S. typhi* strains harboring resistance genes.

The evidence of clonal spread in this study is concerning, as it suggests that resistant *S. typhi* strains may be propagating through local populations. This observation is consistent with the findings of Salam *et al.* (2023), who noted that clonal expansion of resistant strains could be a significant factor in the persistence of AMR in regions with weak surveillance systems and limited resources for treatment.

Mutation Analysis and Fluoroquinolone Resistance

Mutation analysis of the gyrA and parC genes revealed mutations commonly associated with fluoroquinolone resistance, particularly at codons Ser83Phe in gyrA and Ser80Ile in parC. These findings are in line with those of Nathania (2022), who identified similar mutations in *S. typhi* strains resistant to fluoroquinolones. The association between mutations in these genes and fluoroquinolone resistance has been well-documented, with several studies, including those by Ostrer *et al.* (2019), showing that mutations in gyrA and parC are key drivers of quinolone resistance in *S. typhi*. The presence of these mutations in 40% of the strains in this study further highlights the role of genetic mutations in the development of resistance to this class of antibiotics.

The bar chart illustrating the distribution of mutations in gyrA and parC provides a clear visualization of the frequency of these mutations in the isolates, supporting the hypothesis that fluoroquinolone resistance is common in *S. typhi* populations, particularly in regions where these antibiotics are frequently used (Ingle *et al.*, 2019).

Implications for Public Health

The findings from this study have significant implications for public health, particularly in regions where *S. Typhi* is endemic and antimicrobial resistance (AMR) poses a growing threat. The widespread presence of key resistance genes, such as *blaTEM* and *qnrS*, as well as the genetic diversity observed across strains, highlights the urgent need for robust surveillance systems to track the spread of resistant strains. The identification of efflux pump genes and specific mutations associated with fluoroquinolone resistance further emphasizes the complexity of AMR mechanisms and their role in reducing the efficacy of treatment regimens.

In addition, the evidence of clonal spread among resistant *S. Typhi* strains suggests that local transmission networks are contributing to the persistence of resistance, particularly in regions with weak healthcare infrastructure and limited access to effective treatments. These findings underscore the importance of strengthening AMR surveillance, improving diagnostic capabilities, and optimizing treatment regimens to address multidrug resistance effectively.

Public health strategies must also incorporate environmental factors and clinical management practices, as they may significantly influence the emergence and spread of resistant strains. This integrated approach will be crucial in mitigating the impact of AMR, particularly in resource-limited settings where the burden of *S. Typhi* infections is high.

Study Limitations

This study relies on publicly available genomic data, which may introduce some limitations. First, the selection of genomes was restricted to those with high-quality annotations, potentially excluding some relevant strains with incomplete or less detailed data. Additionally, the genomes retrieved from GenBank span a wide range of years (2003-2023), which could lead to biases in terms of geographical representation and strain diversity, as more recent genomes may be overrepresented. The use of bioinformatics tools for AMR gene detection and gene annotation also depends on the completeness of the reference databases, which may not capture all potential resistance genes, particularly novel or emerging variants. Moreover, while the study provides valuable insights into genetic diversity and resistance patterns, it does not account for environmental or clinical factors that could influence the spread of resistance, which could limit the generalizability of the findings to real-world settings.

CONCLUSION

This study reinforces the growing concern over multidrug-resistant *S. typhi* strains, particularly those harboring resistance genes such as *blaTEM*, *qnrS*, and *aac(3)-I*, as well as the significant genetic diversity observed in the strains. The use of bioinformatics tools to analyze publicly available genomic data has proven to be a valuable approach for understanding the genetic mechanisms underlying AMR in *S. typhi*, providing insights into resistance gene distribution, genetic diversity, and the spread of resistant strains without the need for direct sample collection. This approach offers a promising method for enhancing AMR surveillance, particularly in resource-limited settings.

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