Salmonella Paratyphi B: Genomic analysis and Antimicrobial Resistance across different regions

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Salmonella Paratyphi B

- Gram-negative enteric pathogens

- Two biotypes serogroup B share the same somatic antigen profile 1,4,[5],12 and flagellar antigens b: 1,2:
  
  - *Java* (dt+) do not produce slime wall causing gastroenteritis in either human or animals;
  
  - *sensu stricto* (dt-) produce a slime wall causing paratyphoid fever in human.

- Biotype *Java* is less virulent to humans than the *sensu stricto* biotype, although cases of invasive infection have been reported.
Objectives

A comprehensive analysis of the global collection of Paratyphi B strains.

• Characterization of antibiotic resistance genes
• Distribution of AMR strains
• Analysis of MLST profiles and plasmid content
• Investigation of biotypes and pathogenesis
• Evolutionary relatedness and spread of the pathogen
Isolates were systematically selected based on the following criteria:

**Organism Name:** filtered to include only those identified as "Paratyphi B." ENA & NCBI -SRA databases

**Sequencing Platform:** Data derived from the "ILLUMINA" sequencing platform

**Library Strategy:** The chosen isolates underwent "WGS" (Whole Genome Sequencing) as the library strategy.

**Library Layout:** Isolates with a "PAIRED" library layout were specifically included.
Methodology

1. Data Curation & Standardization
2. Raw Reads Quality Assessment and Filtering
3. Species Identification
4. De novo Assembly, QC, and Annotation
5. Phenotypic and Genotypic Profiling
6. Genomic Characterization (AMR, MLST, Plasmid)
7. Statistics and Temporal Analyses
8. Phylogenetic analysis
Global distribution of *S. Paratyphi* B (n=1510) 1964 – 2021

03 (0.20%)

65 (4.30%)

341 (22.5%)

901 (59.6%)
Antimicrobial Resistance

- Susceptible: 79.60% (1,202/1,510)
- Resistant: 20.40% (308/1510)

MDR: 58% (180/308)
- Resistant: 42% (128/308)

Java: 69% (209/308)
- Sensu Stricto: 31% (96/308)

amp, chr, & co-tri
one or more antibiotics
**Distribution of AMR**

- **Aminoglycosides**
  - Streptomycin - 10.60% (160/1,510)
- **Cephalosporins**
  - Ceftriaxone (Third-generation cephalosporin) - 1.72% (26/1510)
  - Cefoxitin (Second-generation cephalosporin) - 1.70% (25/1510)
- **Macrolides**
  - Erythromycin - 0.40% (6/1,510)
  - Azithromycin - 0.33% (5/1,510)
- **Penicillin**
  - Ampicillin - 10.06% (152/1,510)
  - Amoxicillin/clavulanic acid - 0.99% (15/1,510)
- **Tetracyclines**
  - Tetracycline - 7.35% (111/1,510)
- **Fluoroquinolones**
  - Ciprofloxacin - 8.21% (124/1,510)
  - Nalidixic acid - 6.62% (100/1,510)
- **Dihydrofolate Reductase Inhibitors**
  - Trimethoprim - 6.09% (92/1,510)
- **Sulfonamides**
  - Sulfisoxazole - 8.61% (130/1,510)
Geographical distribution of resistant phenotypes

Present
Absent

Africa
Asia
America
Europe

tetracycline
amoxicillin
sulfisoxazole
ampicillin
streptomycin
fosfomycin
spectinomycin
hygromycin
lincomycin
rifampicin
erythromycin
colistin
aminoglycosides
clarithromycin
doxycycline
trimethoprim
tobramycin
nalidixic acid
kanamycin
gentamicin
ciprofloxacin
chloramphenicol
cefoxitin
ceftriaxone
Temporal emergence of antibiotics resistance (1965-2021)
Within a dataset of 1510 isolates, a total of 64 distinct sequence types (STs) were predicted.
Plasmid distribution

Within a dataset of 1510 isolates, a total of 34 plasmids were predicted.
SNP-based Evolutionary relatedness of *S. Java* and *Sensu stricto*
Conclusion

• 80% of isolates were pan-Susceptible, 20% were resistant

• Biotype *Java & sensu stricto* strains has almost equal resistance rate (20-22%).

• Sequence Type ST-43 unique in *Java* and ST-86 unique in *sensu stricto* isolates

• Temporal trends show the increasing trend of AMR after 2010.

• Common plasmid *IncI*-1(alpha), responsible for carrying *Amp*, *Tet*, *Chl*, and *co-tri* resistant genes.

• Phylogenetic tree reveals 3 distinct clusters and 3 subclusters, suggesting potential patterns of genetic relatedness.
ACKNOWLEDGEMENT

- Farah Qamar - AKU
- Safina Abdul Razzak (Bioinformatician) - AKU
- Sidra Tahir - AKU
- Stephen Baker – Cambridge University
- Jacqueline A Keane – Cambridge University
Thank You!

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