

13th
INTERNATIONAL
CONFERENCE

TYPHOID &
OTHER INVASIVE
SALMONELLOSES

December 5-7, 2023 | Kigali, Rwanda



آغا خان یونیورسٹی
THE AGA KHAN UNIVERSITY

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



Inclusion criteria

Isolates were systematically selected based on the following criteria:

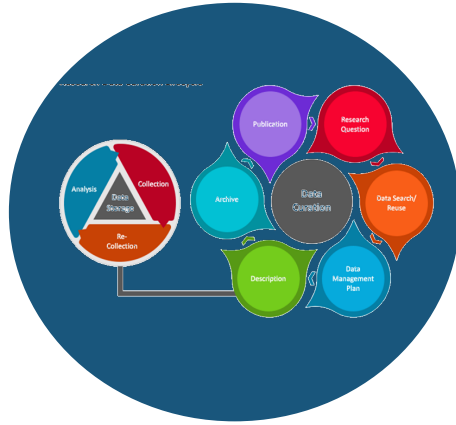
Organism Name: filtered to include only those identified as "Paratyphi B." ENA & NCBI -SRA databases

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

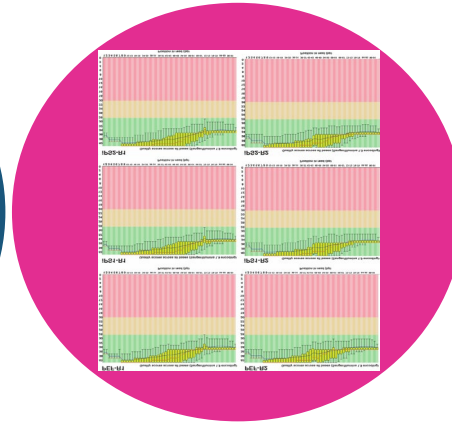
Library Strategy: The chosen isolates underwent "WGS" (Whole Genome Sequencing) as the library strategy.

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

Methodology



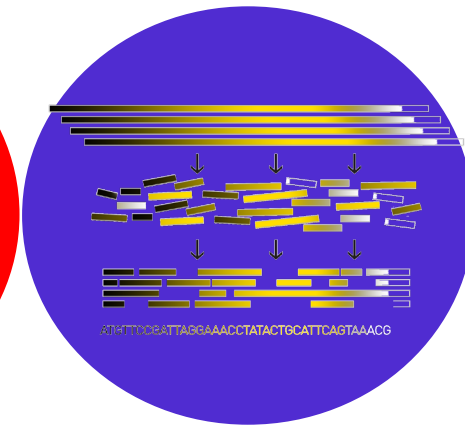
1. Data Curation & Standardization



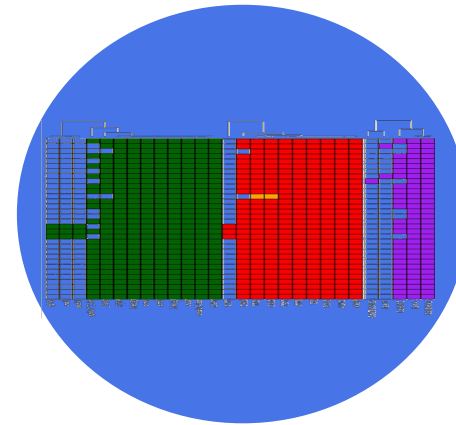
2. Raw Reads Quality Assessment and Filtering



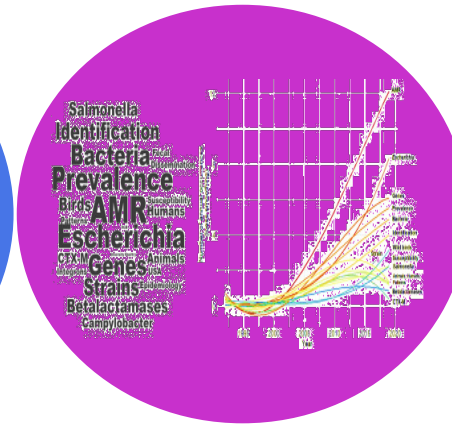
3. Species Identification



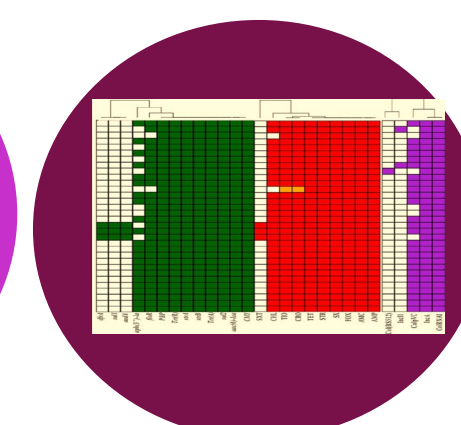
4. *De novo* Assembly, QC, and Annotation



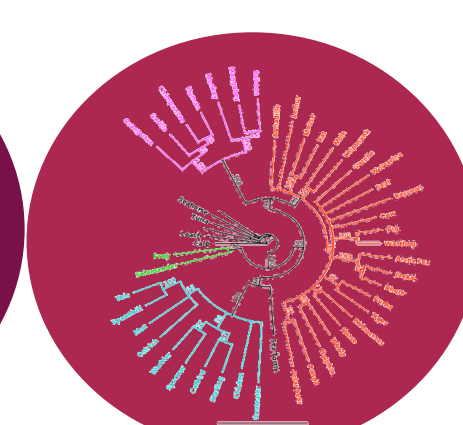
5. Phenotypic and Genotypic Profiling



6. Genomic Characterization (AMR, MLST, Plasmid)

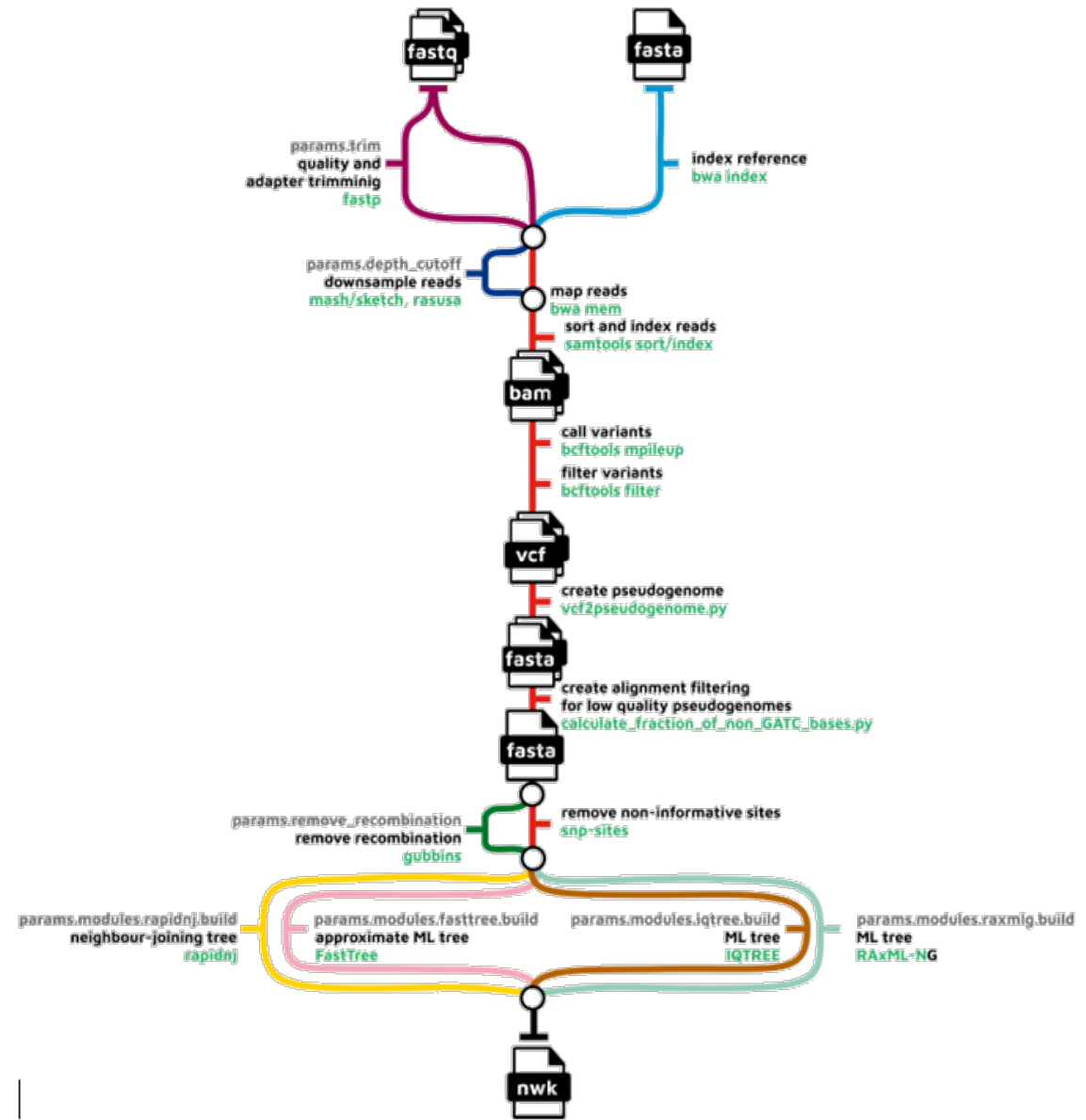


7. Statistics and Temporal Analyses

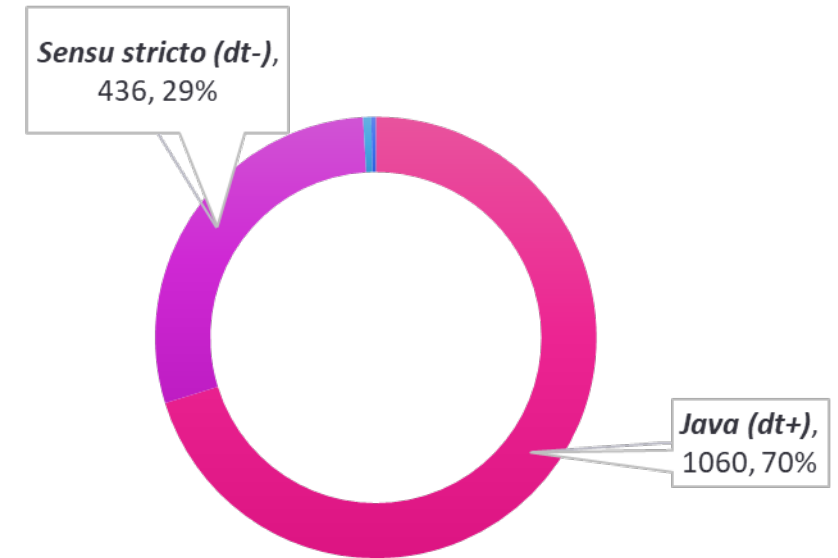
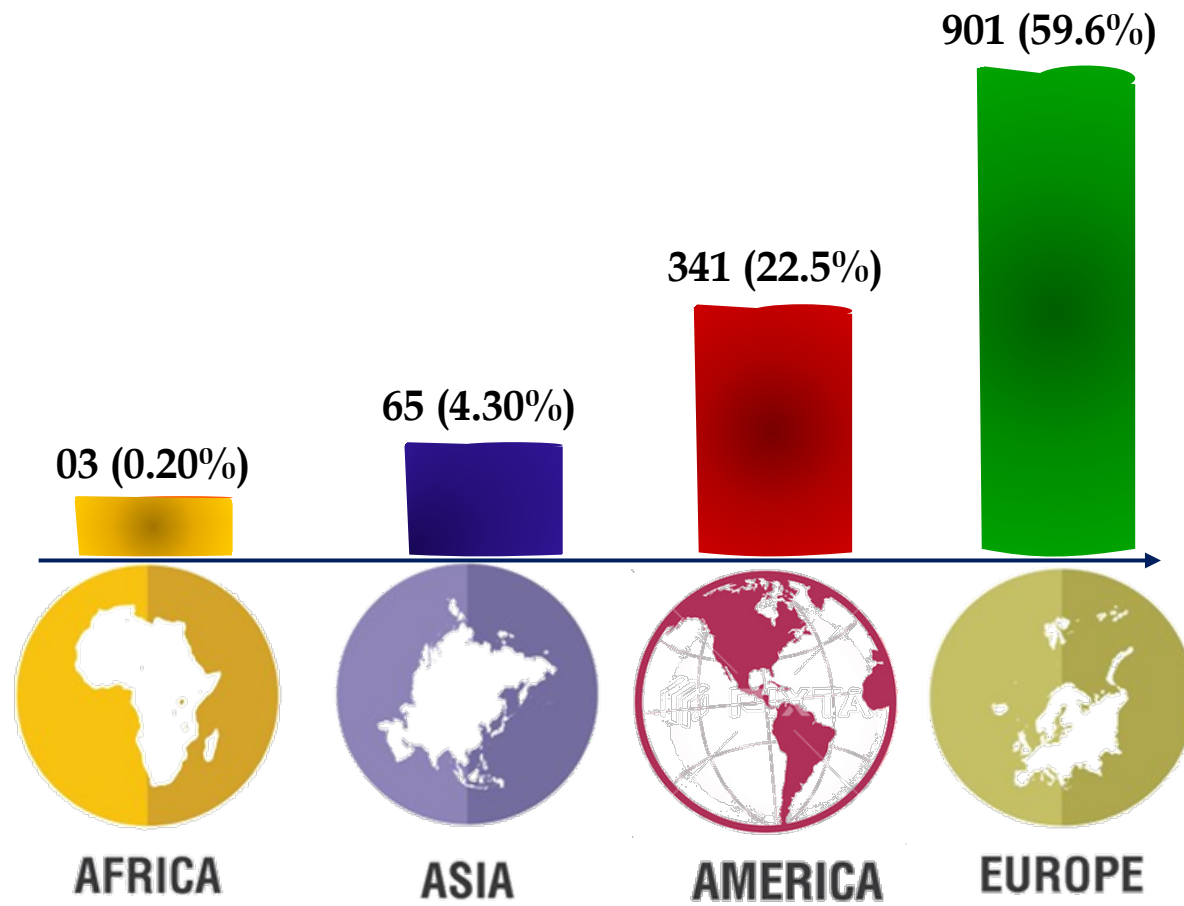


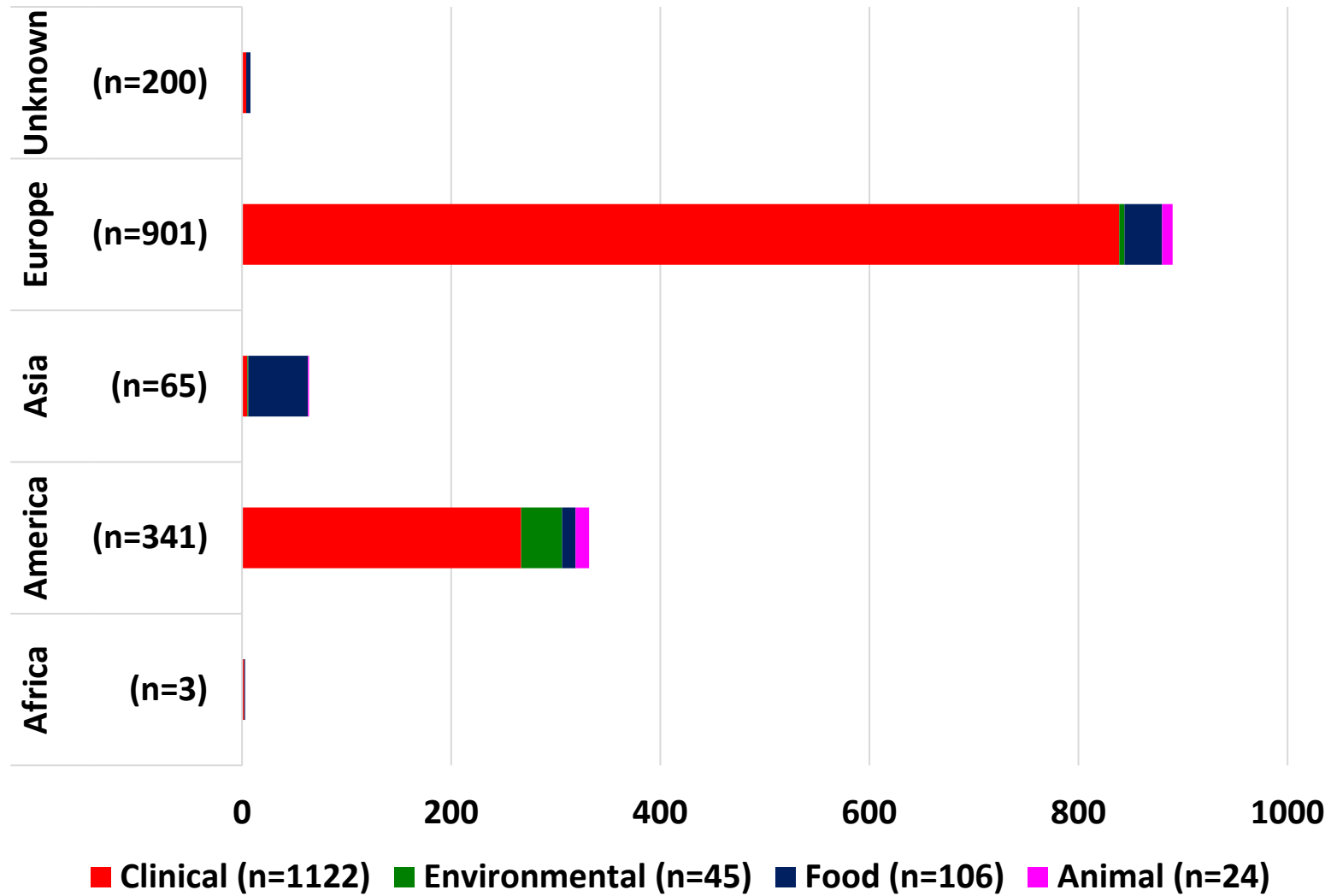
8. Phylogenetic analysis

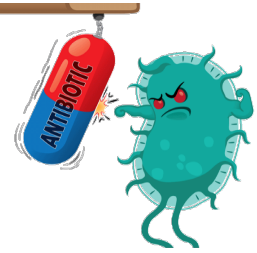
nf-core



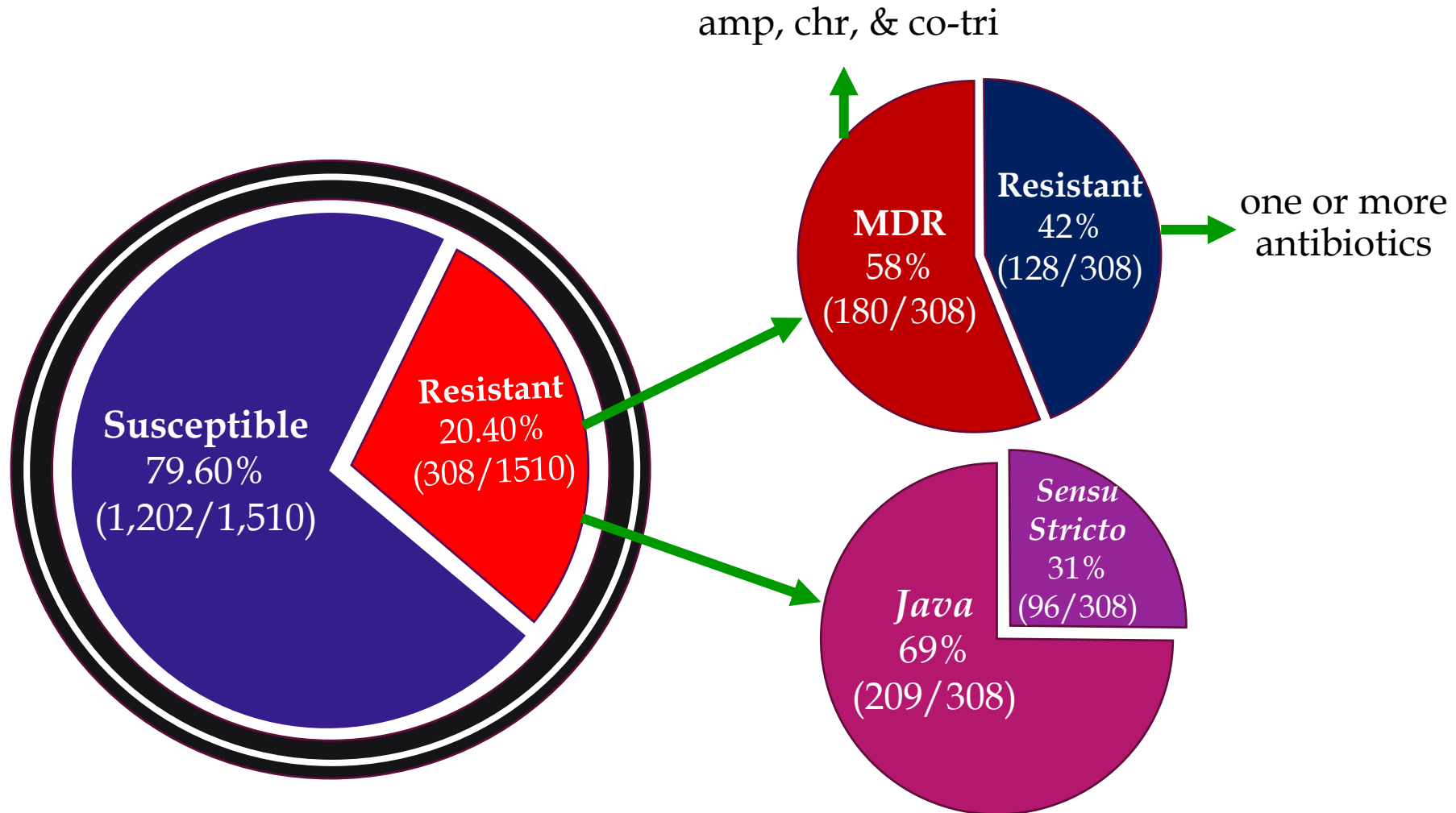
Global distribution of *S. Paratyphi* B (n=1510) 1964 - 2021



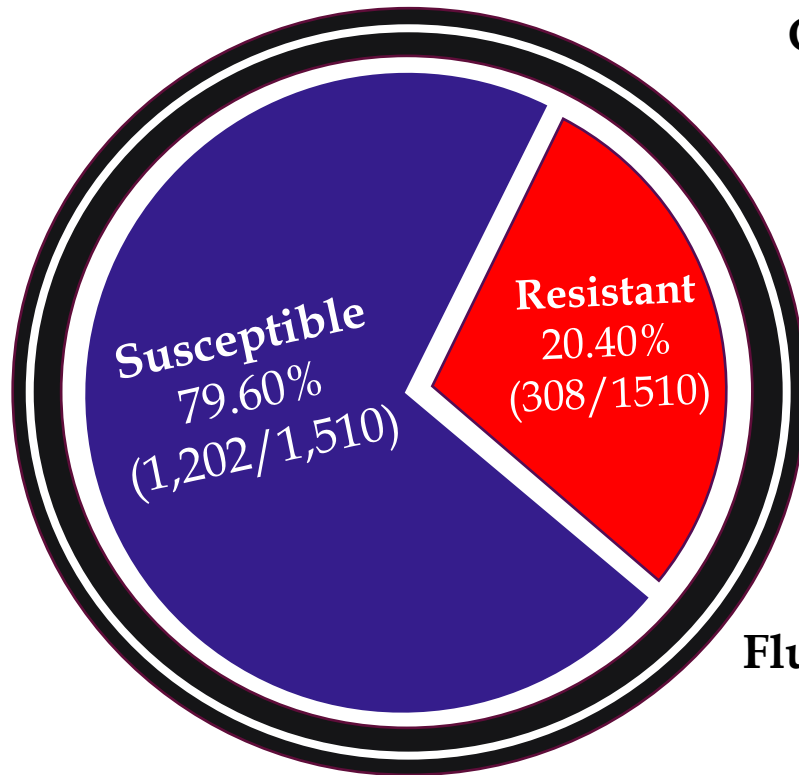




Antimicrobial Resistance



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)

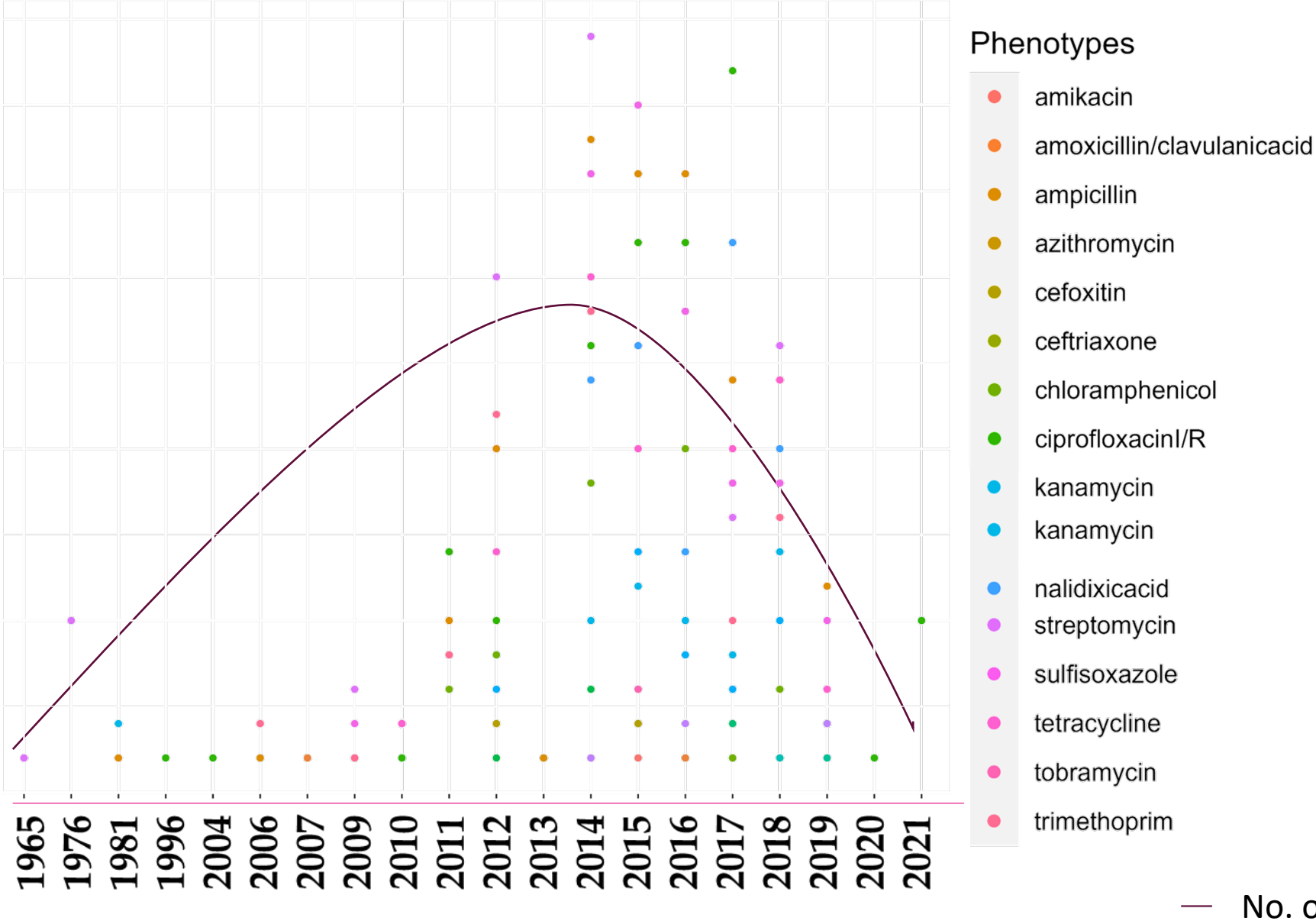
Dihydrofolate
Reductase
Inhibitors

• Trimethoprim - 6.09% (92/1,510)

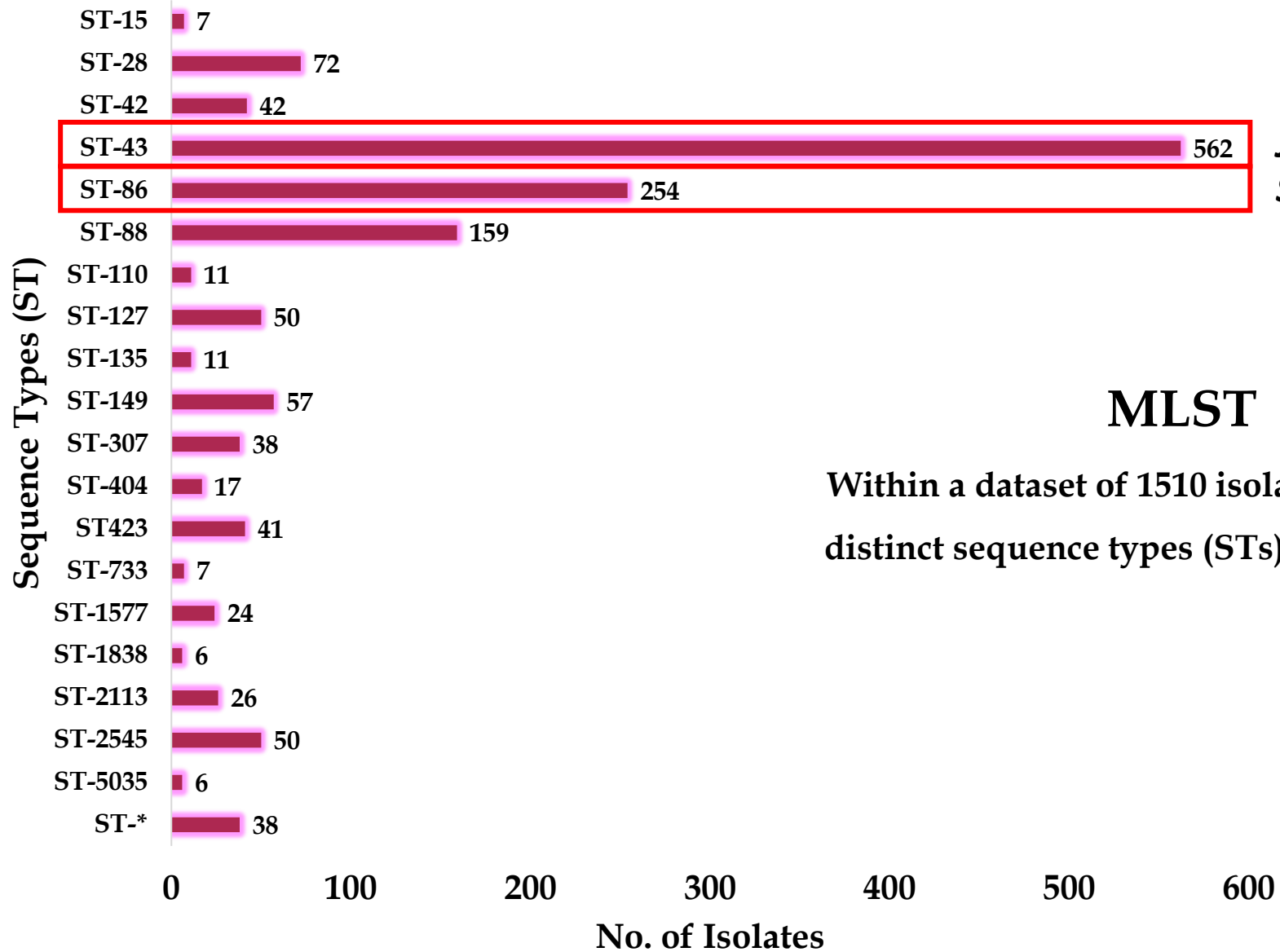
Sulfonamides

• Sulfisoxazole - 8.61% (130/1,510)

Temporal emergence of antibiotics resistance (1965-2021)



Distribution of MLST



Java biotype
Sensu Stricto biotype

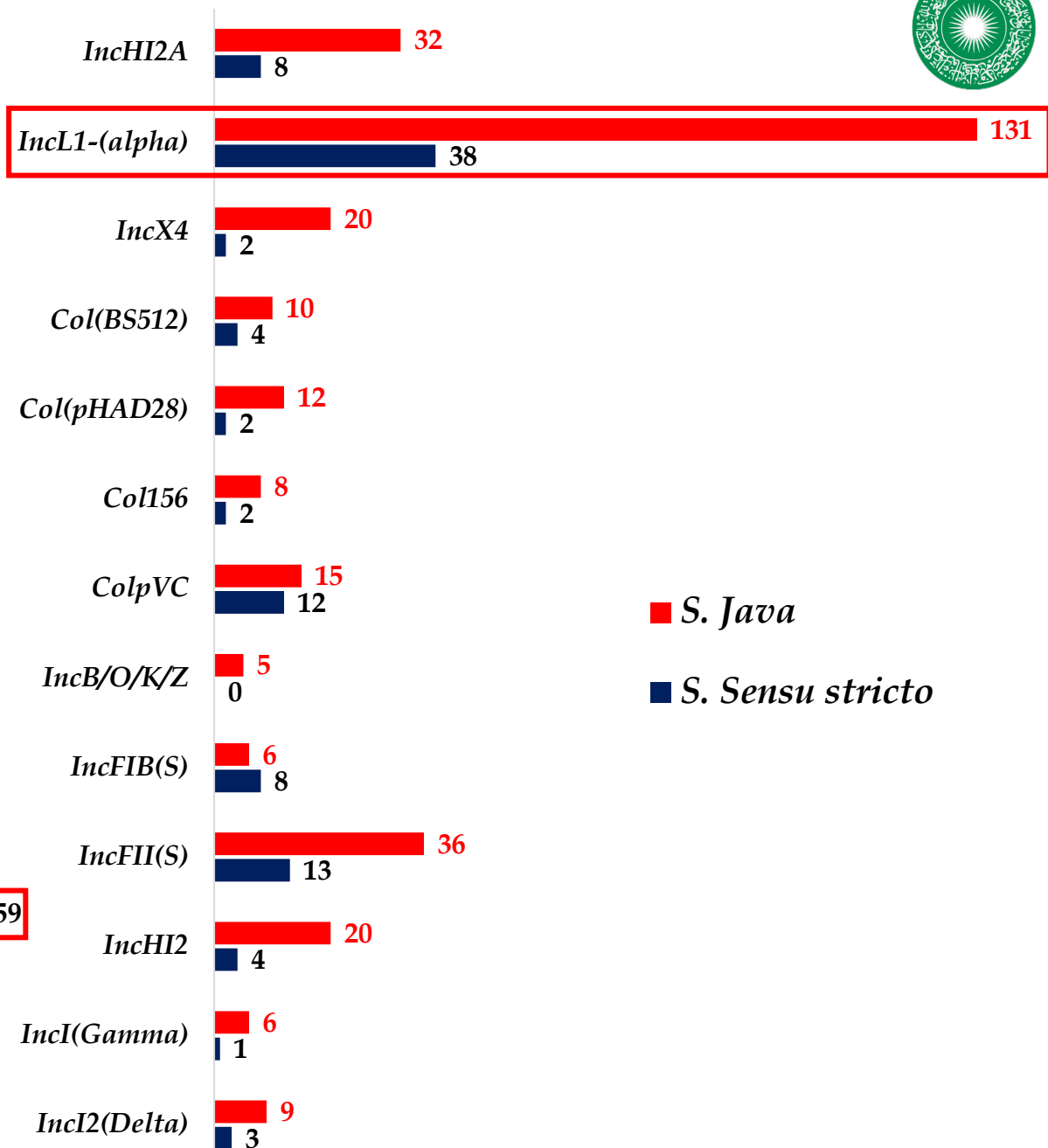
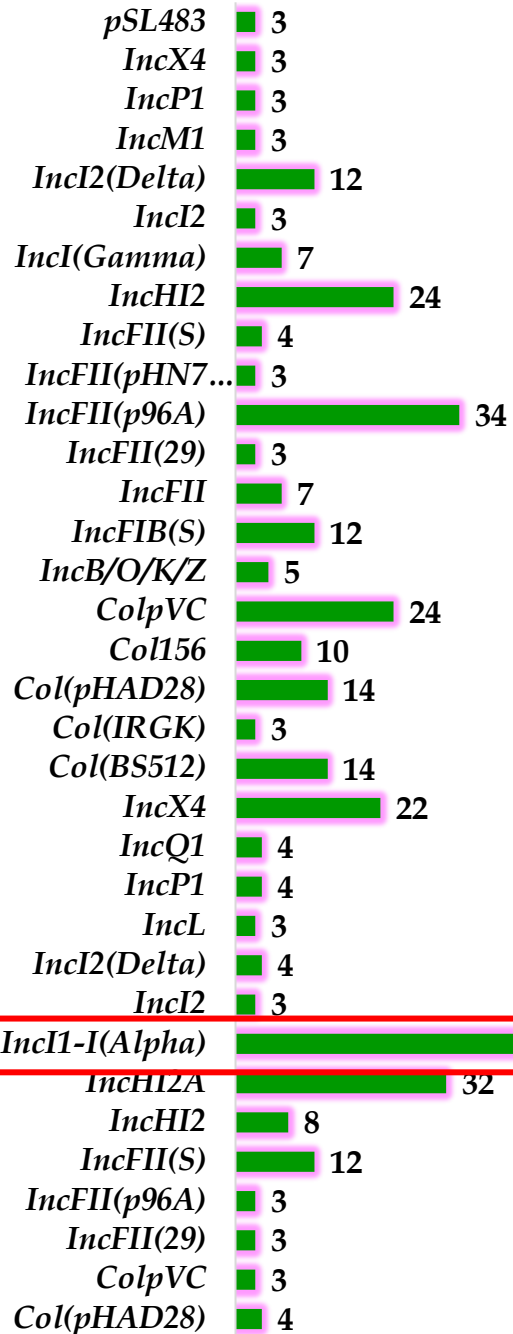
MLST

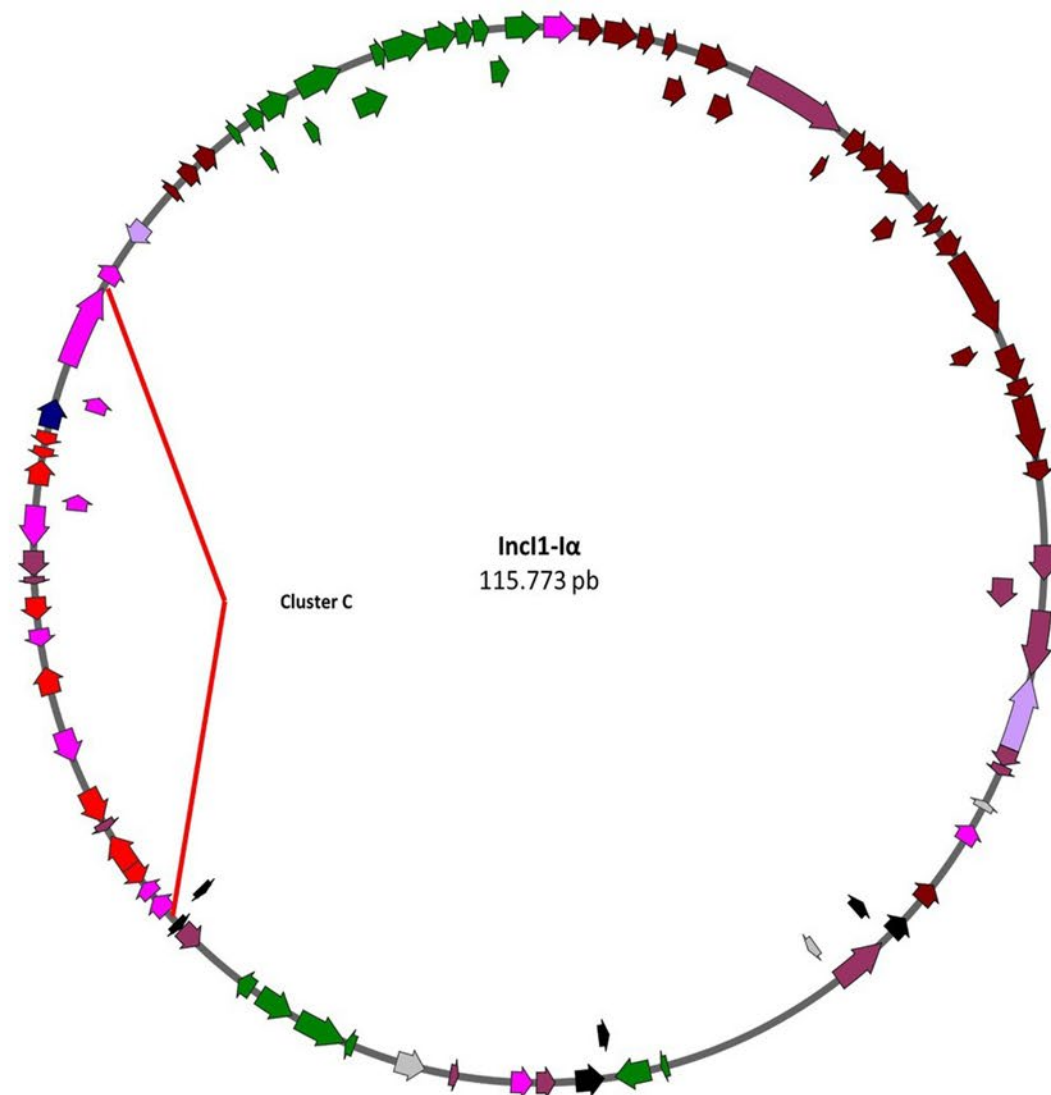
Within a dataset of 1510 isolates, a total of 64 distinct sequence types (STs) were predicted.



Plasmid distribution

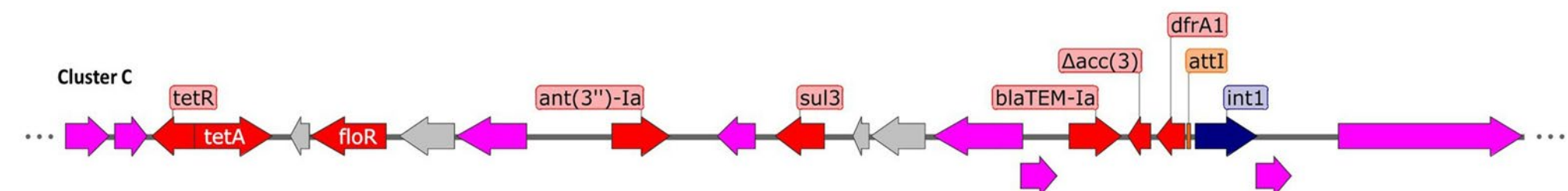
Within a dataset of 1510 isolates, a total of 34 plasmids were predicted.





IncI1- α
115.773 pb

Cluster C



Cluster C

tetR

tetA

floR

ant(3'')-Ia

sul3

blaTEM-Ia

$\Delta acc(3)$

dfrA1

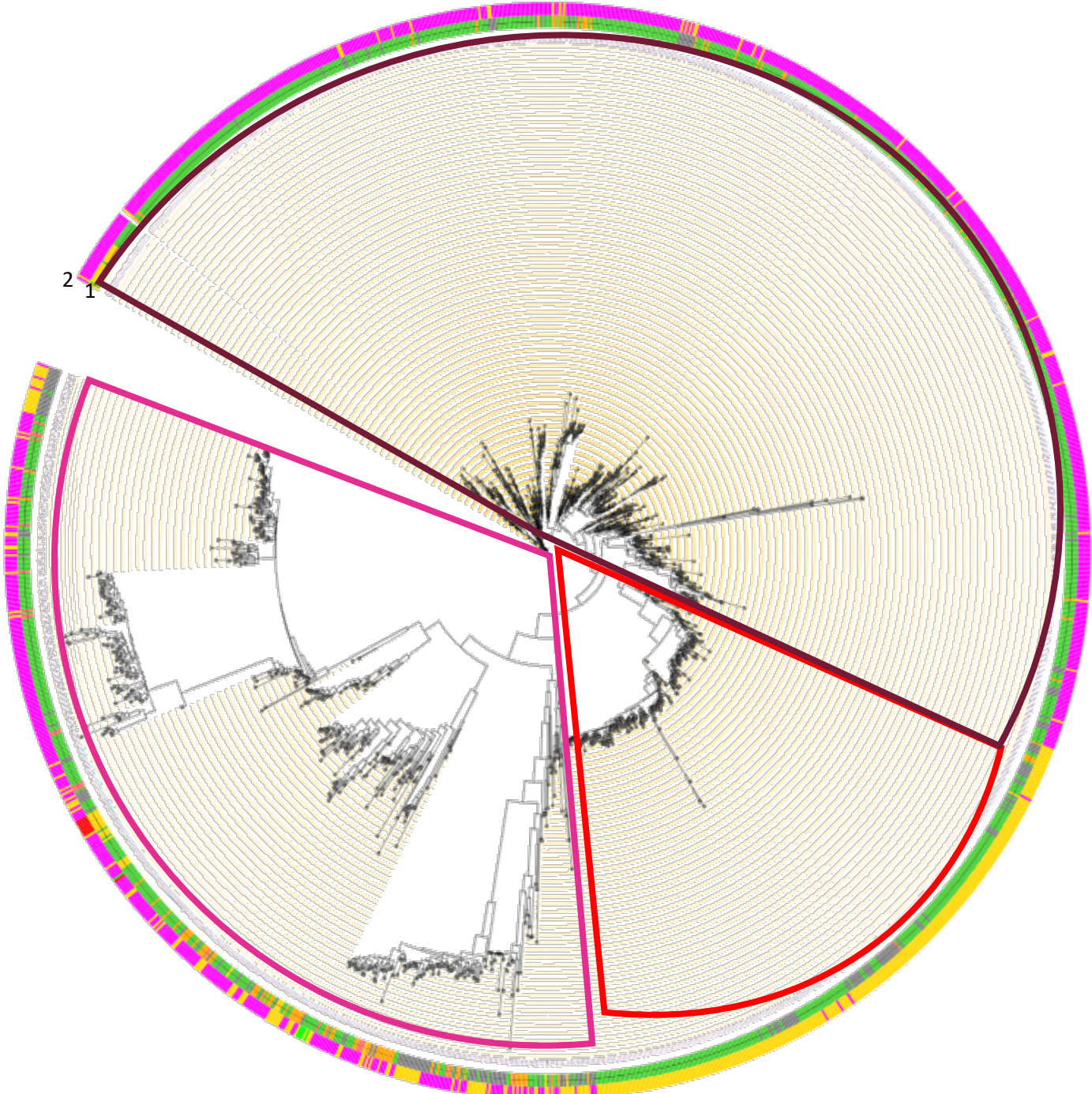
attI

int1

SNP-based Evolutionary relatedness of *S. Java* and *Sensu stricto*

Biotypes 2	
Yellow	Sensu Stricto
Magenta	Java
Red	Monophasic
Green	ParaB

Source 1	
Red	Animal
Green	Clinical
Yellow	Environmental
Orange	Food
Grey	NA



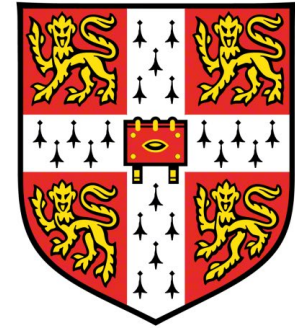
Conclusion



- 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 *Incl-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



UNIVERSITY OF
CAMBRIDGE

Thank You!



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