

Diversity and Antimicrobial Resistance of *Salmonella* Paratyphi A: A Global Typhoid Genomics Consortium initiative

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Kigali, Rwanda

Global Typhoid Genomics Consortium

2021-present

>200 members
>50 countries

Consortium coordinators:



Kathryn Holt
LSHTM



Zoe Dyson
LSHTM



Megan Carey
LSHTM



Stephen Baker
Univ. Cambridge



David Aanensen
Univ. Oxford

Our Mission:

We aim to engage the global typhoid research community in order to aggregate *Salmonella* Typhi & Paratyphi A genomic data to monitor the emergence and spread of drug resistance and inform targeted public health action.

Consortium goals:

1. Encourage prompt sharing of typhoid genome data for public health benefit
2. Facilitate the extraction and reporting of key data of public health relevance
3. Promote and facilitate the dissemination and use of information derived from typhoid genomic data to monitor antimicrobial resistance and post-vaccination impact

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RESEARCH ARTICLE



Global diversity and antimicrobial resistance of typhoid fever pathogens: Insights from a meta-analysis of 13,000 *Salmonella Typhi* genomes

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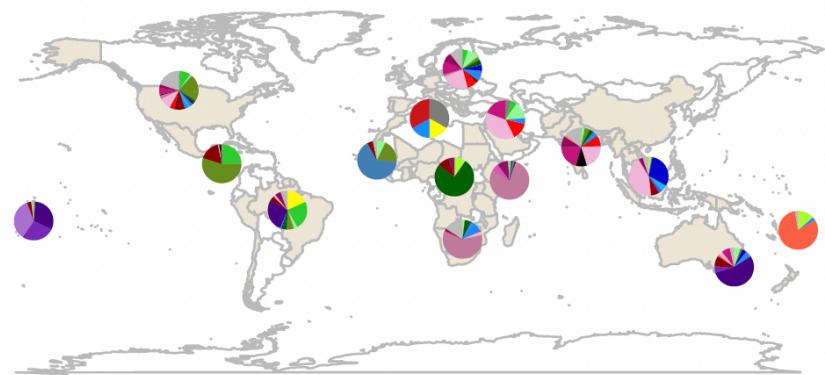
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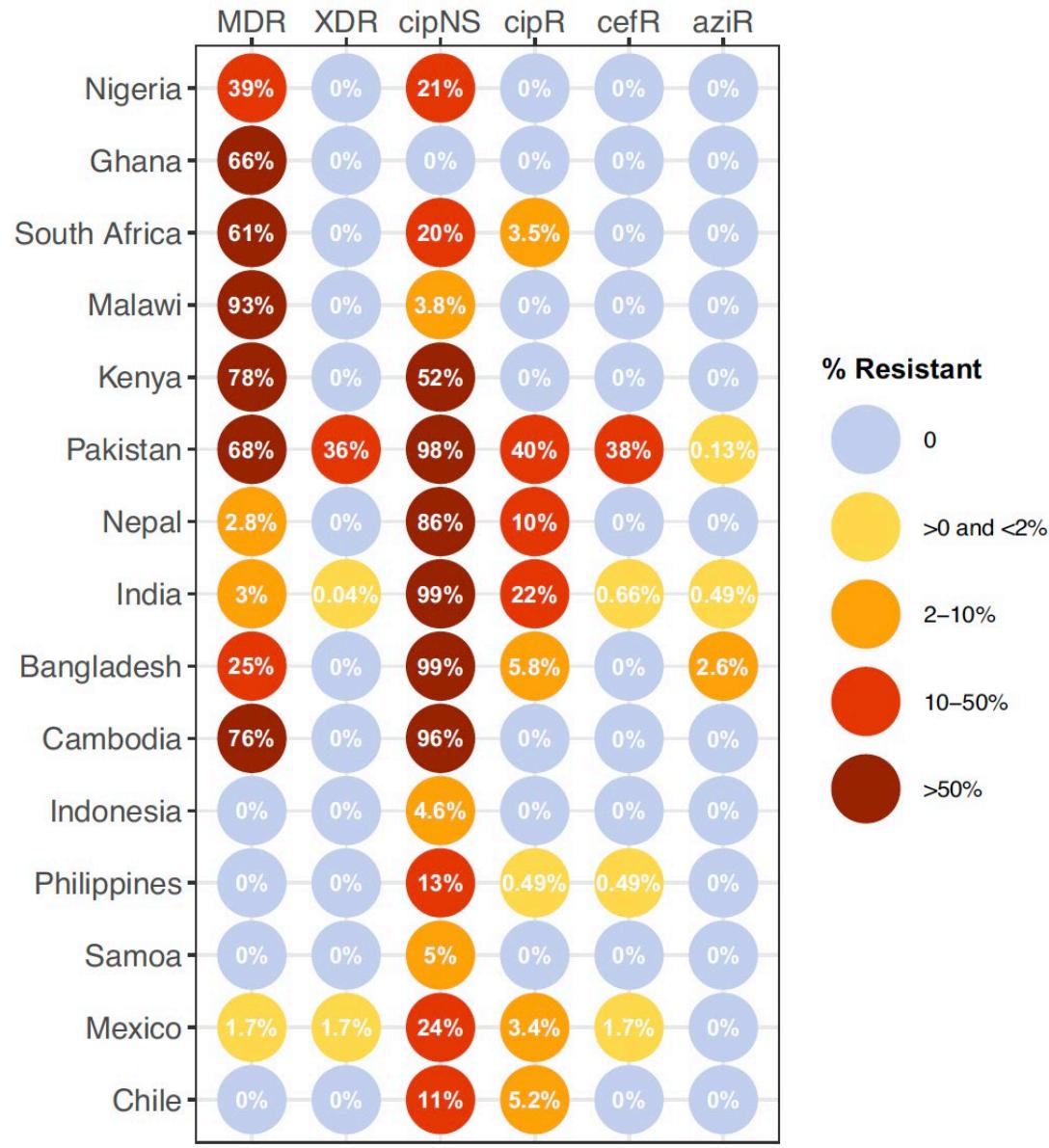
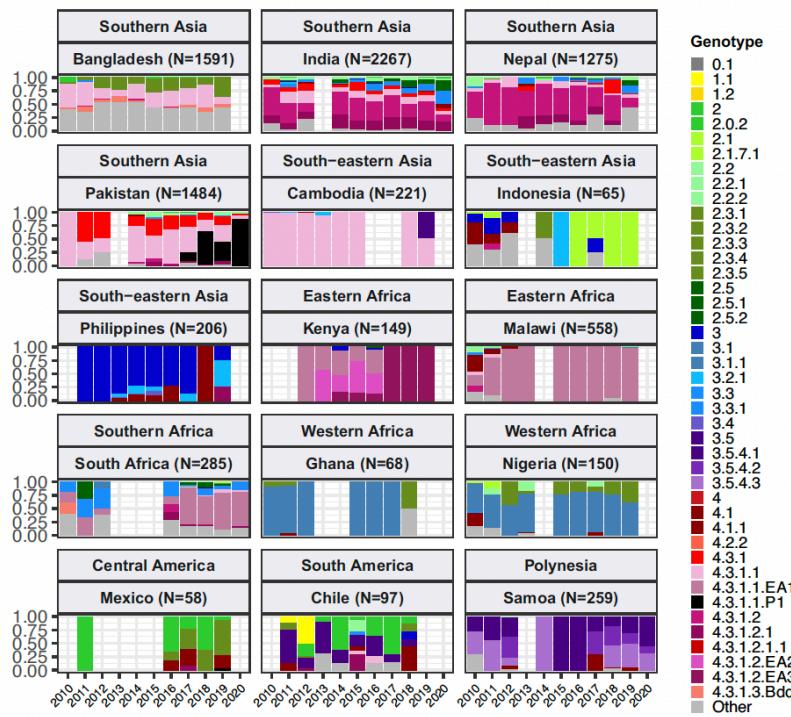
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Genetic diversity of Typhi from 13k genomes

a) Genotype prevalence by world region, 2010–2020

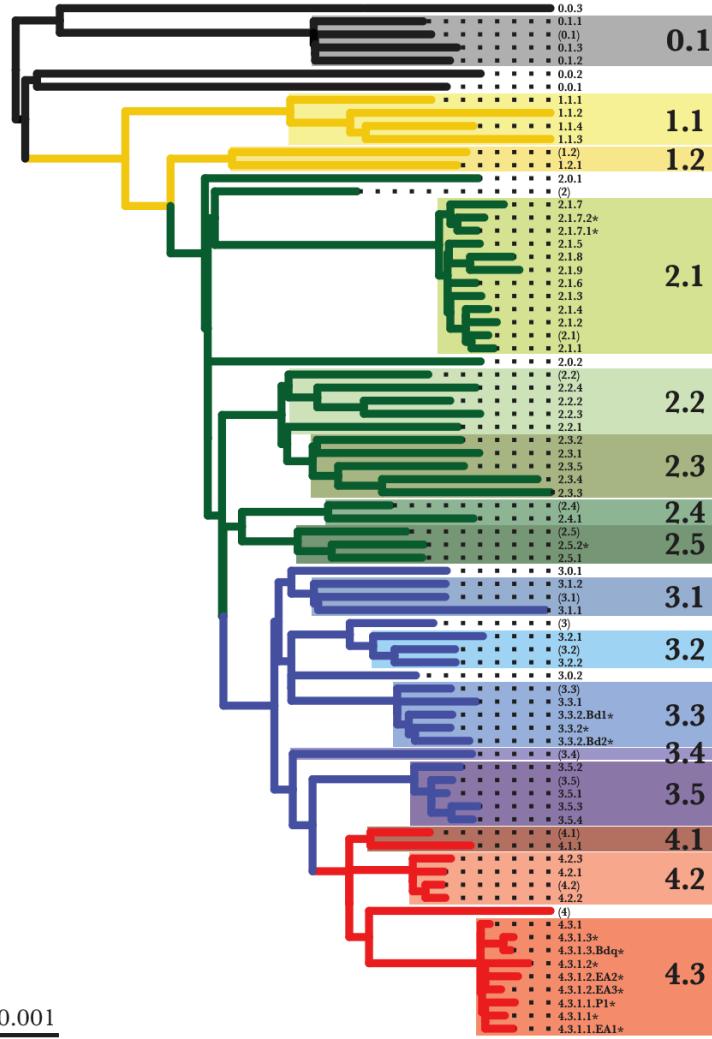


b) Annual genotype prevalence, for countries with at least 50 genomes



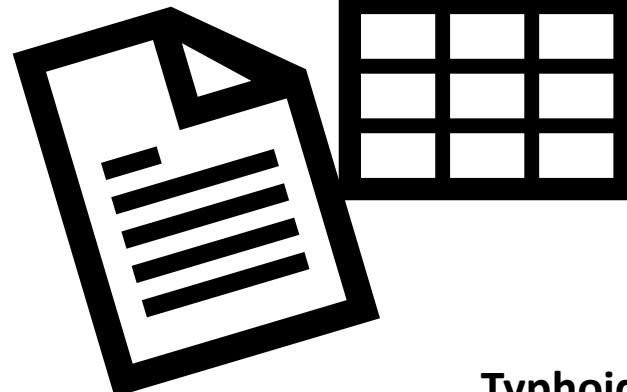
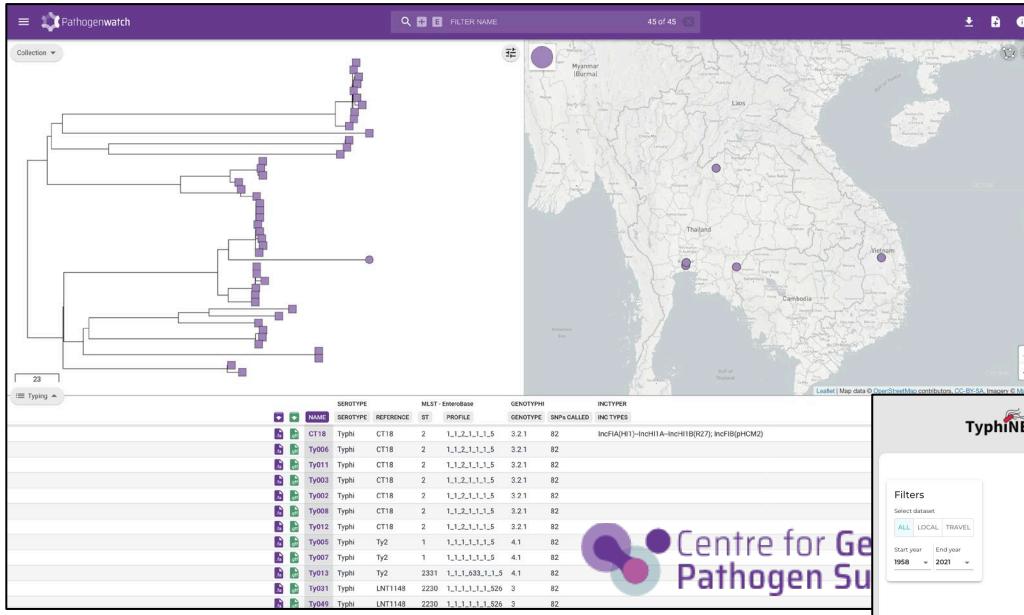
Global Typhoid Genomics Consortium Resources

GenoTyphi genotyping software

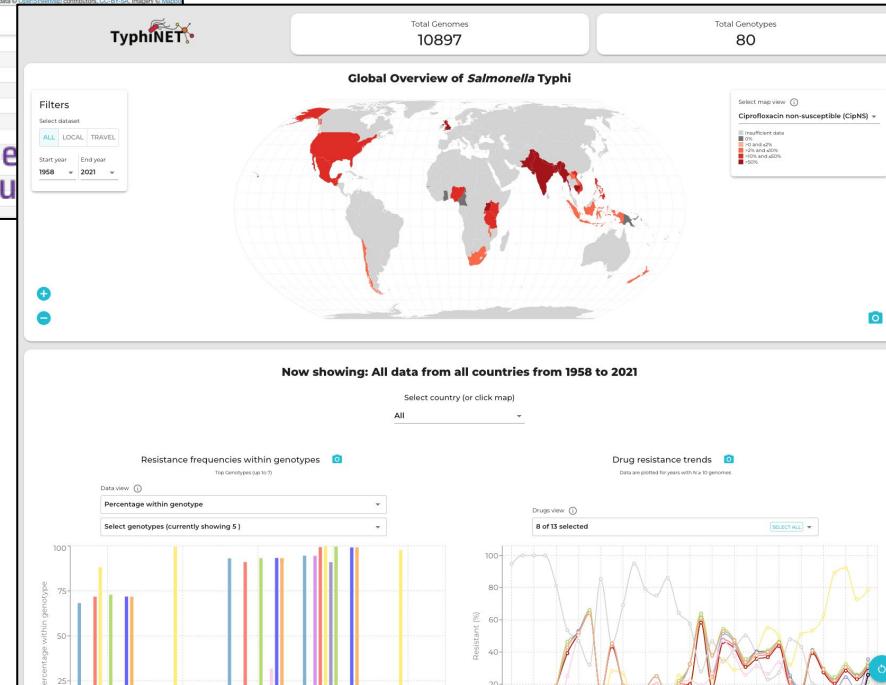


github.com/typhoidgenomics/genotypphi

Typhi Pathogenwatch: <http://pathogen.watch>



TyphiNET surveillance dashboard: <http://typhi.net>



Typhoid Genomics Metadata Template: <https://bit.ly/typhiMeta>

Global Typhoid Genomics Consortium Working Groups

1. Typhi transmission dynamics & phylodynamics
2. GenoTyphi Mykrobe software development
3. GenoTyphi genotyping scheme
4. Paratyphi A genetic epidemiology & software tools

Paratyphi A special interest group

Motivation

To curate a global collection of Paratyphi A whole genome sequences to better understand the global distribution of Paratyphi A pathogen variants, their transmission dynamics, and antimicrobial resistance for public health benefit.

Goals and aims

1. Extend the current GTGC standardised metadata template for use with Paratyphi A data and long-read nanopore data
2. To better understand the global genetic epidemiology of Paratyphi A, including spatio-temporal distribution of AMR pathogen variants, their emergence, and transmission dynamics
3. Increase the accessibility of the Paratype genotyping framework via Mykrobe and Pathogenwatch

Collaboration

- Contacted corresponding authors who have published at least a single Paratyphi A genome
- Responses from >90 consortium members in >40 countries

Working groups

1. Statistical analysis of AMR and pathogen genotypes
2. Phylodynamic analysis of pathogen transmission dynamics
3. Accessible software tools to facilitate the analysis of Paratyphi A genome data



Jaspreet Mahindroo
Imperial College

Working group leads:



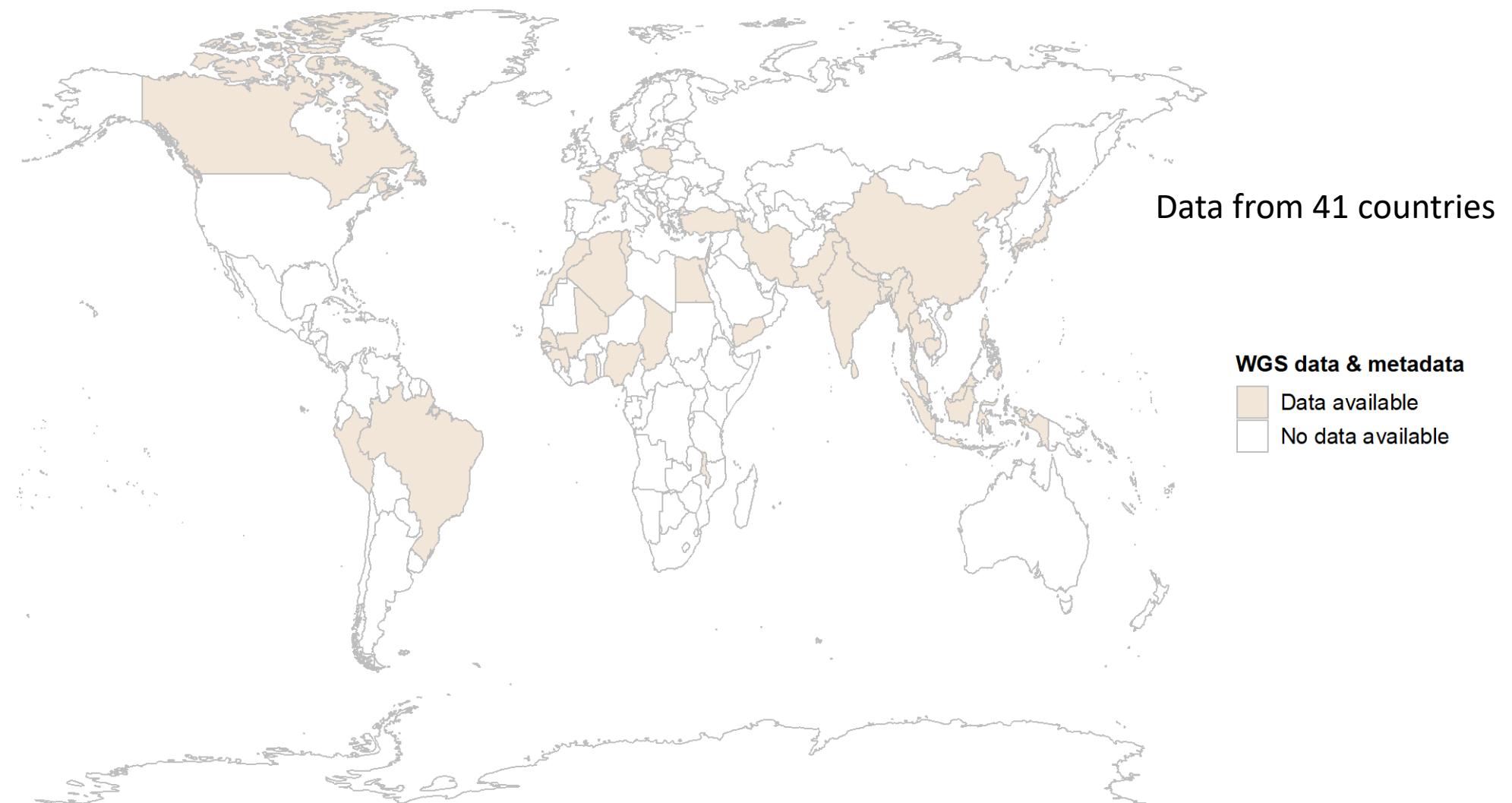
Yogesh Hooda
CHRF



Zoe Dyson
LSHTM

Public genome meta-analysis: samples available

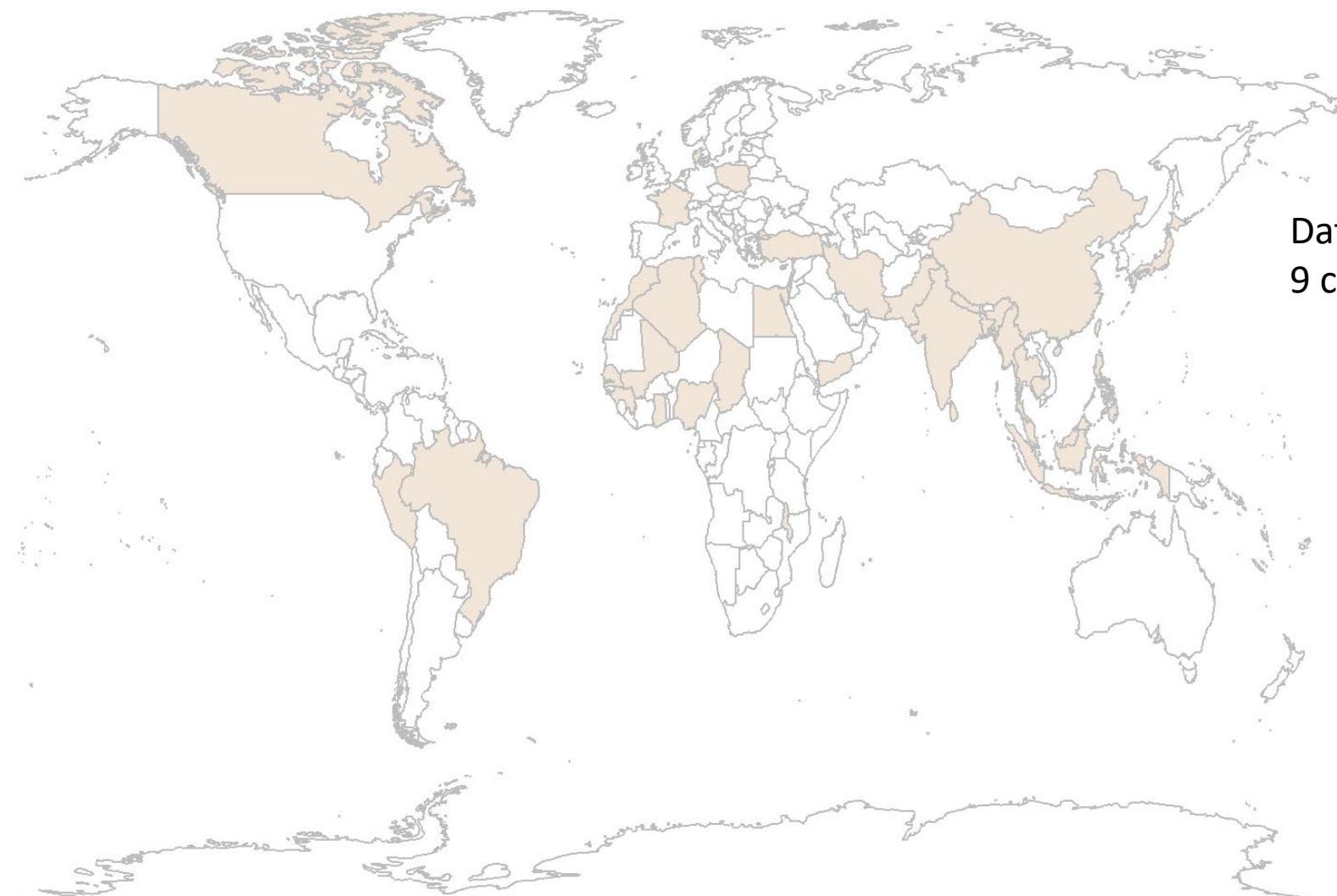
Distribution of public Paratyphi A WGS data



n=2,561 genomes published prior to July 2023

Public genome meta-analysis: samples available

Distribution of public Paratyphi A WGS data



Data from 41 countries
9 countries with ≥ 10 genomes

WGS data & metadata

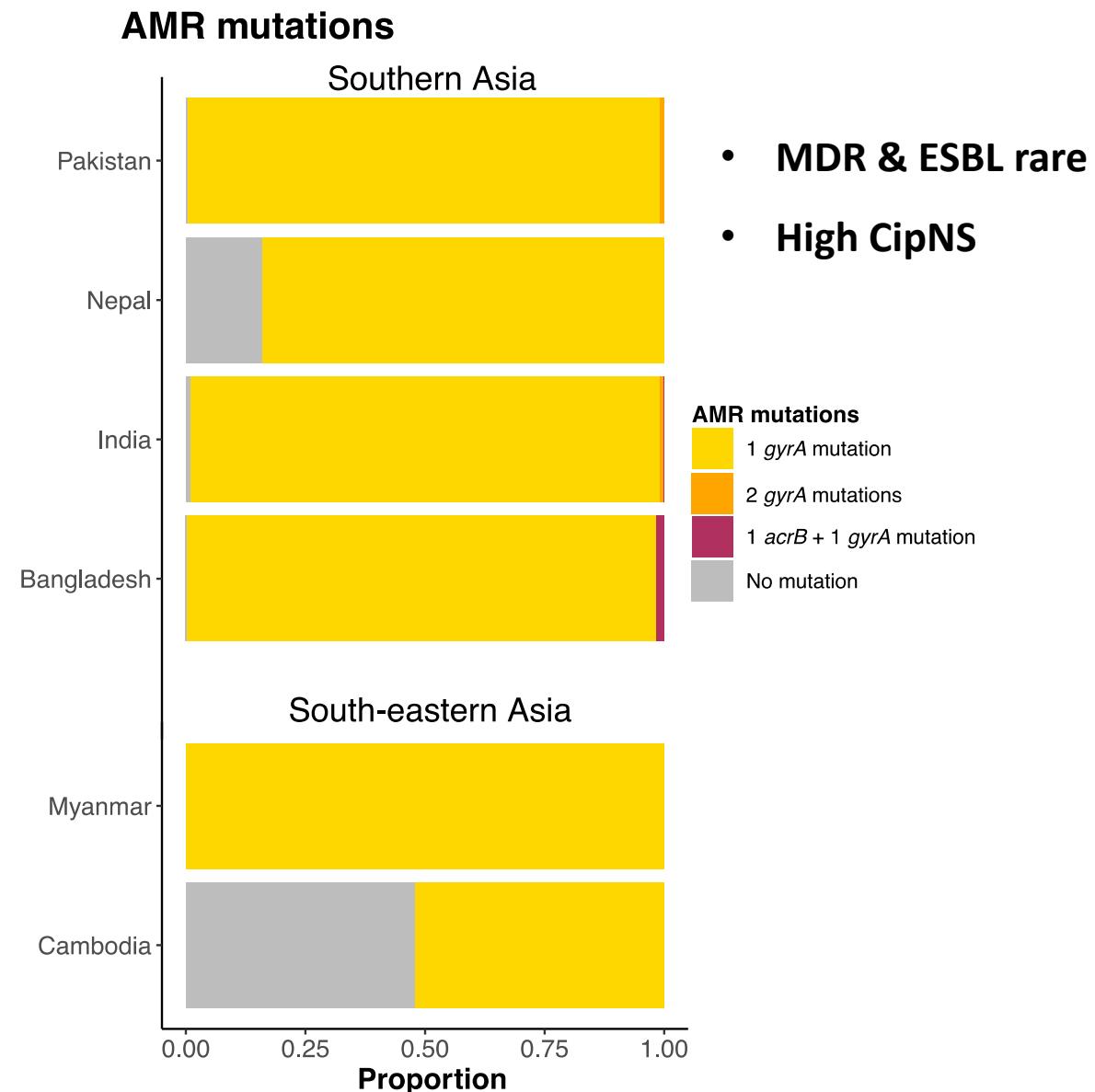
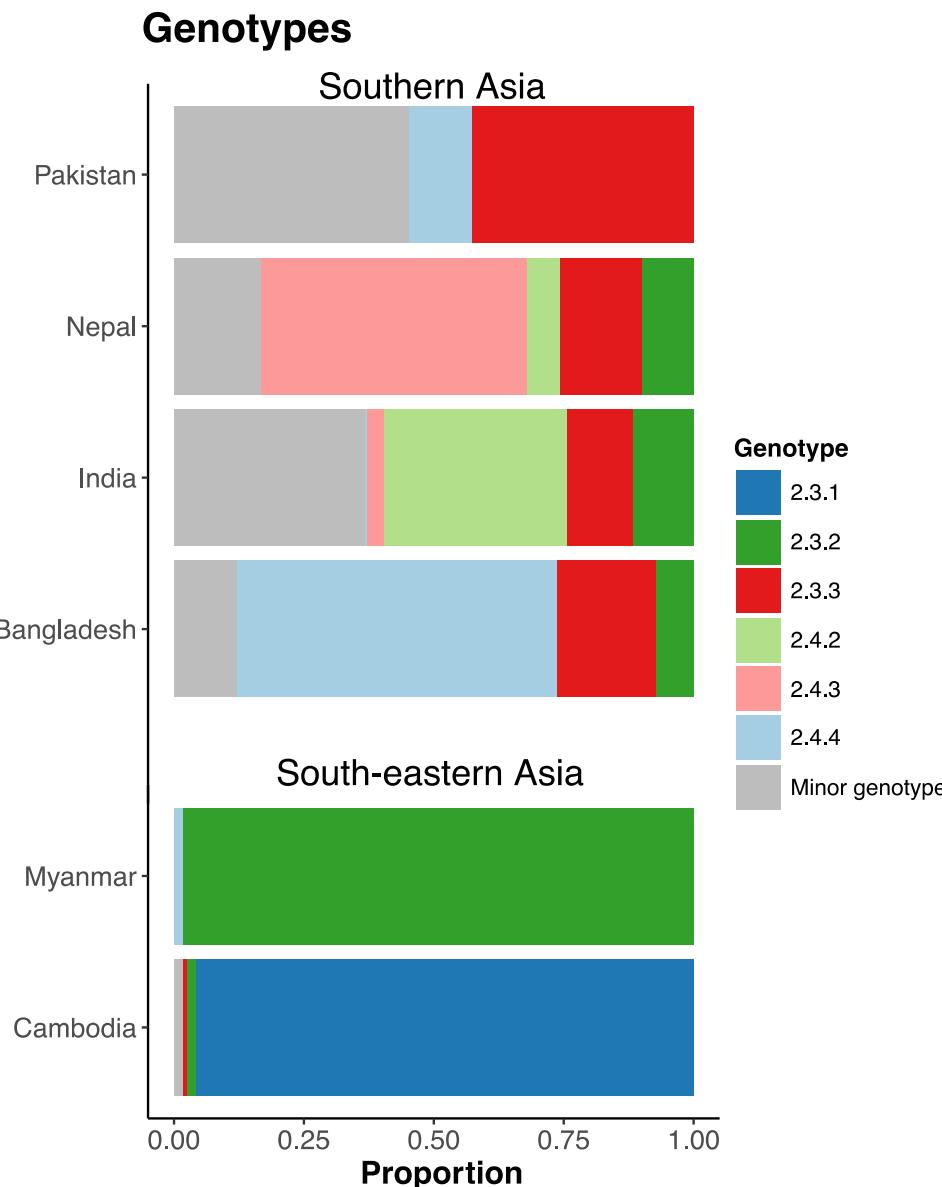
- Data available
- No data available

Number of WGS

- 200
- 400
- 600

n=2,561 genomes published prior to July 2023

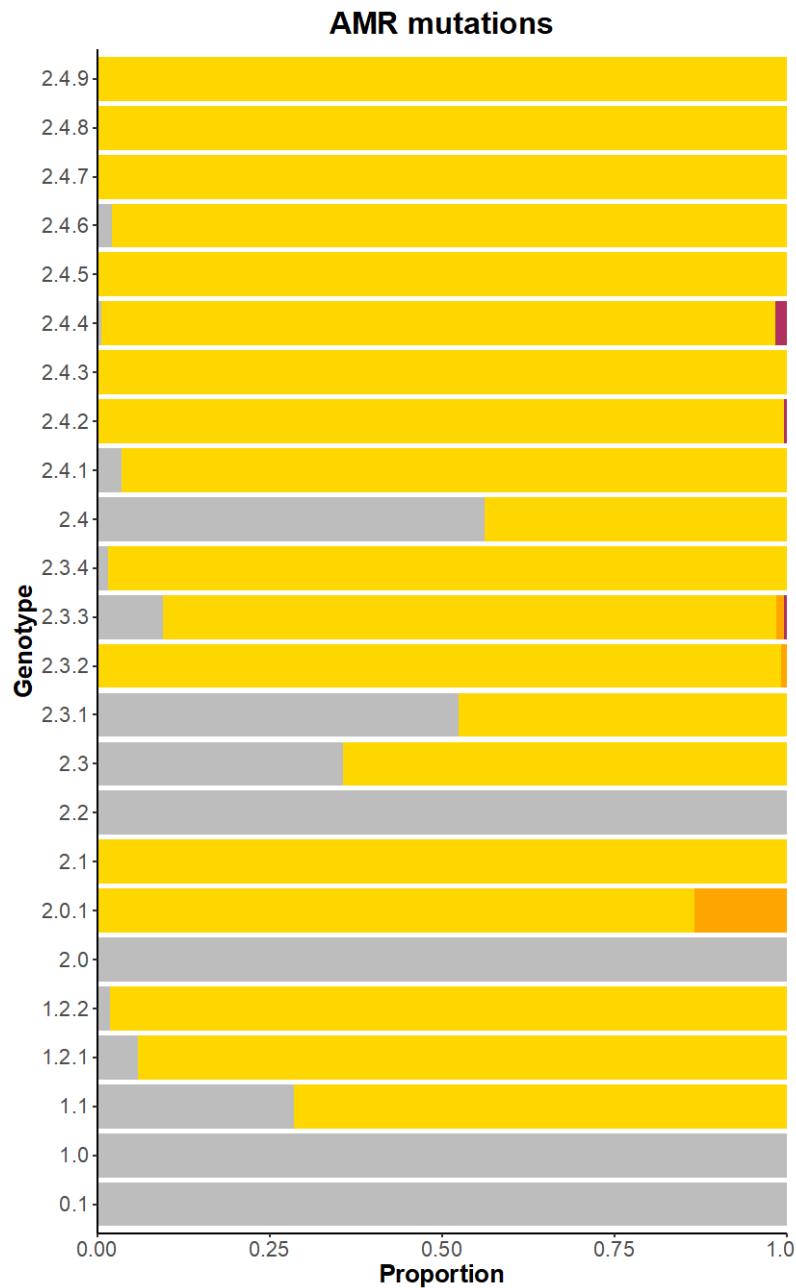
Public genome meta-analysis: genotype & AMR prevalence



Minor genotypes present at <20%

Endemic countries with $n \geq 20$ non-targeted sequences post 2010

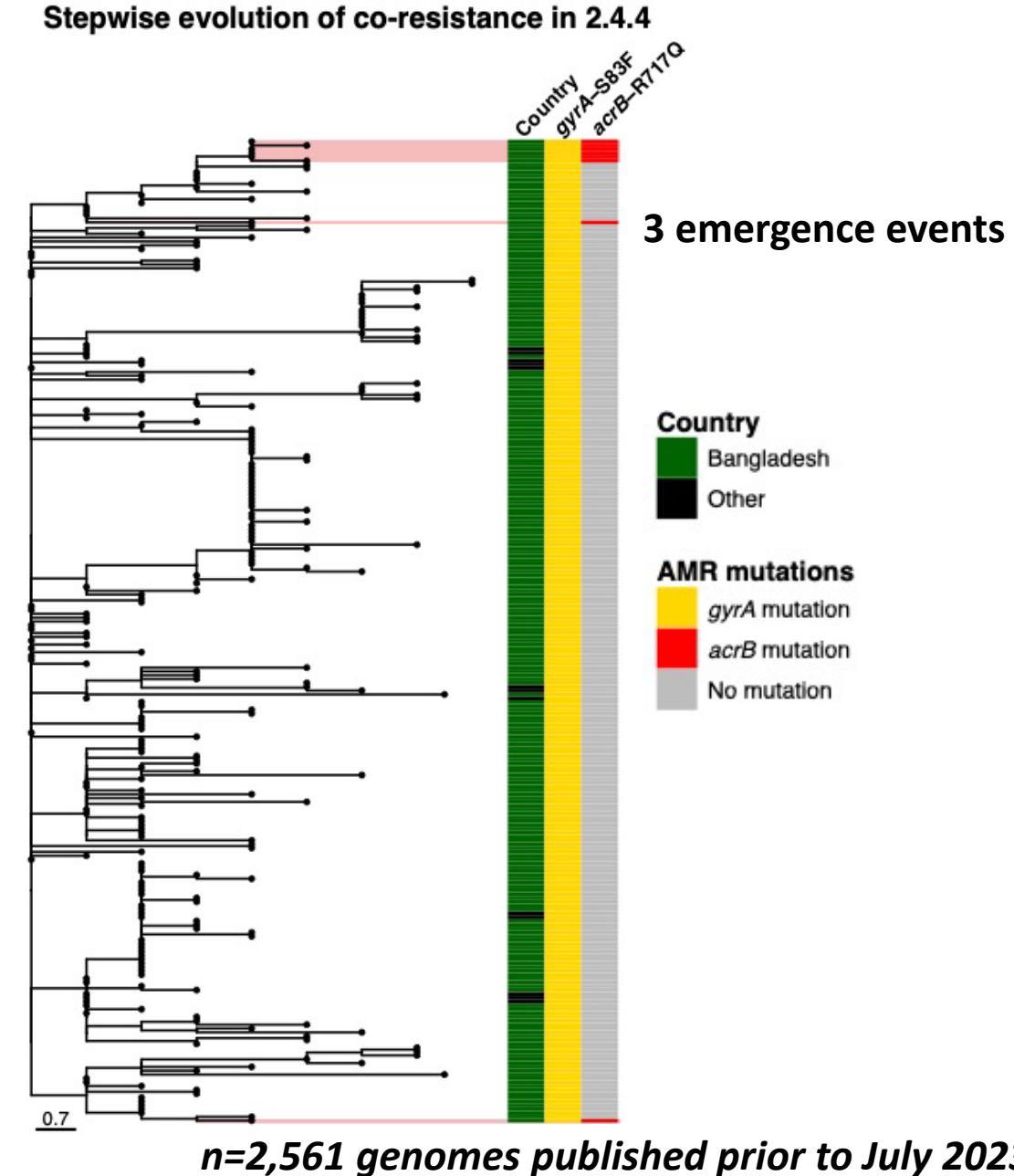
Public genome meta-analysis: variants of concern



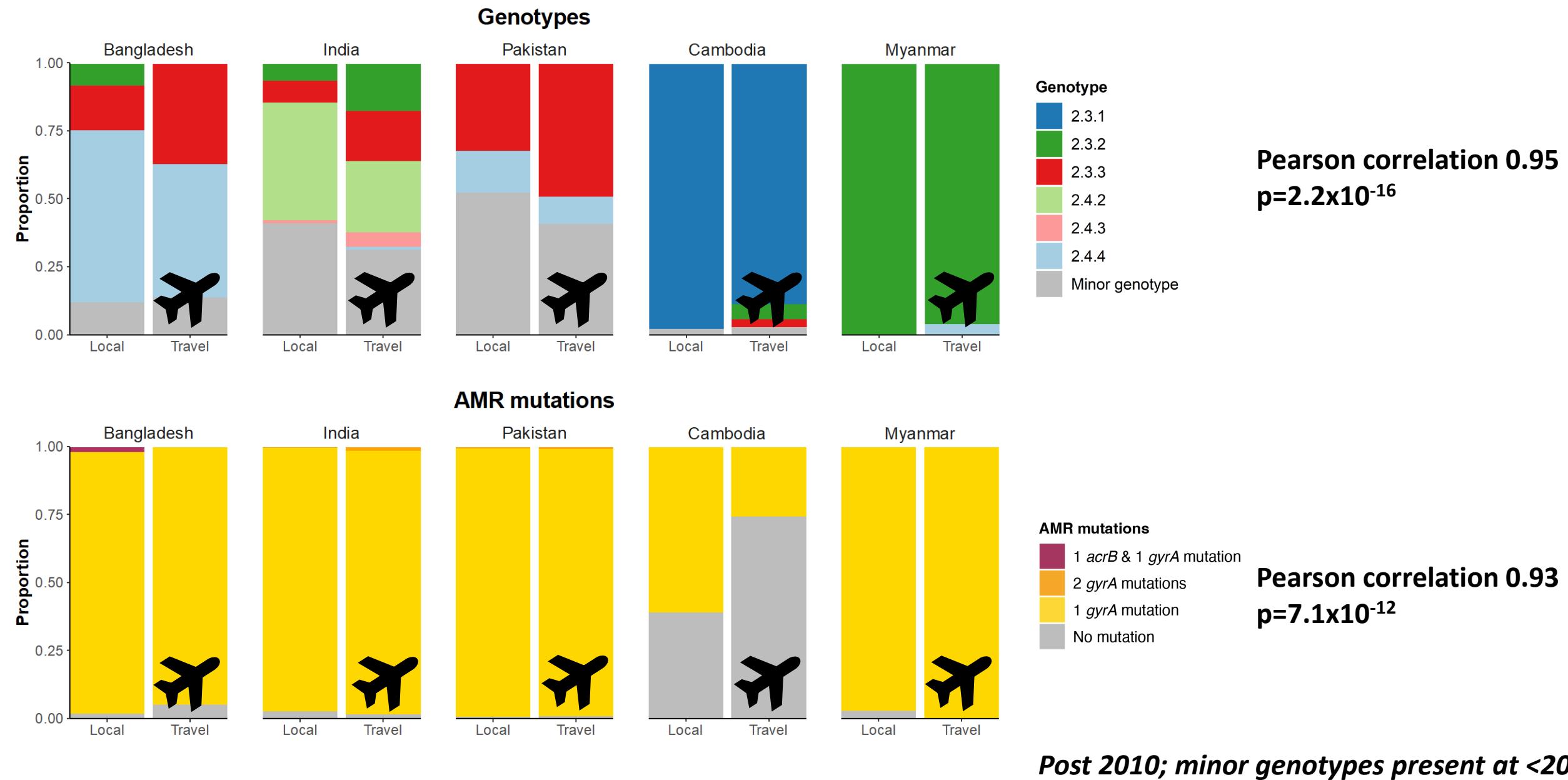
- Increased Ciprofloxacin MIC
- Ciprofloxacin & Azithromycin co-resistance

AMR mutations

- 1 *acrB* + 1 *gyrA* mutation
- 2 *gyrA* mutations
- 1 *gyrA* mutation
- No mutation



Travel-associated cases predict endemic populations



Future plans

- **Inaugural special interest group meeting in January 2024**
- **Formal working group analyses**
 - Integrate ~800 more genomes into the GTGC collection
 - Statistical analysis of genotype and AMR prevalence
 - Phylogenetic analysis of transmission dynamics
 - Develop accessible software solutions for Paratyphi A data analysis
- **Inform Paratyphi A control and intervention strategies**
 - Empirical therapy
 - Baseline data ahead of potential future vaccination programmes

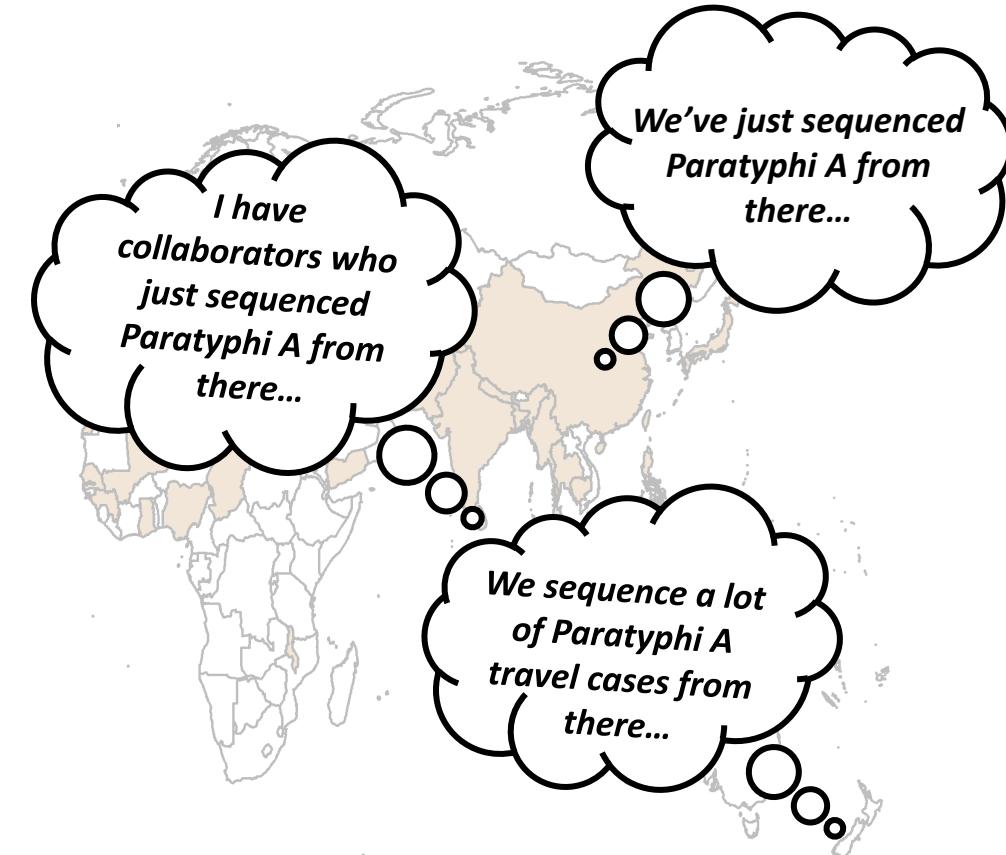
How to get involved

Seeking:

- Paratyphi A genomes and metadata
- Contributors to working group analyses

How to contribute:

- Membership questionnaire:
<https://bit.ly/ParatyphiREG>
- Come speak to us or email
typhinetinfo@gmail.com



Acknowledgements & further information

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Global Typhoid Genomics Consortium

<http://typhoidgenomics.org>

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LSHTM, UK

Prof Kathryn Holt

Dr Megan Carey

Typhoid Genomics Consortium

Consortium membership

<http://bit.ly/typhiREG>

<http://bit.ly/typhiMOU>

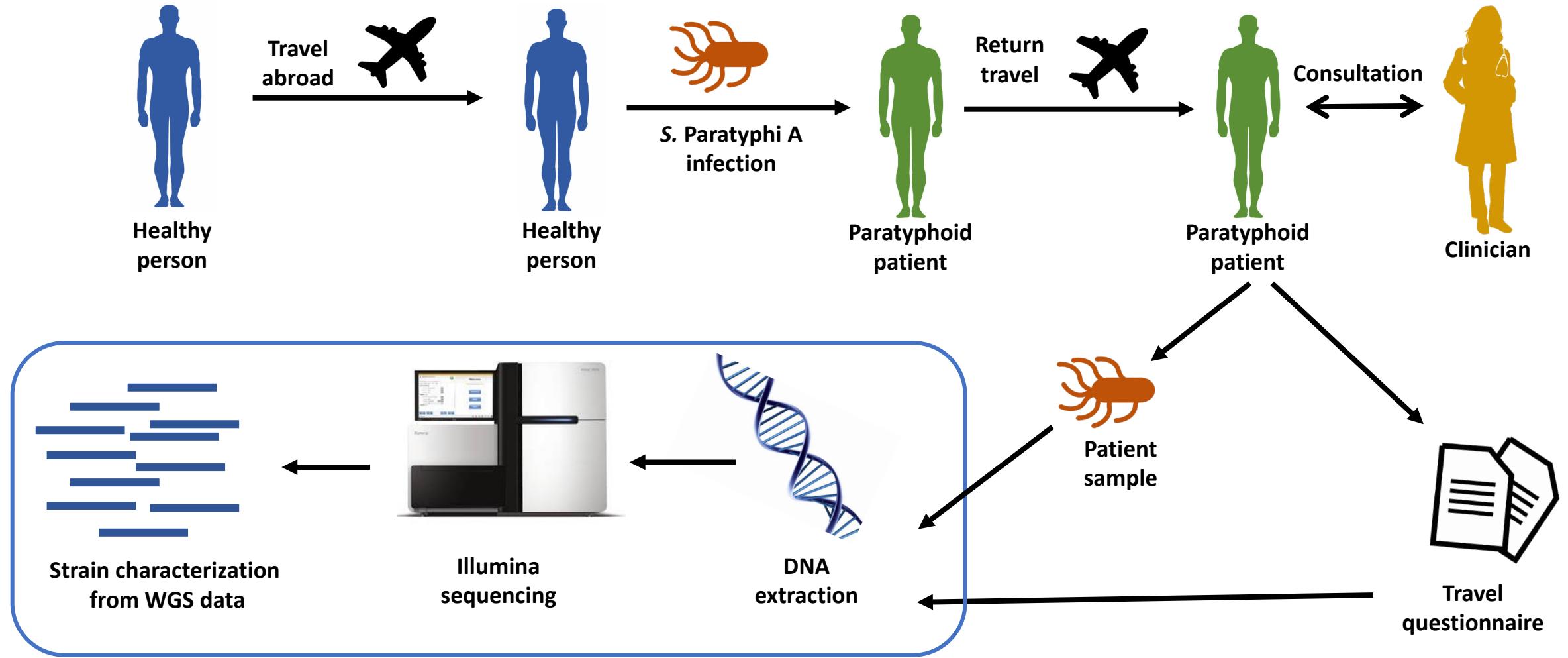
Paratyphi A working group membership

<https://bit.ly/ParatyphiREG>

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LSHTM ISSF3 Pump Priming Grant

Travel-associated paratyphoid cases



Public Health Laboratory e.g. UKHSA