

TyphINET

AMR surveillance dashboard



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TargetAMR webinar, February 5th 2026

Acknowledgements



Kat Holt



Louise Cerdeira



Megan Carey



Vandana Sharma

Global Typhoid Genomics Consortium

<https://typhoidgenomics.org>

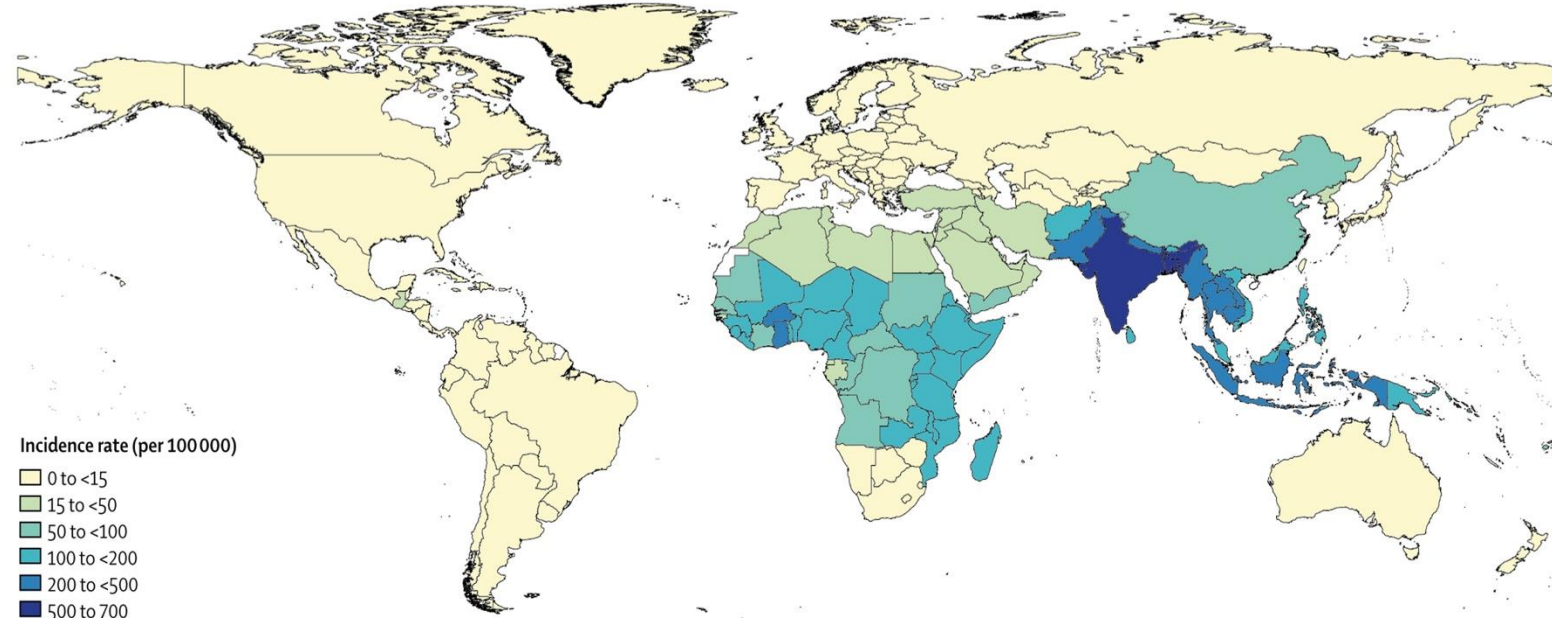
Typhoid fever: a global public health threat

Salmonella Typhi

- Gram-negative bacterium
- *Salmonella enterica* serovar
- Human restricted

Typhoid fever

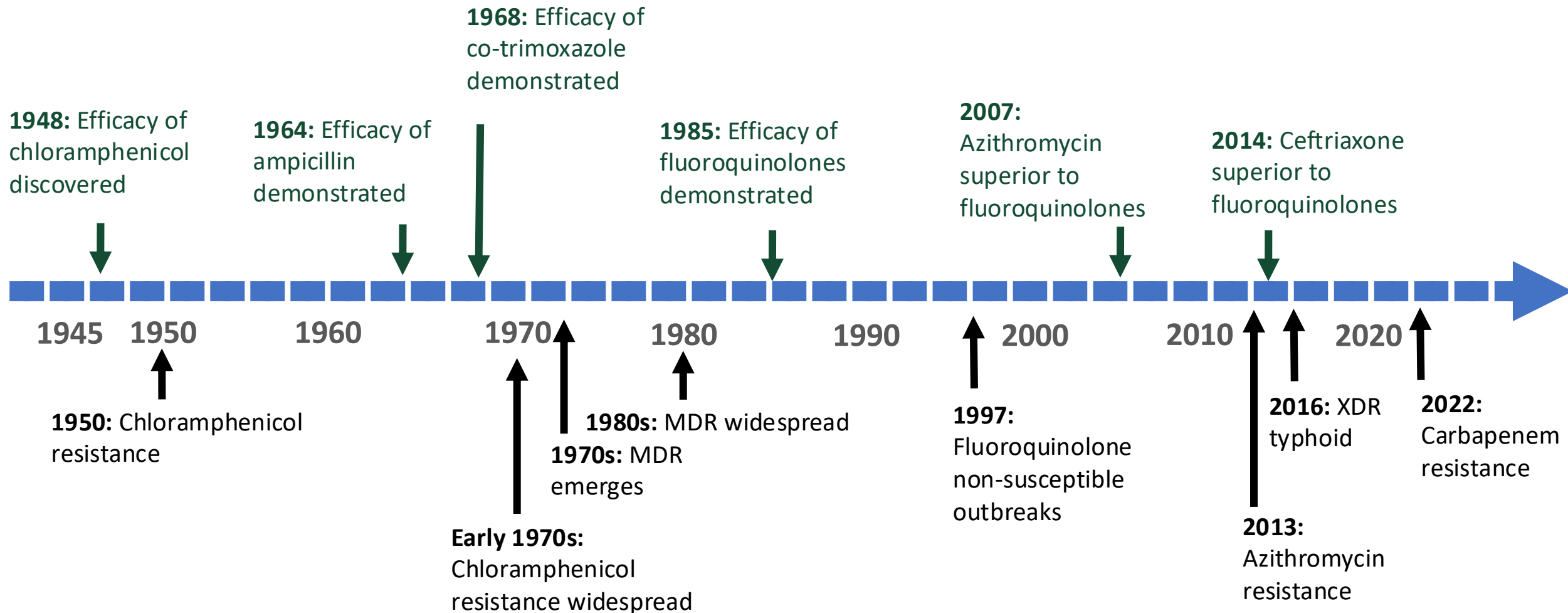
- Systemic infection
- ~10 million illnesses annually
- >100,000 mortalities annually
- Transmitted faeco-orally
- Endemic in many LMIC settings
- Asymptomatic carriage
- Antimicrobial resistance



Global burden of typhoid fever (GBD 2017, Lancet Inf Dis)



Antimicrobial resistance (AMR) & typhoid



AMR emergence in S. Typhi. Andrews et al. 2018, Parry et al. 2007; Hooda et al. 2020; Ain et al. 2022; Nizamuddin et al. 2023; Simon et al. 2025; Vasanthaiah et al. 2025; Priya et al. 2025

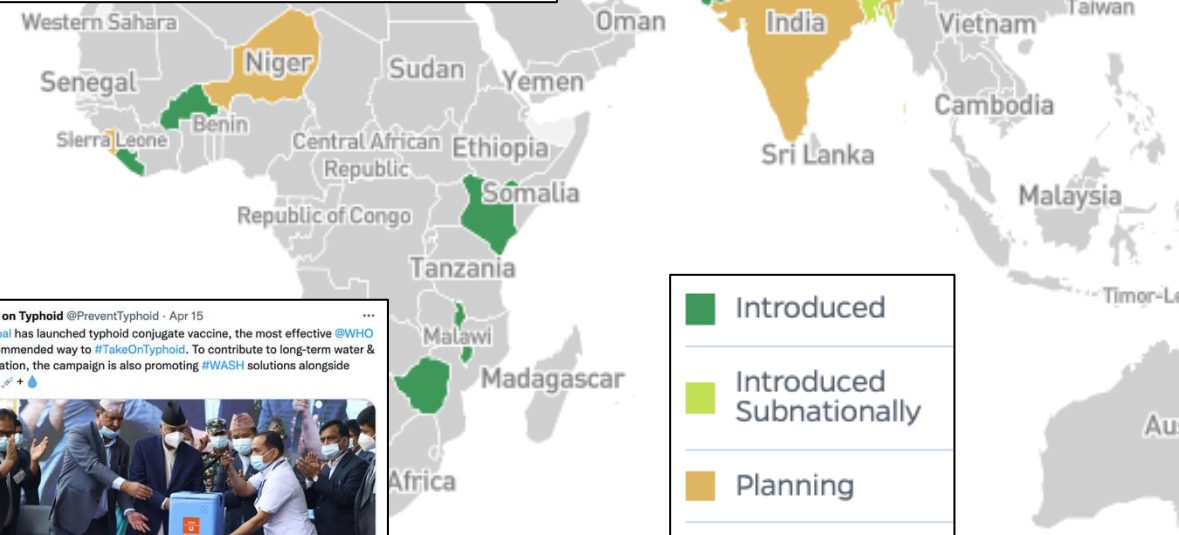
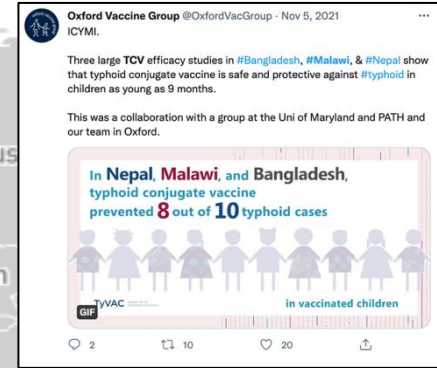
Control options for typhoid fever

Antimicrobial chemotherapy

Typhoid vaccines

- Until recently mainly for travelers to endemic regions
- 2018 WHO prequalified Vi conjugate vaccine
- 6 months of age
- 81-97% efficacy
- Introduced in Nepal, Bangladesh, Pakistan, Zimbabwe, Burkina Faso, Malawi, Fiji, Samoa, ...

WaSH (Water, sanitation, and hygiene)



Genomic surveillance of typhoid



Genomics is increasingly used as a **core method for pathogen characterisation** in research and public health laboratories



Genomic characterisation of AMR is **robust, reproducible, and informative**

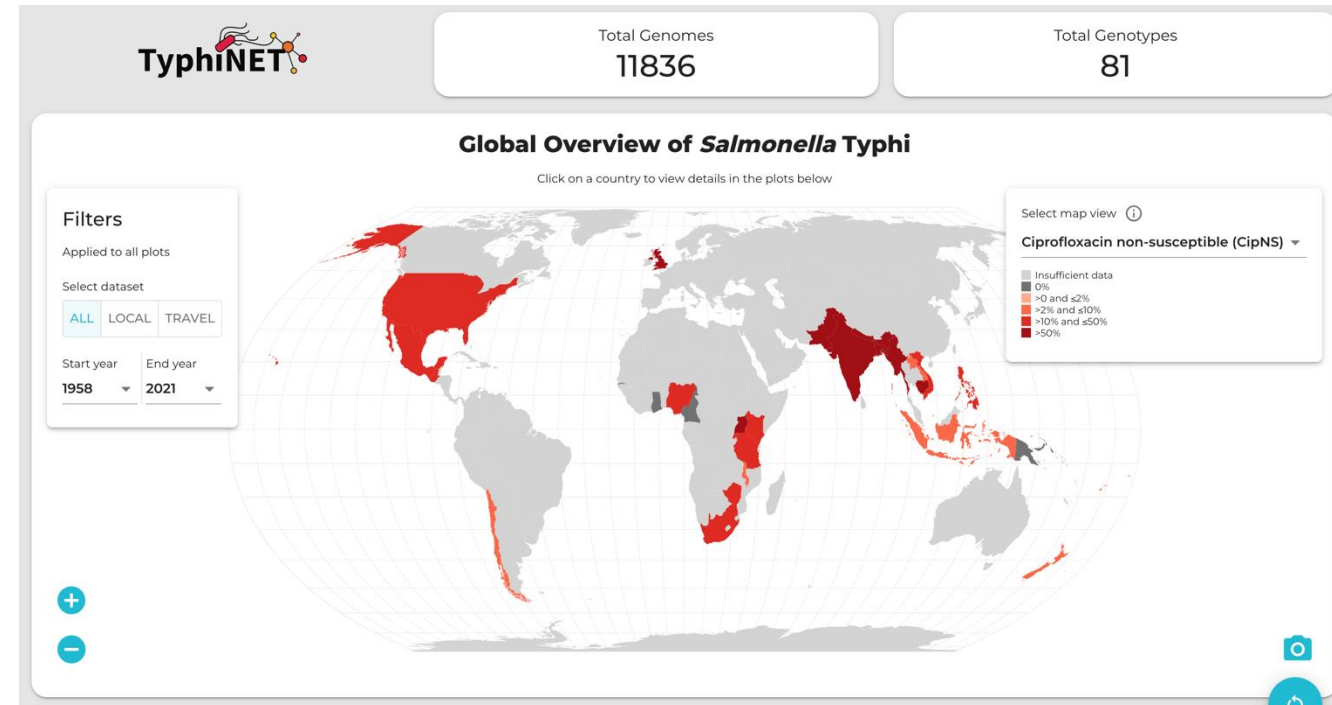


Genome data are **easily stored, shared, re-analysed and re-interpreted** as knowledge develops


TyphiNET dashboard objectives

- Unite typhoid WGS data
- Accessible & open access interface
- Representative genotype & AMR frequencies
- Query by location & time
- Identify trends
- Downloadable data, plots & reports
- Guide empirical therapy & targeting of intervention strategies, policy decision making

<https://www.typhi.net>

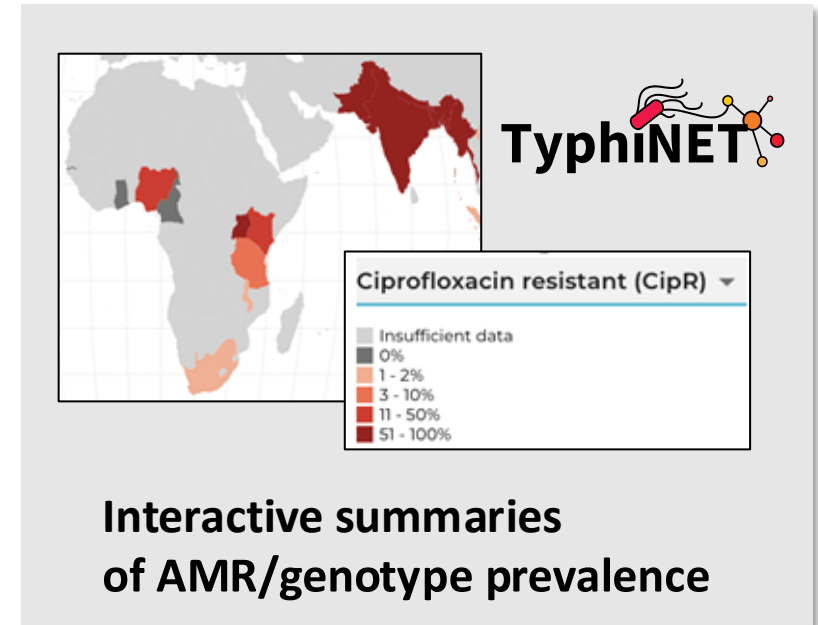


From data to knowledge



Country	Year
Kenya	2020
Kenya	2020
Pakistan	2020
Pakistan	2020
Pakistan	2020

**Sequence
+ metadata**



Microbiology lab

PH Policy makers



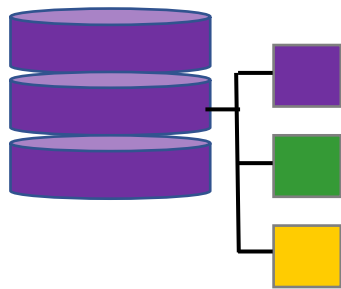
From data to knowledge

NCBI, ENA

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Sequence
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Typing tools
MLST, serotype, AMR

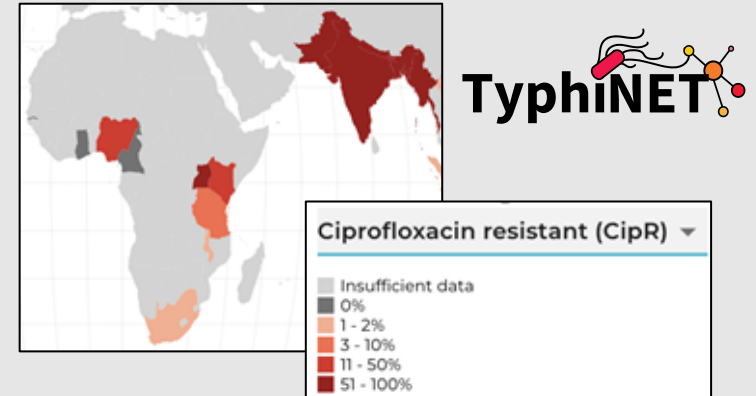


Organism-specific
analytics

Pathogenwatch,
Enterbase, PubMLST
NCBI Pathogens

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Kenya	2020	EA2	S
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Pakistan	2020	P1	R
Pakistan	2020	P1	R

Sample-level
information



Interactive summaries
of AMR/genotype prevalence

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PH Epidemiologists

Bioinformaticians

PH Policy makers



From data to knowledge

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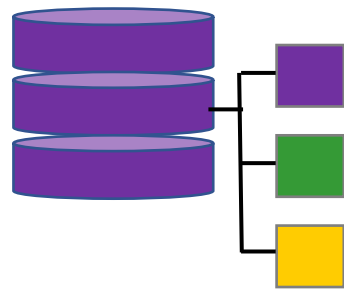
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Typing tools
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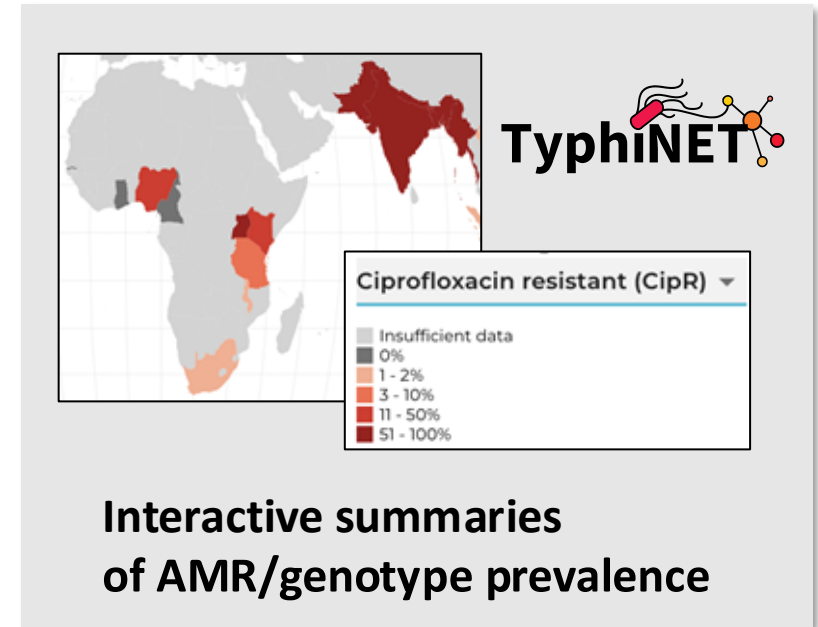
Organism-specific analytics

Database content & functionality

Pathogenwatch, Enterobase, PubMLST, NCBI Pathogens

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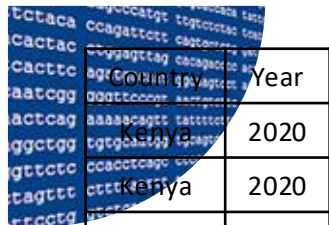
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From data to knowledge

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Pakistan	2020

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+ metadata**



Microbiology lab

Global Typhoid Genomics Consortium

2021-present

>200 members
~50 countries

Our Mission:

We aim to engage the global typhoid research community in order to aggregate *Salmonella* Typhi 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

Founders/coordinators:



Kathryn Holt
LSHTM



Zoe Dyson
LSHTM



Megan Carey
LSHTM



Stephen Baker
Univ. Cambridge



David Aanensen
Univ. Oxford

Typhi metadata template

Validated Typhi Metadata Template - v3

File Edit View Insert Format Data Tools Extensions Help

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A1 Data Accession


	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Data Accession	Study Accession	Sample Accession	DisplayName	Repeat Isolate	Year	Month	Day	Age	Sex	Country	City	Latitude	Longitude	Accuracy
2	REQUIRED (access	REQUIRED (e.g. NC	REQUIRED (e.g. NCBI BioSan	REQUIRED	REQUIRED (leave	REQUIRED	REQUIRED (Numer	REQUIRED (Numer	REQUIRED (in yea	REQUIRED	REQUIRED	OPTIONAL	OPTIONAL (Patient	OPTIONAL (Patient	OPTIONAL Pa
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Typhi Metadata Template Instructions Lab Code Master List

T
Purpose of Sampling
REQUIRED
Targeted [Cluster Investigation] ▼
Targeted [AMR investigation] ▼
Targeted [Other] ▼
Non Targeted [Reference lab] ▼
Non Targeted [Surveillance Study] ▼
Non Targeted [Routine diagnostics] ▼
Non Targeted [Other] ▼
Not Provided ▼

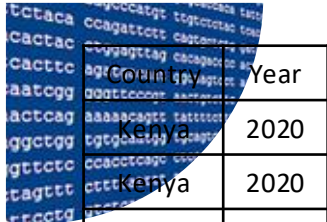
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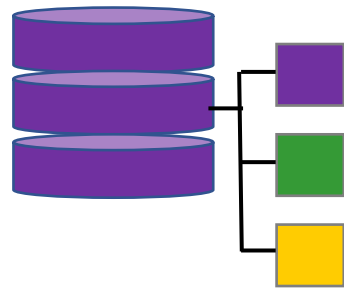
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NCBI, ENA

Typing tools
MLST, serotype, AMR



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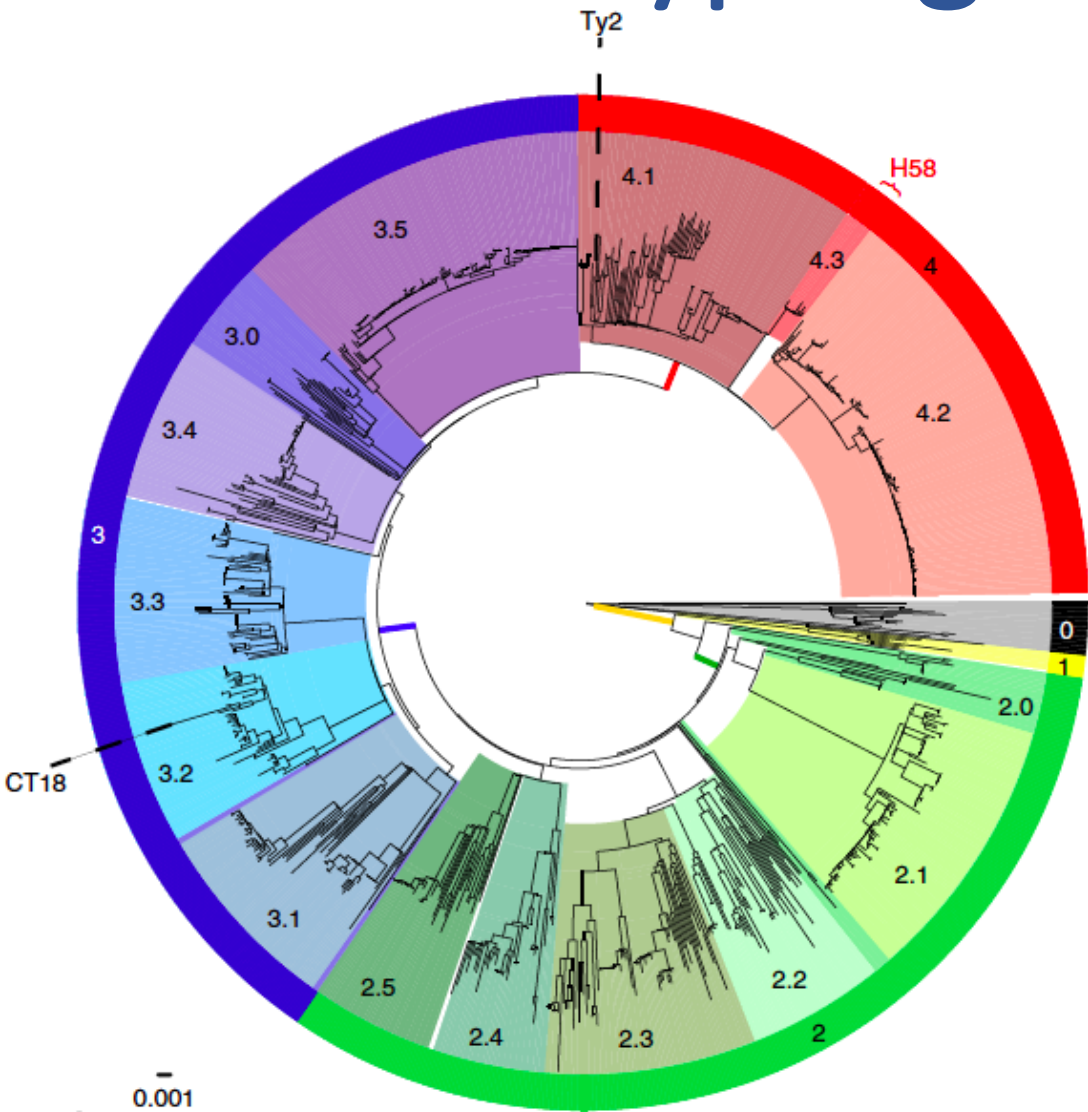
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analytics**



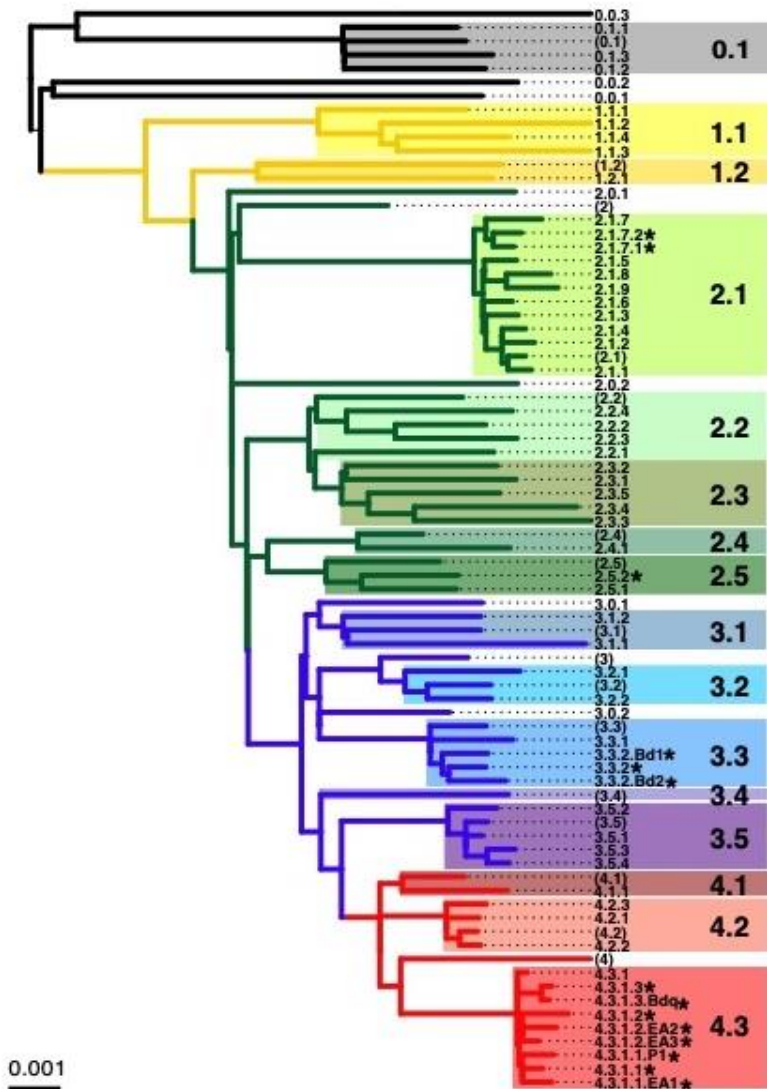
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Bioinformaticians

GenoTyphi genotyping framework

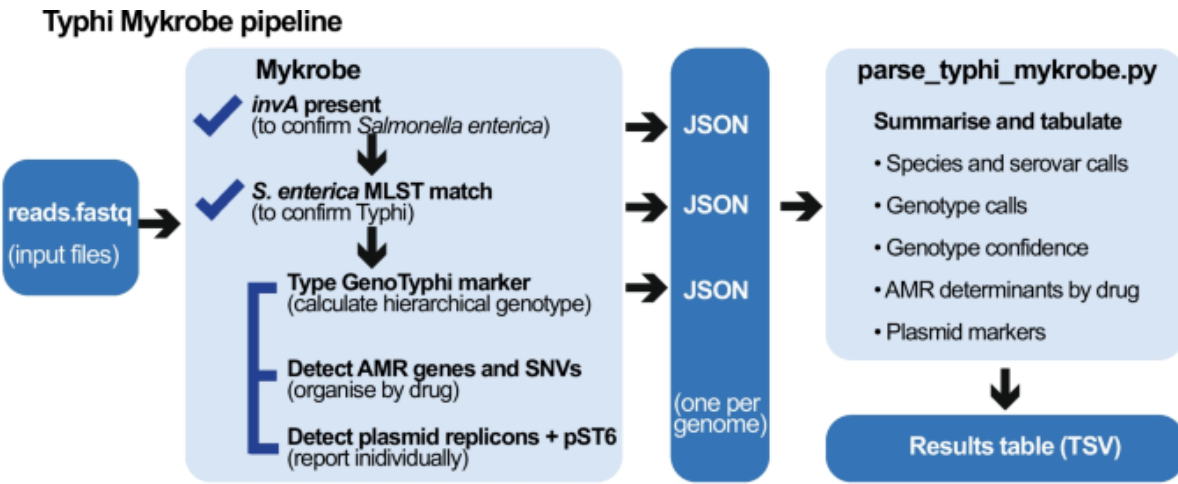
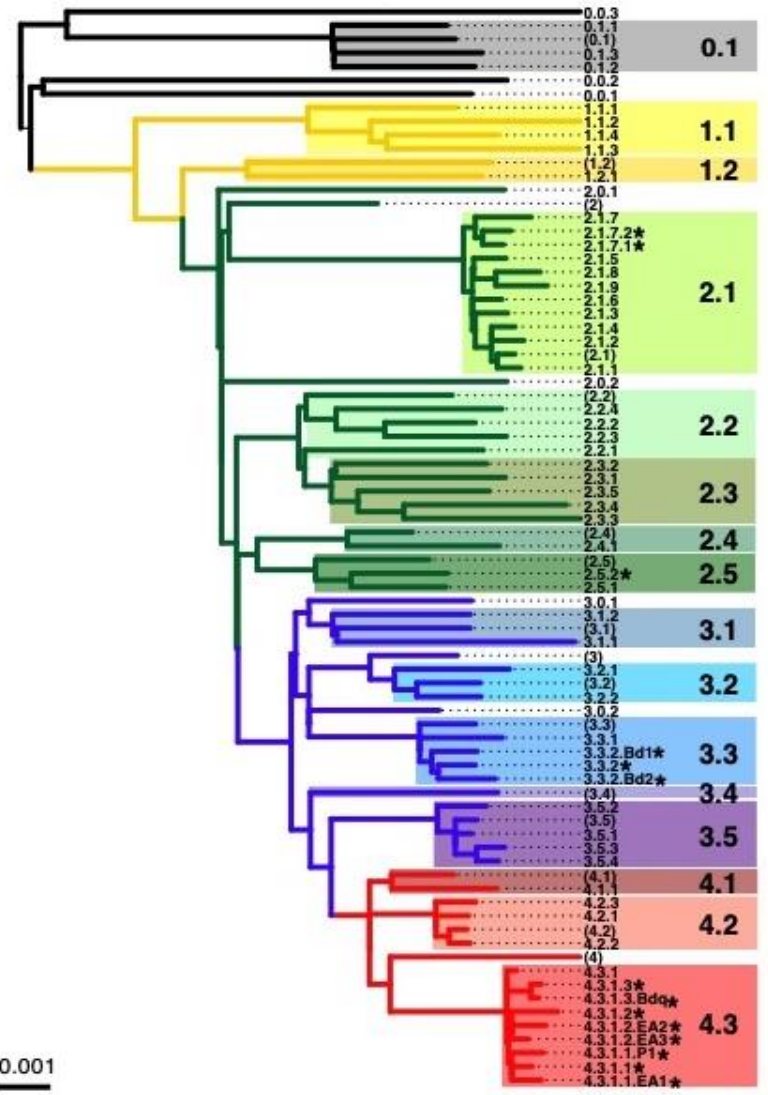


Global population structure of Salmonella Typhi
Wong et al. 2016, Nat Commun



Updated *S. Typhi* genotyping framework
Dyson & Holt 2021, J Infect Dis; github.com/katholt/genotyphi

Typhi Mykrobe: genotyping from reads



AMR determinants included in Typhi Mykrobe

Drug	Acquired genes	Point mutations
ampicillin	<i>bla</i> TEM-1, <i>bla</i> OXA-7	
azithromycin	<i>ereA</i> , <i>ermB</i> , <i>mphA</i>	AcrB-717
carbapenems	<i>bla</i> KPC-2, <i>bla</i> NDM-5, <i>bla</i> VIM-1, <i>bla</i> IMP-27, <i>bla</i> OXA-48	
ceftriaxone	<i>ampC1</i> , <i>bla</i> CTX-M-15, <i>bla</i> OXA-134, <i>bla</i> SHV-12	
chloramphenicol	<i>catA1</i> , <i>cmlA1</i>	
ciprofloxacin	<i>qnrB1</i> , <i>qnrD1</i> , <i>qnrS1</i>	GyrA-83, GyrA-87, GyrB-464F, ParC-80, ParC-84
sulfonamides	<i>sul1</i> , <i>sul2</i>	
trimethoprim	<i>dfrA1</i> , <i>dfrA5</i> , <i>dfrA7</i> , <i>dfrA14</i> , <i>dfrA15</i> , <i>dfrA17</i> , <i>dfrA18</i>	
tetracycline	<i>tetA(A)</i> , <i>tetA(B)</i> , <i>tetA(C)</i> , <i>tetA(D)</i>	

Plasmids included in Typhi Mykrobe

Group	Plasmid probe target
AMR-linked replicons	IncFIBK, IncHI2A, IncI1, IncL/M, IncN, IncX1, IncX3, IncY
IncHI1 targets	IncHI1A, IncHI1BR27, IncFIAHI1 (rep markers); C19241A (marker of PST6 lineage)
Non-AMR plasmids	IncFIB_pHCM2 (cryptic), pBSSB1 (z66 flagellin), pO111

Typhi Mykrobe genotypes + AMR + mobile elements

Ingle et al. 2025, *Genome Med*; github.com/typhoidgenomics/genotyphi

Accuracy of Typhi AMR genotyping

Table 1. Evaluation of genotypic analysis for the prediction of resistance phenotypes for *S. Typhi*

Genotype resistance is classified as having one or more genetic marker/mutation.

Antibiotic	MIC no.*	Phenotype: susceptible		Phenotype: resistant	
		Genotype: resistant	Genotype: susceptible	Genotype: resistant	Genotype: susceptible
AMX	1034	0	726	308	0
AMX-CL	1034	0	726	308	0
CAZ	1034	0	983	51	0
CRO	1034	0	983	51	0
ETP	1034	0	1034	0	0
GEN	1034	0	1034	0	0
CIP	1034	0	83	950	1
AZM	1034	0	1034	0	0
TMP	1034	1	704	328	1
FOS	1013	0	1012	1	0
TET	1034	0	1006	28	0
SXT	1034	0	698	336	0
CHL	1034	0	711	323	0
COL	1034	0	1034	0	0
Total combinations	14 455	–	–	–	–

99.9% concordance


AMX, Amoxicillin; AMX-CL, amoxicillin/clavulanic acid; CAZ, ceftazidime; CIP, ciprofloxacin; CRO, ceftriaxone; ETP, ertapenem; GEN, gentamicin; AZM, azithromycin; TMP, trimethoprim; FOS, fosfomycin; TET, tetracycline; SXT, trimethoprim/sulphonamide; CHL, chloramphenicol; COL, colistin.


Numbers in bold relate to discrepancies between genotype and phenotype.

*The number of isolates that had phenotypic MIC testing.

From data to knowledge

 **Missing metadata**

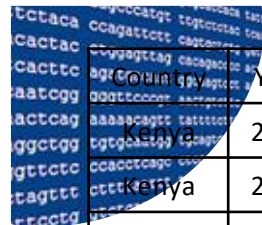
 **Missing tools for AMR interpretation**

 **Database content & functionality**

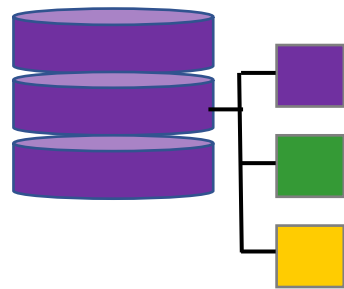
NCBI, ENA

Typing tools
MLST, serotype, AMR

Pathogenwatch,
Enterobase, PubMLST
NCBI Pathogens



Country	Year
Kenya	2020
Kenya	2020
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Country	Year	Genotype	Cipro
Kenya	2020	EA2	S
Kenya	2020	EA2	S
Pakistan	2020	P1	R
Pakistan	2020	P1	R
Pakistan	2020	P1	R

Sequence + metadata

Organism-specific analytics

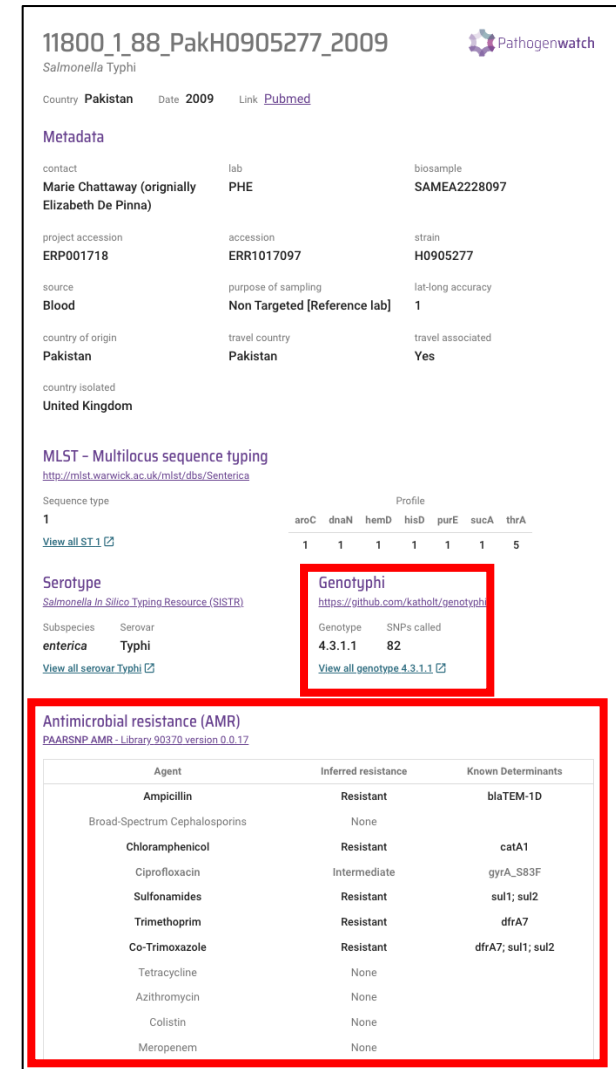
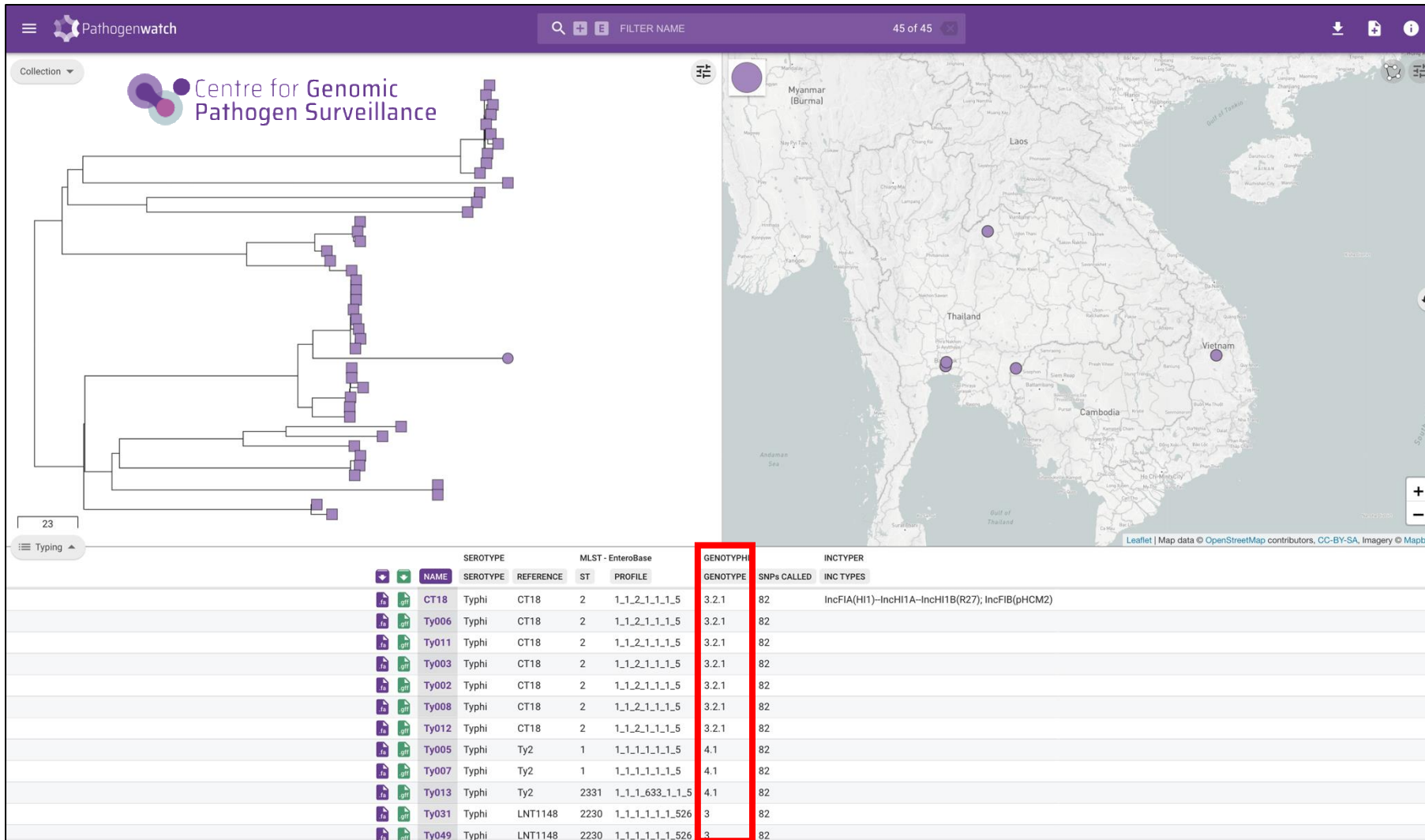
Sample-level information

 Microbiology lab

PH Epidemiologists

Bioinformaticians

Typhi Pathogenwatch



GenoTyphi genotyping + AMR detection available via Typhi Pathogenwatch online data analysis platform

Argimon et al. 2021, Nat Commun

Central hub for typhoid data

Pathogenwatch

GENOMES
COLLECTIONS
UPLOAD
DOCUMENTATION

Search

Salmonella Typhi

Public

Date

Viewing 70 of 161 collections

Sort by **Created: Most Recent**

<div style="display: flex; justify-content: space-between; align-items: flex-start;"> <div> <p>Rutanga et al. (2023) <i>Salmonella Typhi</i></p> <p>S. Typhi genomes from Rwanda</p> </div> <div style="text-align: right; font-size: 0.8em;"> <p> 51 genomes 5 months ago</p> </div> </div>	<div style="display: flex; justify-content: space-between; align-items: flex-start;"> <div> <p>South Africa NICD Typhi <i>Salmonella Typhi</i></p> <p>Typhi genomes contributed by the South Africa NICD to the Global Typhoid Genomics Consortium project</p> </div> <div style="text-align: right; font-size: 0.8em;"> <p> 281 genomes 5 months ago</p> </div> </div>	<div style="display: flex; justify-content: space-between; align-items: flex-start;"> <div> <p>Ashton et al. (2023) <i>Salmonella Typhi</i></p> <p>The rapid emergence of Salmonella Typhi with decreased ciprofloxacin susceptibility following an increase in ciprofloxacin prescriptions in Blantyre, Malawi</p> </div> <div style="text-align: right; font-size: 0.8em;"> <p> 20 genomes 6 months ago</p> </div> </div>
<div style="display: flex; justify-content: space-between; align-items: flex-start;"> <div> <p>Dyson et al. (2023) <i>Salmonella Typhi</i></p> <p>Genomic epidemiology and antimicrobial resistance transmission of Salmonella Typhi and Paratyphi A at three urban sites in Africa and Asia</p> </div> <div style="text-align: right; font-size: 0.8em;"> <p> 729 genomes 6 months ago</p> </div> </div>	<div style="display: flex; justify-content: space-between; align-items: flex-start;"> <div> <p>US CDC Typhi <i>Salmonella Typhi</i></p> <p>Typhi genomes contributed by US CDC to the Global Typhoid Genomics Consortium project</p> </div> <div style="text-align: right; font-size: 0.8em;"> <p> 887 genomes 8 months ago</p> </div> </div>	<div style="display: flex; justify-content: space-between; align-items: flex-start;"> <div> <p>Chattaway et al. (2021) <i>Salmonella Typhi</i></p> <p>Phylogenomics and antimicrobial resistance of Salmonella Typhi and Paratyphi A, B and C in England, 2016-2019</p> </div> <div style="text-align: right; font-size: 0.8em;"> <p> 635 genomes 8 months ago</p> </div> </div>
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CLEAR FILTERS

From data to knowledge

Missing metadata

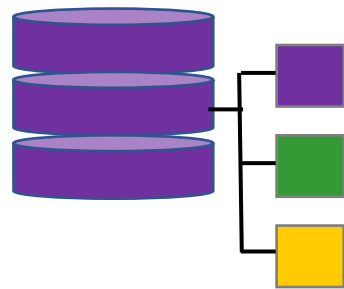
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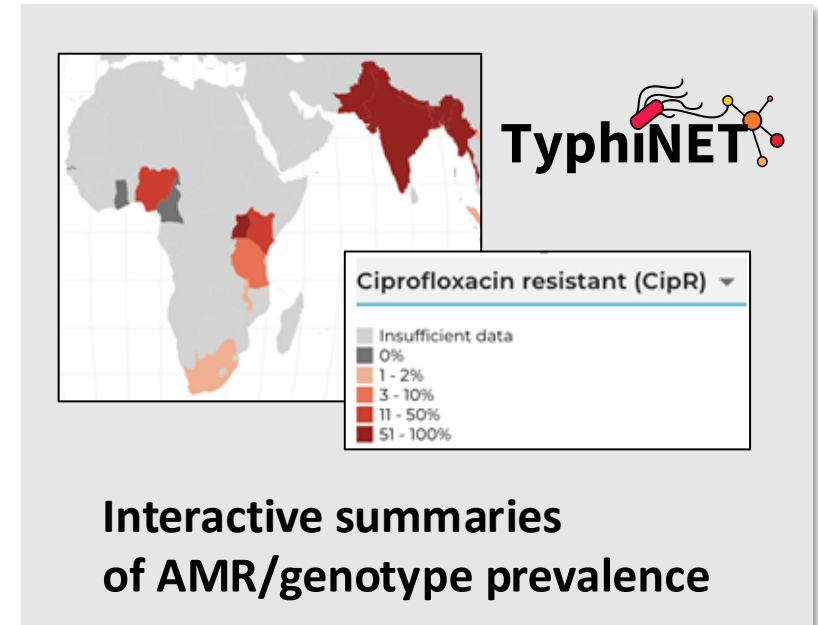
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Microbiology lab

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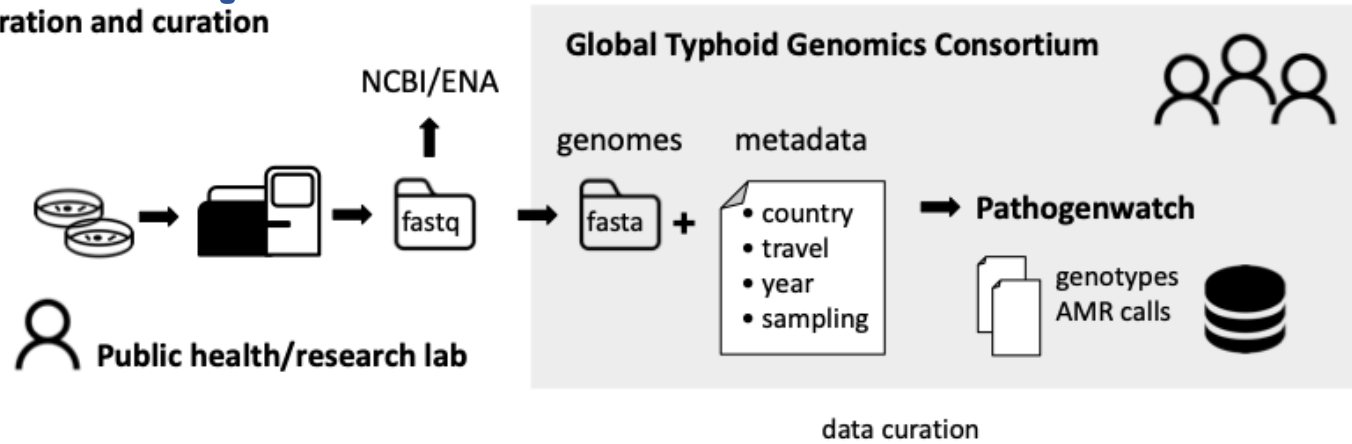
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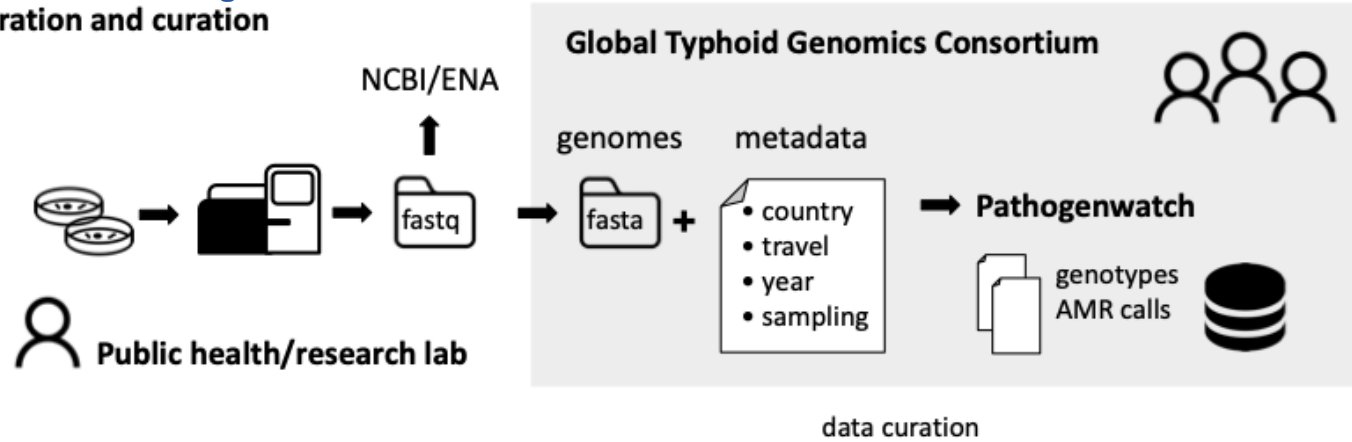
TyphiNET implementation

Data generation and curation



TyphiNET implementation

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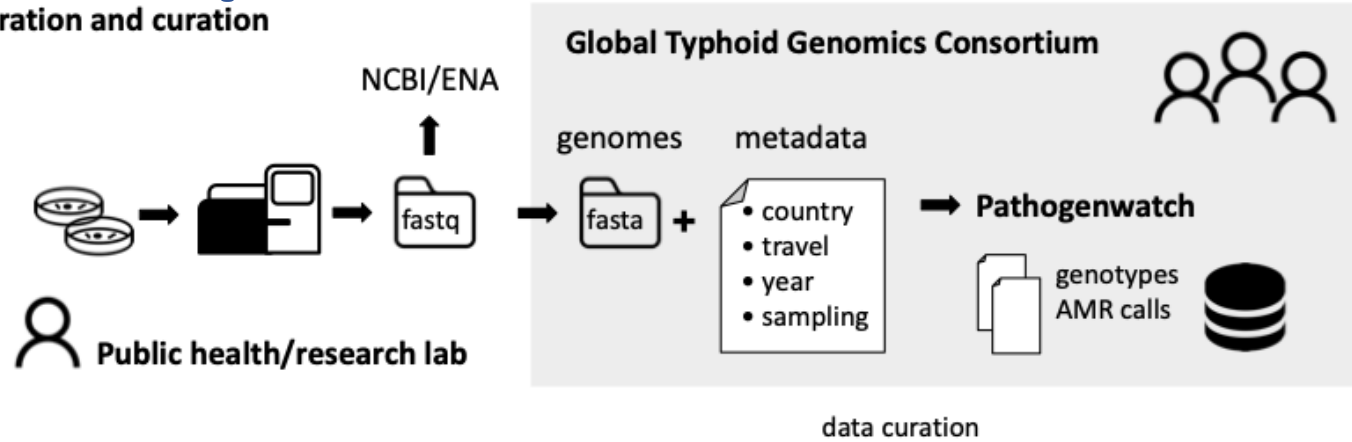


Data extraction



TyphiNET implementation

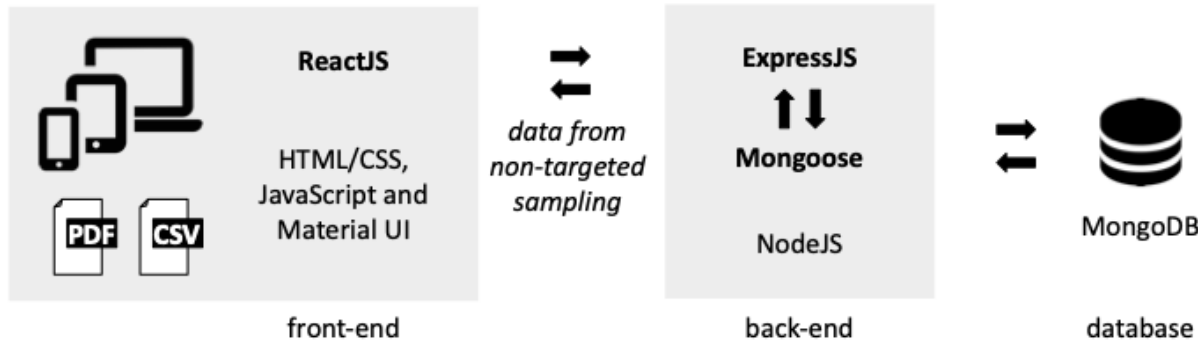
Data generation and curation



Data extraction



TyphiNET Dashboard



TyphiNET: Global overview



Total Genomes
11836

Total Genotypes
81

Global Overview of *Salmonella* Typhi

Click on a country to view details in the plots below

Filters

Applied to all plots

Select dataset

ALL LOCAL TRAVEL

Start year

1958

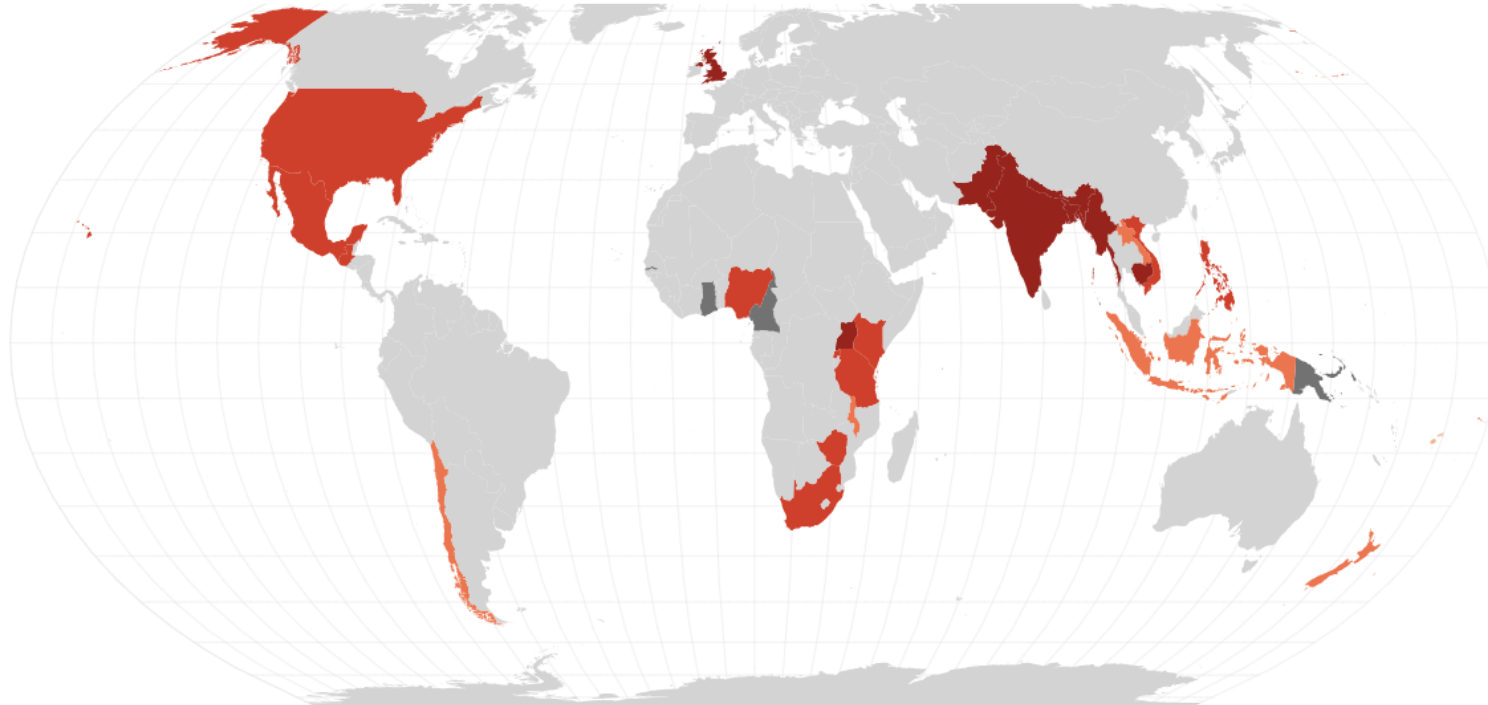
End year

2021

Select map view ⓘ

Ciprofloxacin non-susceptible (CipNS) ▾

- Insufficient data
- 0%
- >0 and ≤2%
- >2% and ≤10%
- >10% and ≤50%
- >50%



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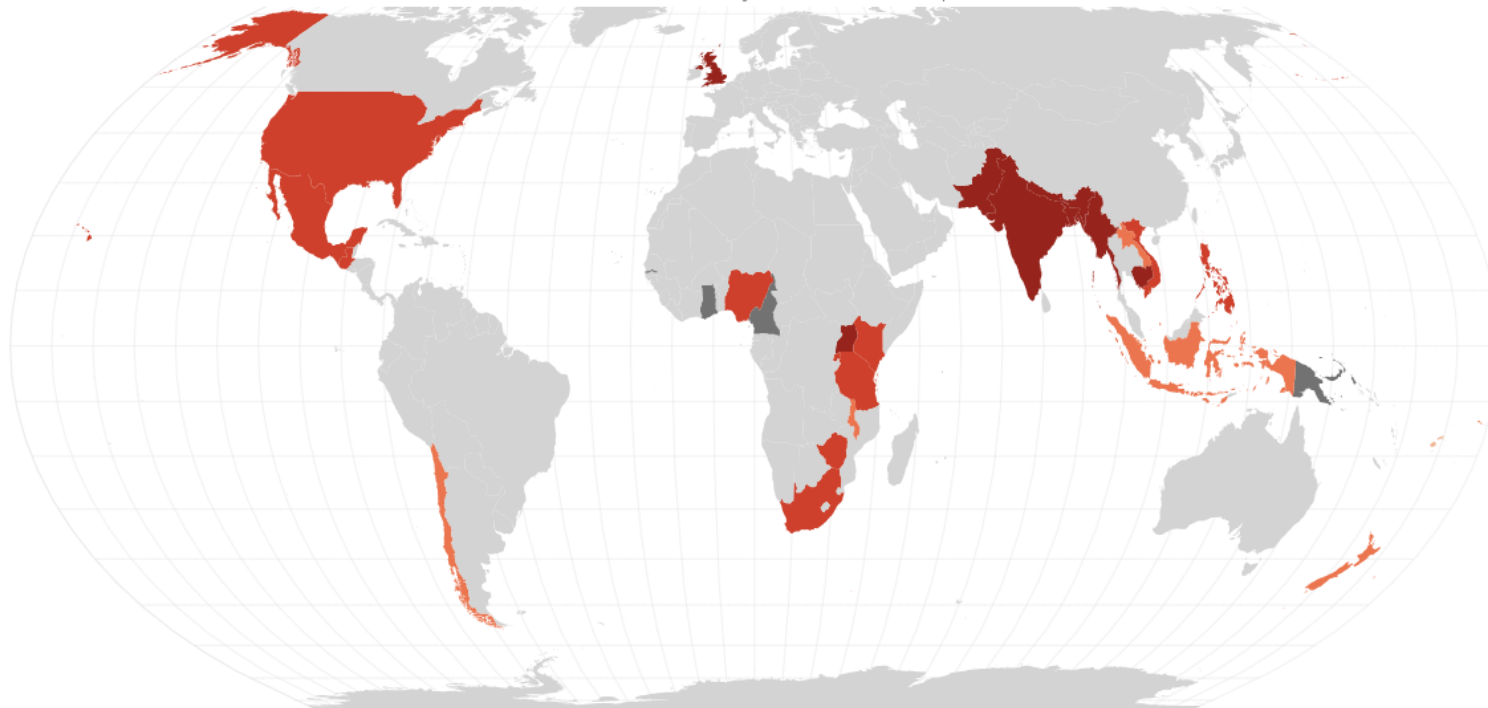
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1958 2021



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<https://www.typhi.net>

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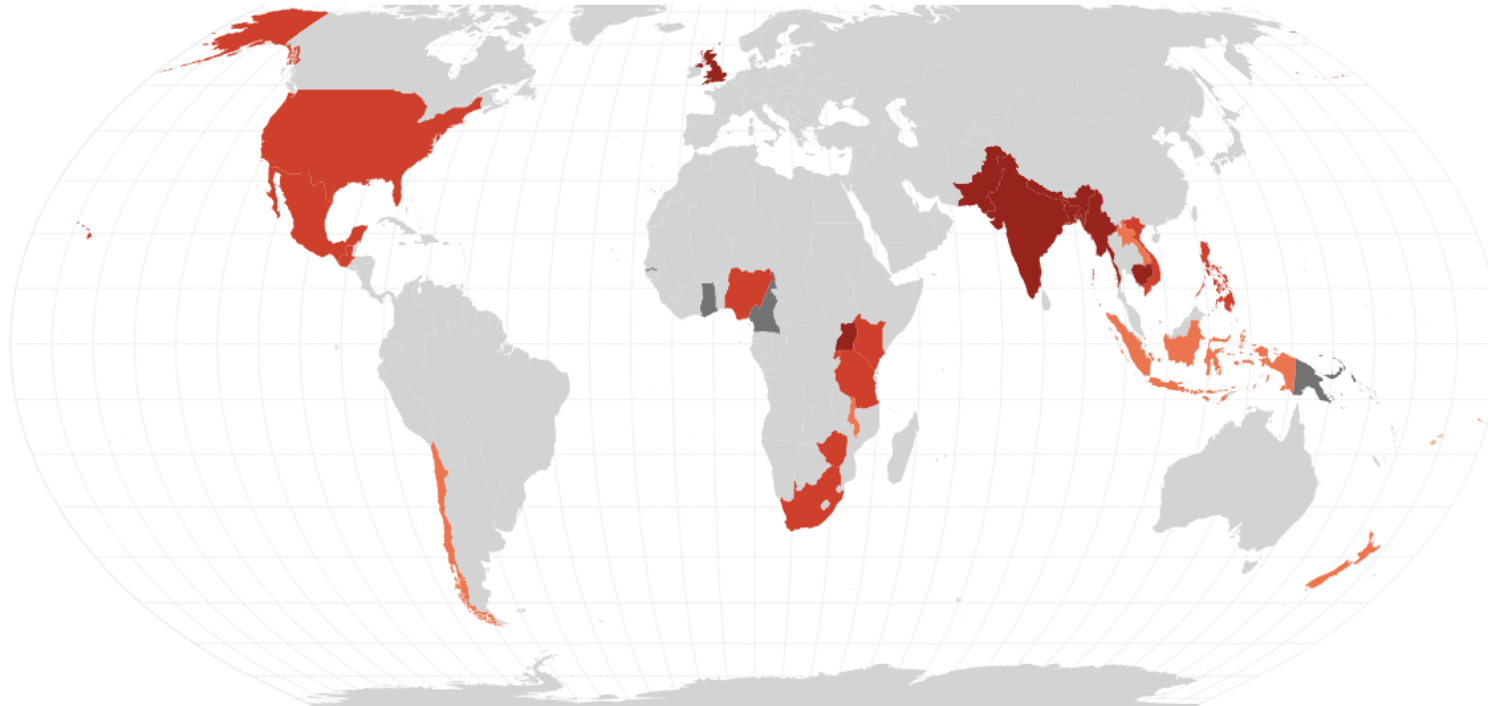
ALL LOCAL TRAVEL

Start year

1958

End year

2021



Select map view ⓘ

Ciprofloxacin non-susceptible (CipNS)

Multidrug resistant (MDR)

Extensively drug resistant (XDR)

Ceftriaxone resistant

Azithromycin resistant

Ciprofloxacin non-susceptible (CipNS)

Ciprofloxacin resistant (CipR)

Pansusceptible

Dominant Genotype

Genotype prevalence

H58 genotype

No. Samples

TyphiNET: Global overview



Total Genomes
11836

Total Genotypes
81

Global Overview of *Salmonella* Typhi

Click on a country to view details in the plots below

Filters

Applied to all plots

Select dataset

ALL LOCAL TRAVEL

Start year End year

1958 2021



Select map view ⓘ

Ciprofloxacin non-susceptible (CipNS) ▾

- Insufficient data
- 0%
- >0 and ≤2%
- >2% and ≤10%
- >10% and ≤50%
- >50%



TyphiNET: Global overview



Total Genomes
11836

Total Genotypes
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Global Overview of *Salmonella* Typhi

Click on a country to view details in the plots below

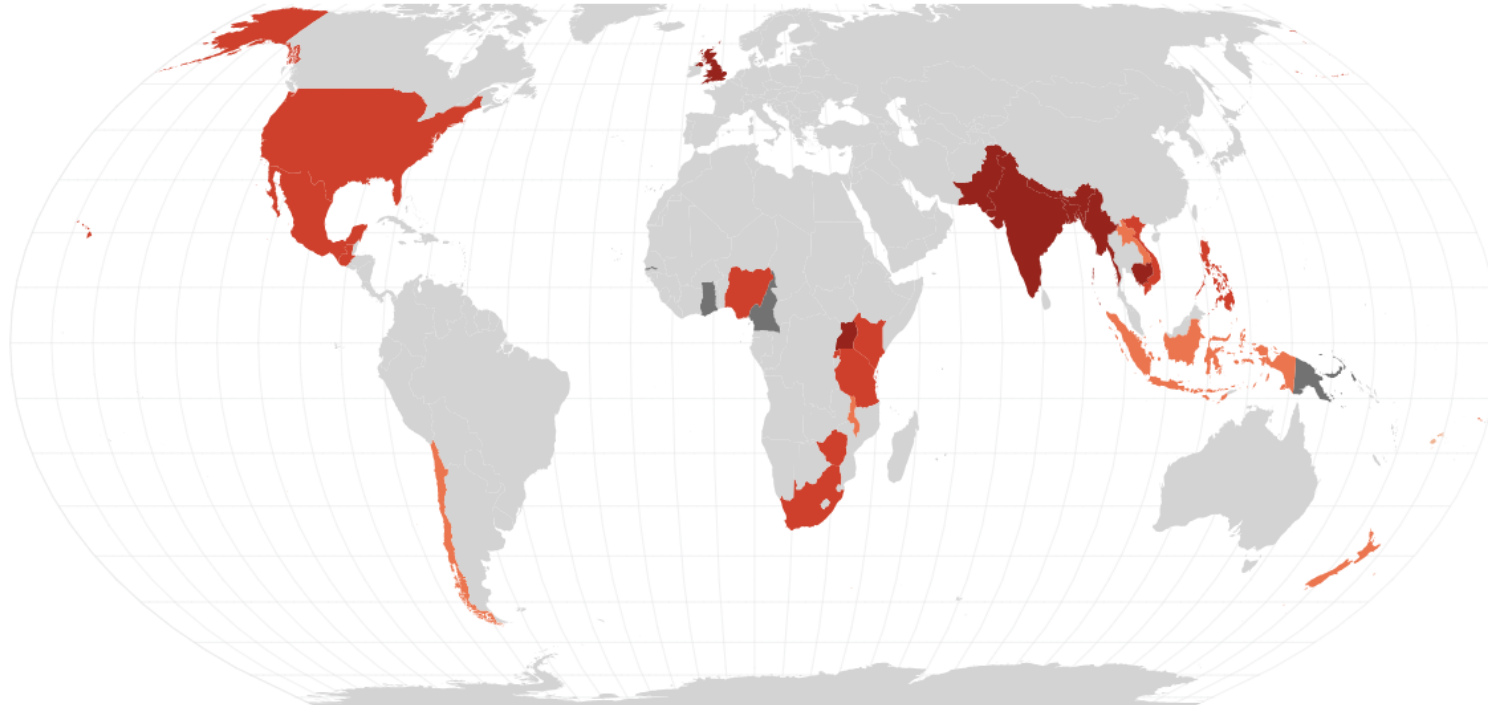
Filters

Applied to all plots

Select dataset

ALL LOCAL TRAVEL

Start year: 1958 End year: 2021



Select map view ⓘ

Ciprofloxacin non-susceptible (CipNS) ▾

- Insufficient data
- 0%
- >0 and ≤2%
- >2% and ≤10%
- >10% and ≤50%
- >50%



<https://www.typhi.net>

TyphiNET: Global overview



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Global Overview of *Salmonella* Typhi

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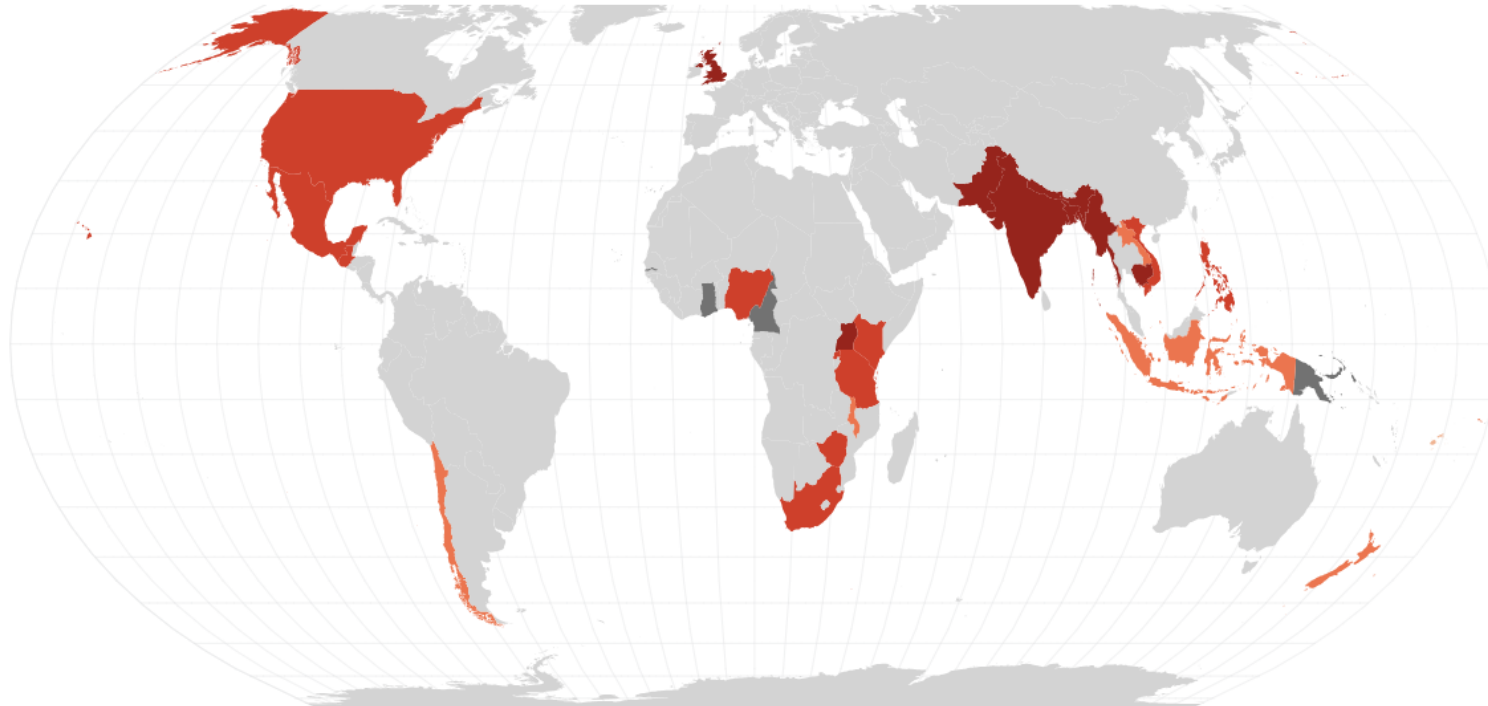
Applied to all plots

Select dataset

ALL LOCAL TRAVEL

Start year End year

1958 2021



Select map view ⓘ

Ciprofloxacin non-susceptible (CipNS) ▾

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- 0%
- >0 and ≤2%
- >2% and ≤10%
- >10% and ≤50%
- >50%



<https://www.typhi.net>

TyphiNET: Pakistan case study



Total Genomes
11836

Total Genotypes
81

Global Overview of *Salmonella* Typhi

Click on a country to view details in the plots below



Filters

Applied to all plots

Select dataset

ALL LOCAL TRAVEL

Start year End year

1958 2021

Select map view ⓘ

Ciprofloxacin non-susceptible (CipNS) ▾

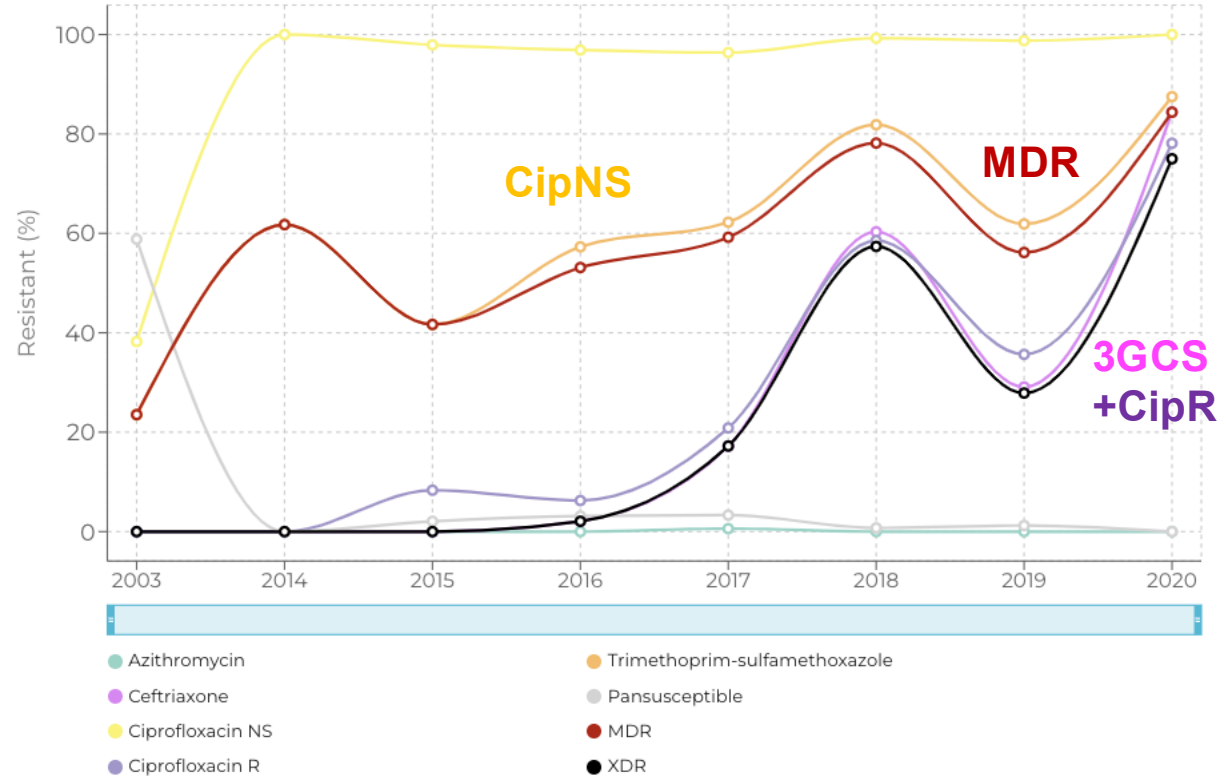
- Insufficient data
- 0%
- >0 and ≤2%
- >2% and ≤10%
- >10% and ≤50%
- >50%



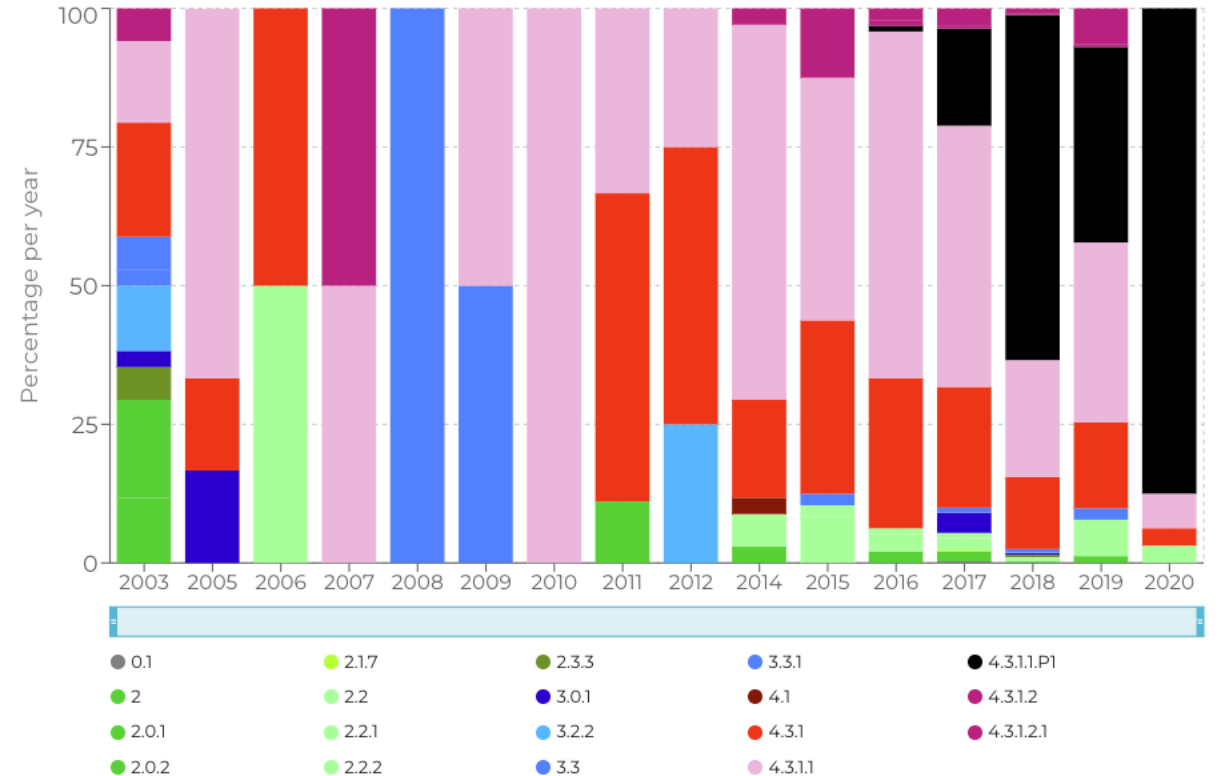
<https://www.typhi.net>

TyphiNET: Pakistan case study

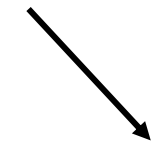
Drug resistance trends



Genotype distribution



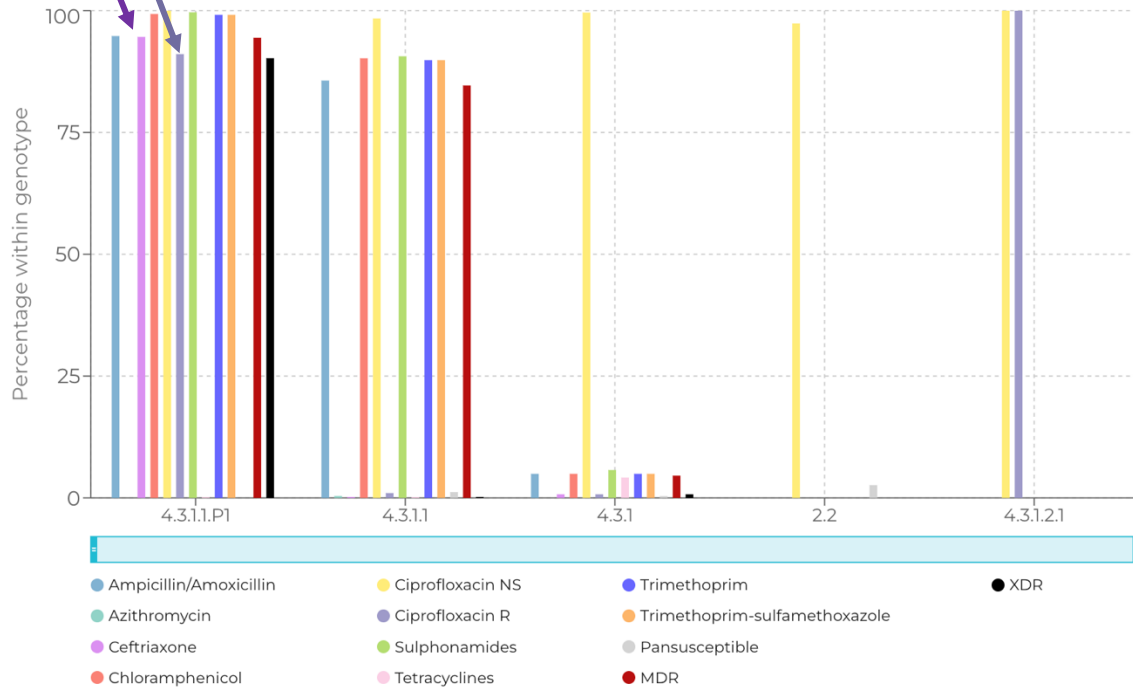
4.3.1.1.P1



TyphiNET: Pakistan case study

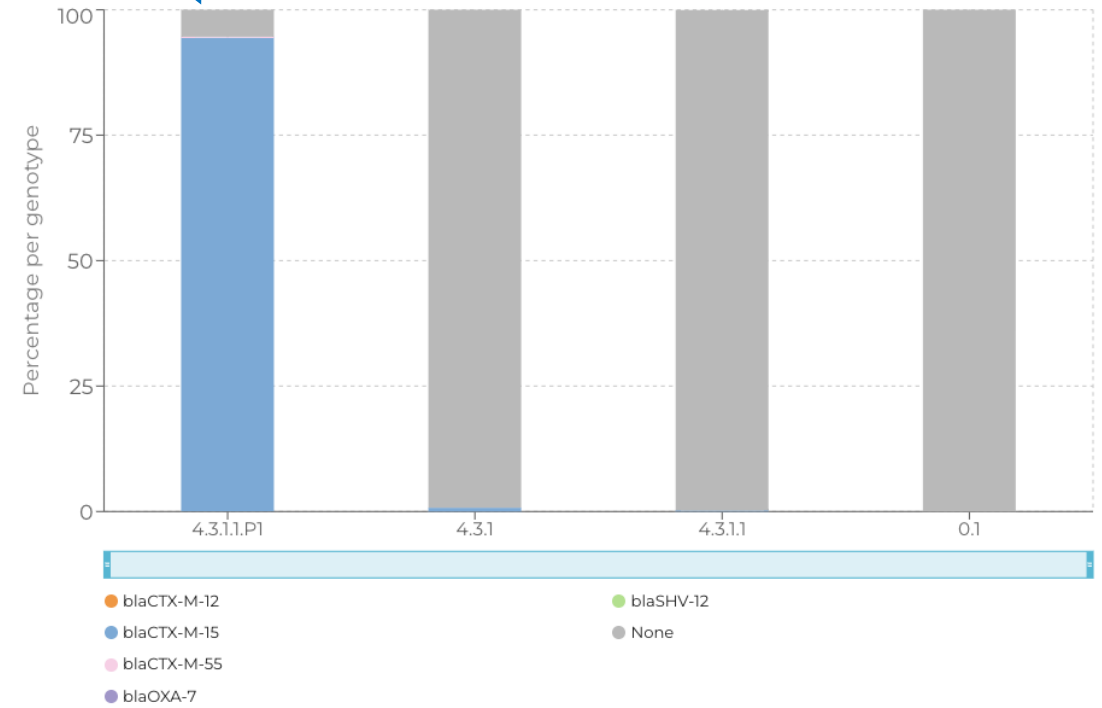
3GCS in 4.3.1.1.P1
+ CipR in 4.3.1.1.P1

Resistance frequencies within genotypes



blaCTX-M-15 in 4.3.1.1.P1 (XDR)

Resistance determinants within genotypes



XDR typhoid in Pakistan



RESEARCH ARTICLE
January/February 2018 Volume 9 Issue 1 e00105-18
<https://doi.org/10.1128/mBio.00105-18>

Emergence of an Extensively Drug-Resistant *Salmonella enterica* Serovar Typhi Clone Harboring a Promiscuous Plasmid Encoding Resistance to Fluoroquinolones and Third-Generation Cephalosporins

[Klemm *et al.* 2018](#)



microorganisms

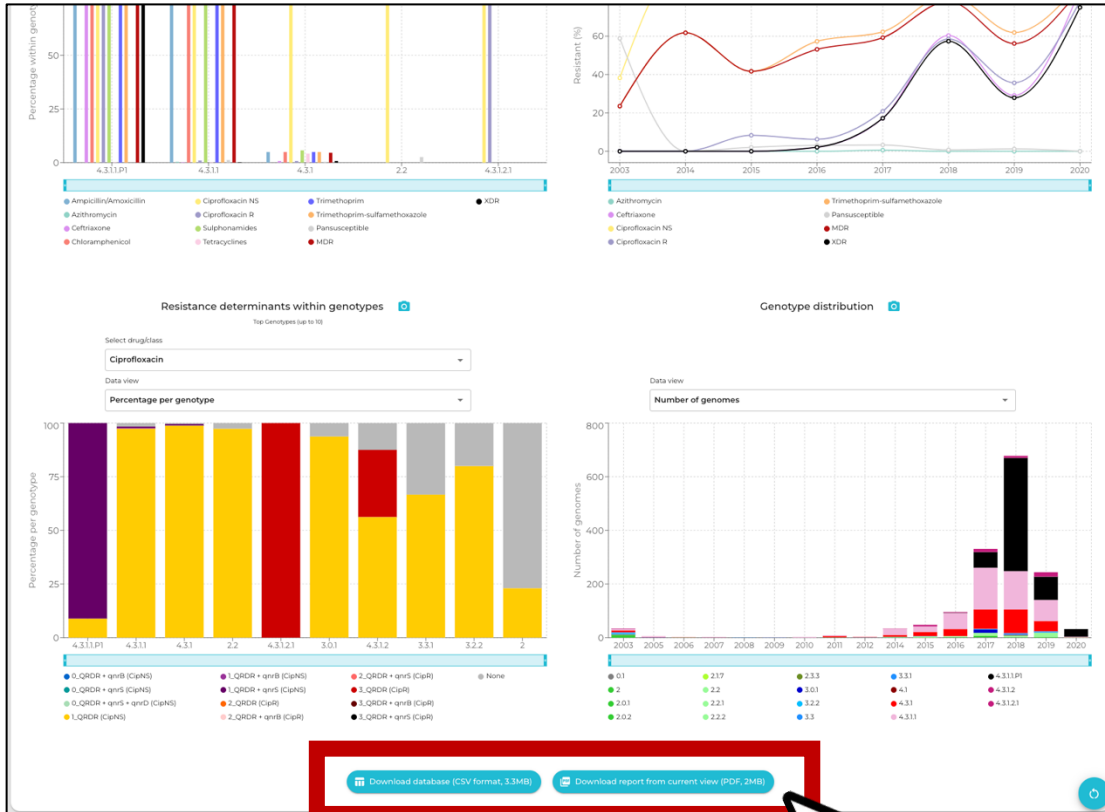


Brief Report

Emergence of Resistance to Fluoroquinolones and Third-Generation Cephalosporins in *Salmonella* Typhi in Lahore, Pakistan

[Rasheed *et al.* 2020](#)

TyphiNET: Downloadable pdf reports



TyphiNET TyphiNET Report for *Salmonella* Typhi

This report was generated at Fri Jun 27 2025 using the TyphiNET visualisation platform that draws genome data from Typhi Pathogenwatch (<https://pathogenwatch.org/>) and TyphiGenomics (<https://www.typhigenomics.org/>).

Source Data
TyphiNET data were last updated on 24 Jun 2025 (<https://github.com/typhoidgenomics/TyphiNET>).

TyphiNET presents data aggregated from studies with the following PubMed IDs (PMID): 27703135, 32883020, 33704480, 33496211.

Individual genome information, including accession numbers, and source information (PubMed ID) is available on the TyphiNET website (<https://www.typhi.net>).

Variable definitions
The genotypes reported here are defined in <https://doi.org/10.1093/infdis/jiab414>.

Travel-associated cases are attributed to 2019, PLoS NTDs, (<https://doi.org/10.1371/journal.pntd.1007137>).

Antimicrobial resistance determinants are defined in [2021, Nat. Commun., \(<https://doi.org/10.1186/s12875-021-1111-1>\)](https://doi.org/10.1186/s12875-021-1111-1).

Abbreviations

- MDR, multi-drug resistant (resistant to trimethoprim-sulfamethoxazole)
- XDR, extensively drug resistant (MDR + ciprofloxacin resistance)
- Ciprofloxacin NS, ciprofloxacin non-susceptible (resistant to ciprofloxacin or mutations in *gyrA/parC/gyrB* genes)
- Ciprofloxacin R, ciprofloxacin resistant and/or genes, see Carey et al. 2023 <https://doi.org/10.1186/s12875-023-1111-1>

Funding
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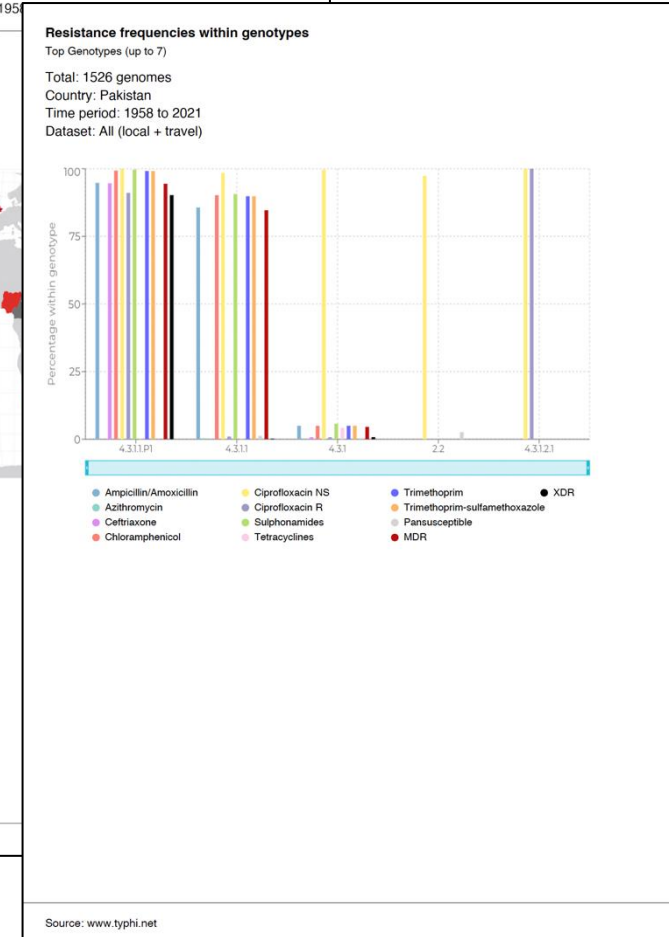
Source: www.typhi.net

Global Overview of *Salmonella* Typhi

Total: 1526 genomes
Country: Pakistan
Time period: 1958 to 2021

Map
Map View: Ciprofloxacin non-susceptible (CipNS)
Dataset: All (local + travel)

Source: www.typhi.net



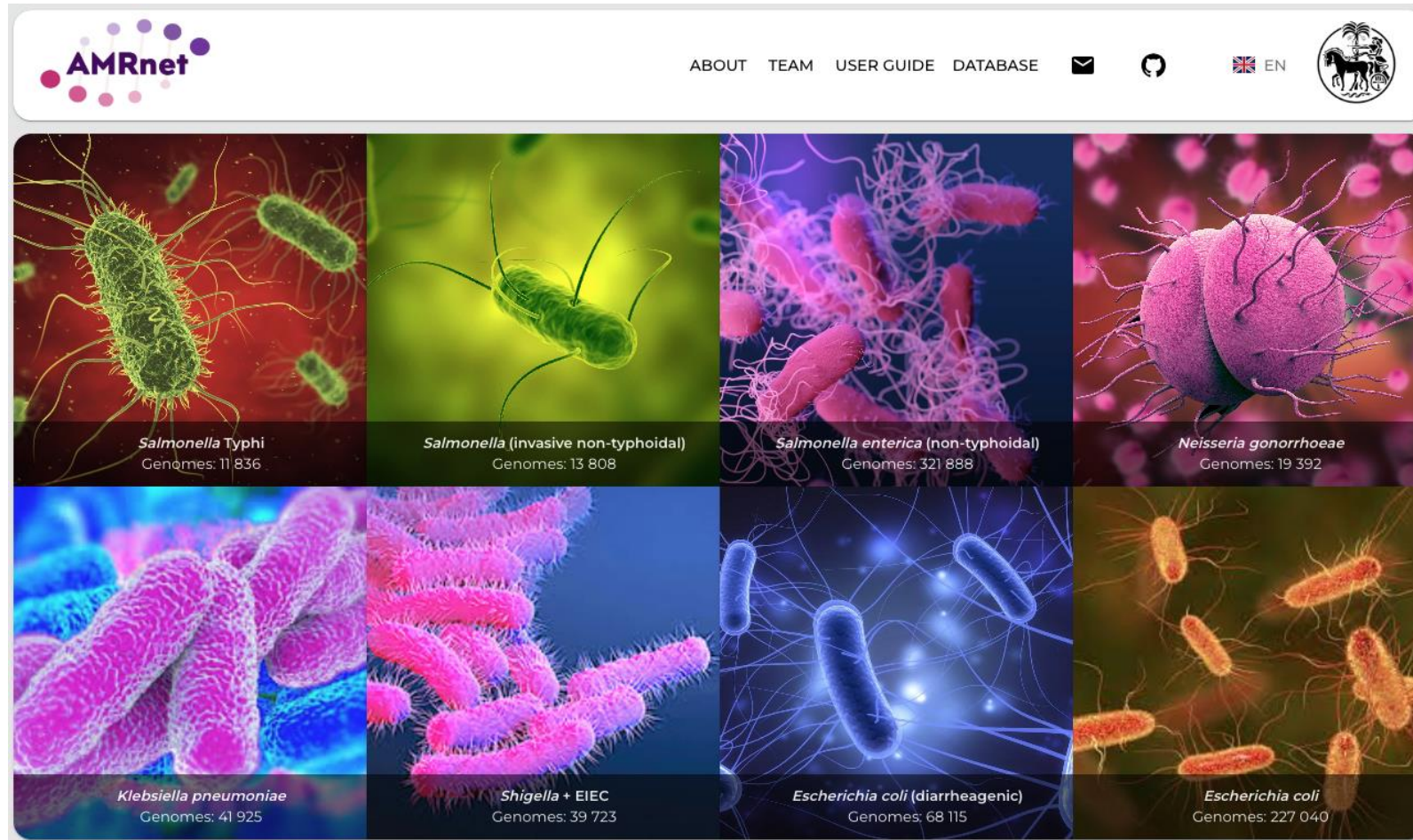
<https://www.typhi.net>

Conclusions

- Open & centralised resource for genomic surveillance
- Global overviews & country level summaries
- Identify temporal and geographical trends
- Applications in guiding empirical therapy, targeting and monitoring of intervention & control strategies, and policy decision making



A dashboard for global genomic surveillance of AMR priority pathogens



Acknowledgements



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Global Typhoid Genomics Consortium

<https://www.typhoidgenomics.org>



<https://www.typhi.net>



<https://www.amrnet.org>