



Genetic environment of *bla*_{TEM-1B} in global *Salmonella* Typhi

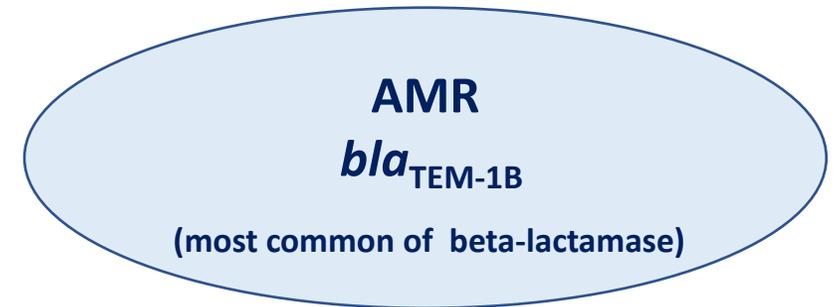
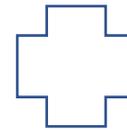
Metagenomic Analysis of Toilet Waste from Three Different Income Areas in Bangkok, Thailand

Genetic environment of *bla*_{TEM-1B} in global *Salmonella* Typhi

Narong Nuanmuang

Introduction

- *Salmonella* Typhi
 - a gram-negative bacterium
 - fecal-oral route transmission
 - only humans as a reservoir
 - typhoid fever
 - a burden on developing countries
 - a major worldwide public health concern



1. Global sharing of data (ENA / NCBI)

Metadata (Years, Continents, Sources)
& Whole genome sequences (until to 12th July 2022)



2. Genomic analysis with bioinformatics tools

KmerFinder, SISTR, AMRPlusFinder,
PlasmidFinder, MGE, Flankophile

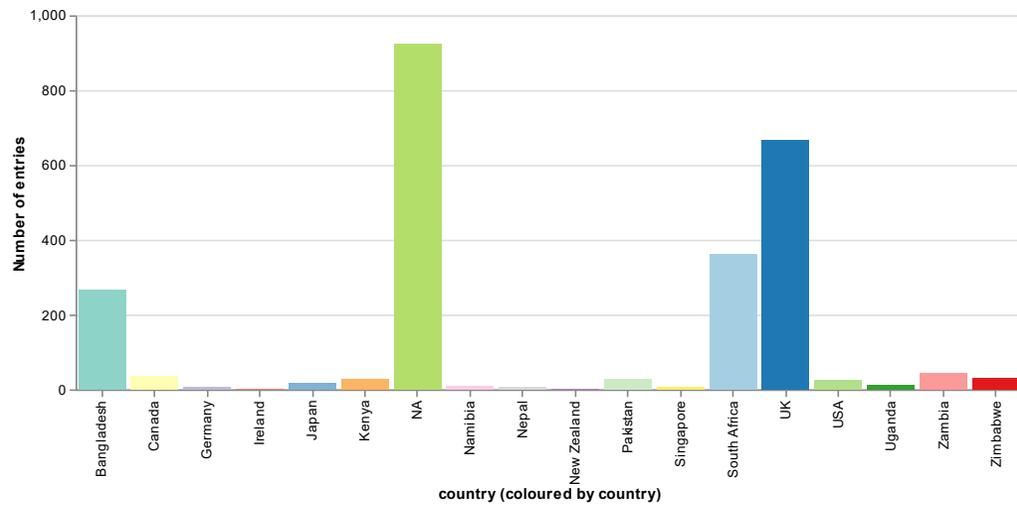


3. Visualization

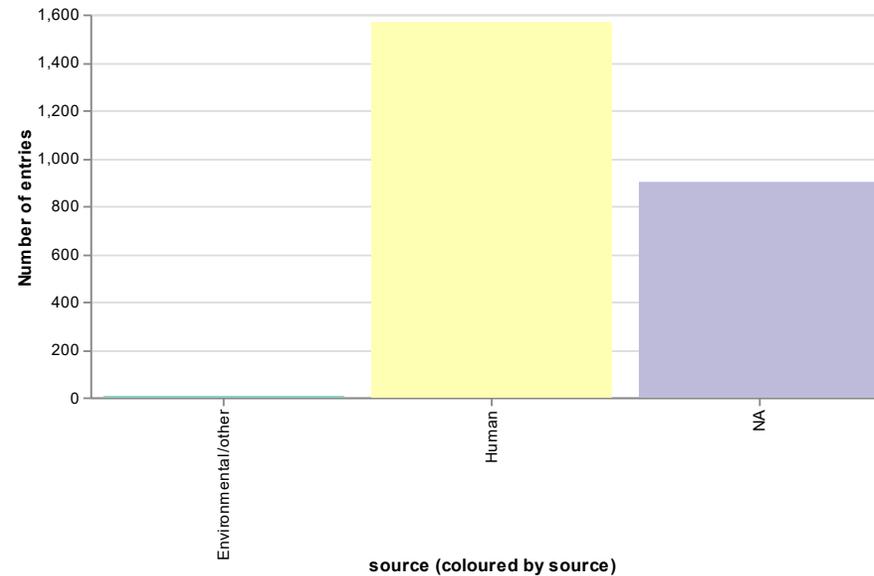
Microreact, Flankophile

Results (1)

A) Countries



B) Isolation source



C) ST-type

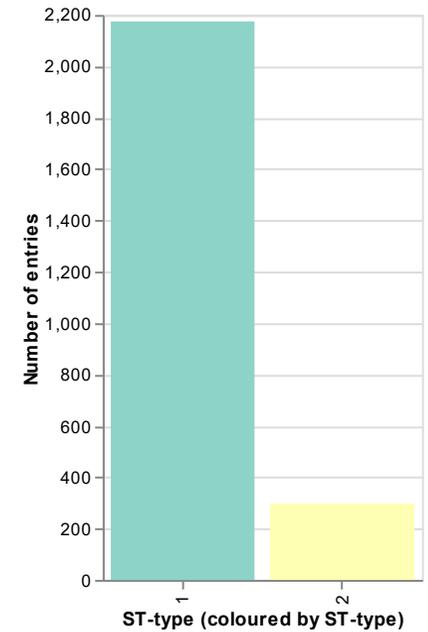
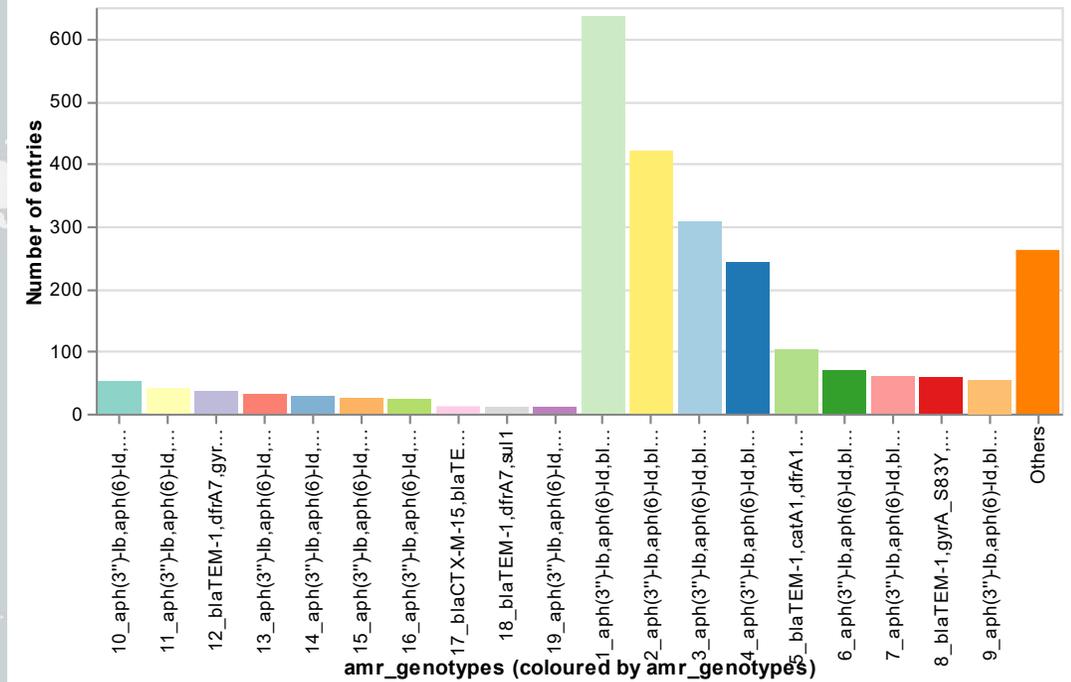


Fig.1 The distribution of global *Salmonella* Typhi carried bla_{TEM-1} (n=2,476) divided by countries (A), isolation source (B), and ST-type (C) visualized by Microreact.

Results (2)

A) *bla*_{TEM-1} profiles are divided by countries

B) *bla*_{TEM-1} profiles



- 1_aph(3'')-lb,aph(6)-ld,bla TEM-1,catA1,dfrA7,gyrA_S83F,sul1,sul2
- 2_aph(3'')-lb,aph(6)-ld,bla TEM-1,catA1,dfrA7,sul1,sul2
- 3_aph(3'')-lb,aph(6)-ld,bla TEM-1,catA1,dfrA7,sul1,sul2,tet(B)
- 4_aph(3'')-lb,aph(6)-ld,blaCTX-M-15,bla TEM-1,catA1,dfrA7,gyrA_S83F,qnrS1,sul1,sul2
- 5_blaTEM-1,catA1,dfrA15,sul1,tet(B)

Fig.2 The distribution of global *Salmonella* Typhi carried *bla*_{TEM-1} following antimicrobial resistance (AMR) profiles shown in the world map (A) and bar chart (B) visualized by Microreact.

Results (3)

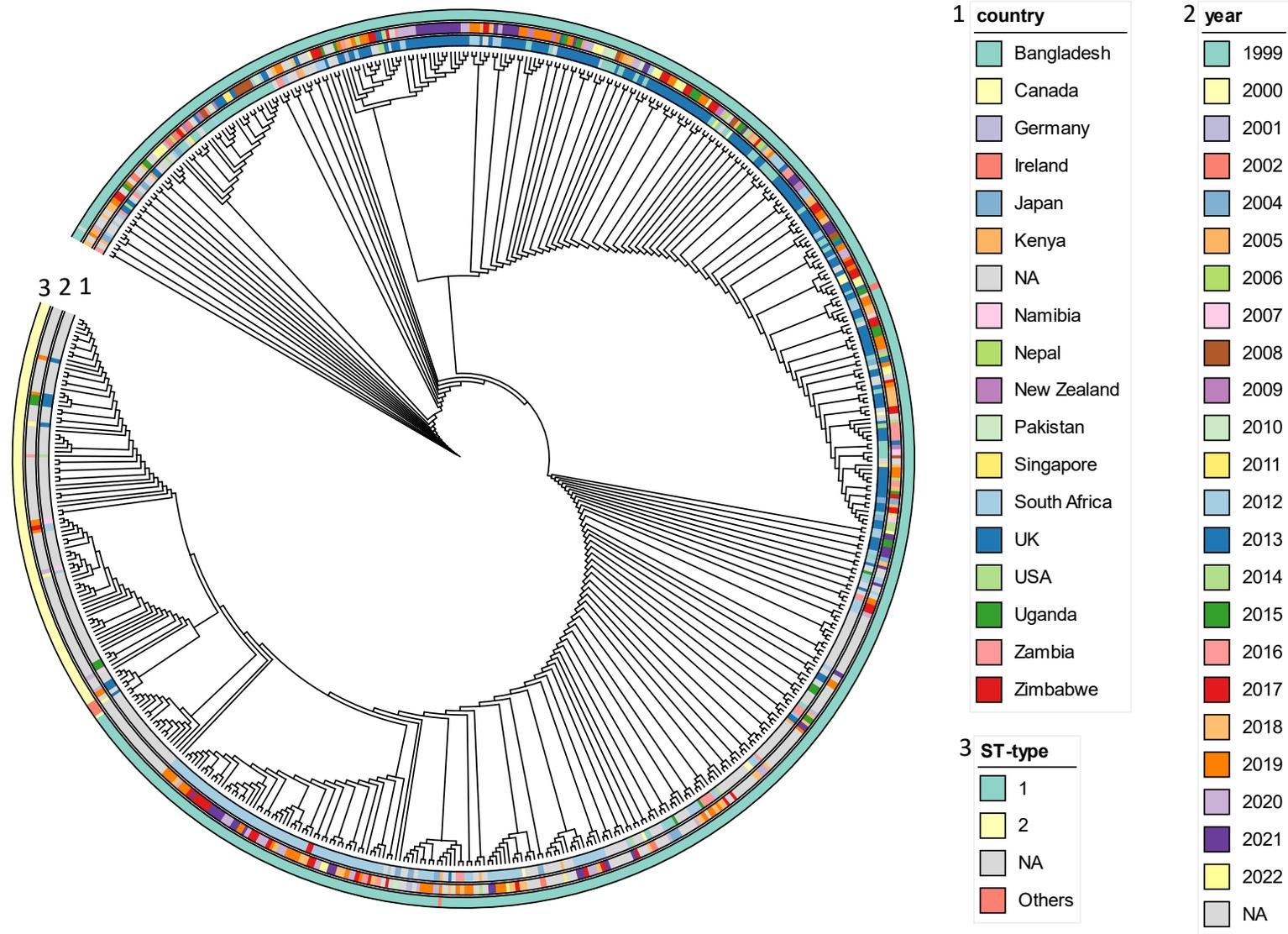
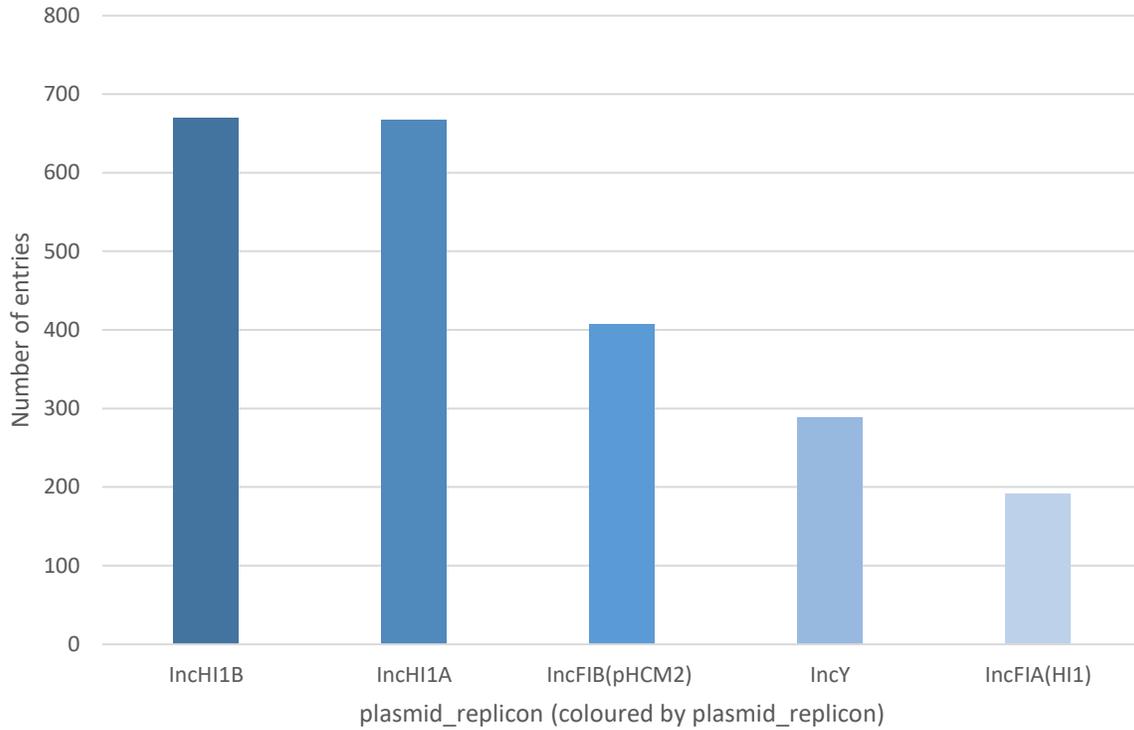


Fig.3 Phylogeny distribution of global *Salmonella* Typhi carried *bla*_{TEM-1}.

Results (4)

A) Plasmid replicon



B) MGE

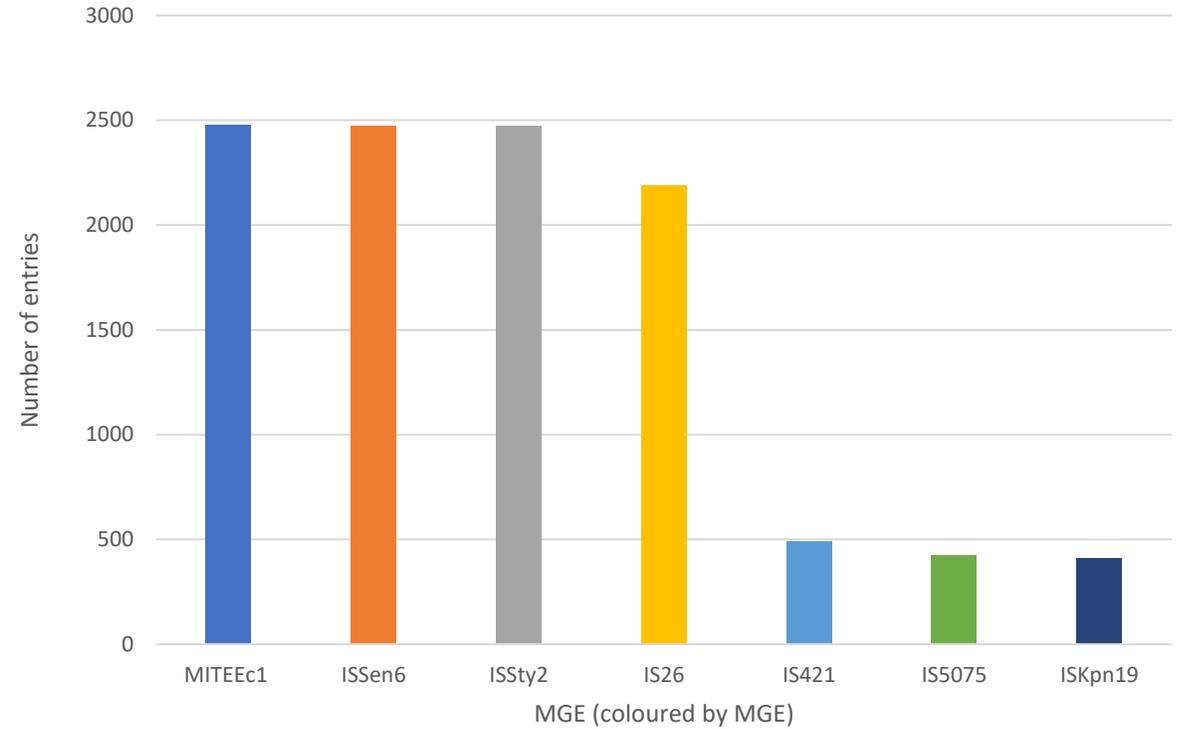


Fig.4 The most common plasmid replicon (A) and MGE (B) found in global *Salmonella* Typhi carried *bla*_{TEM-1}.

Results (5)

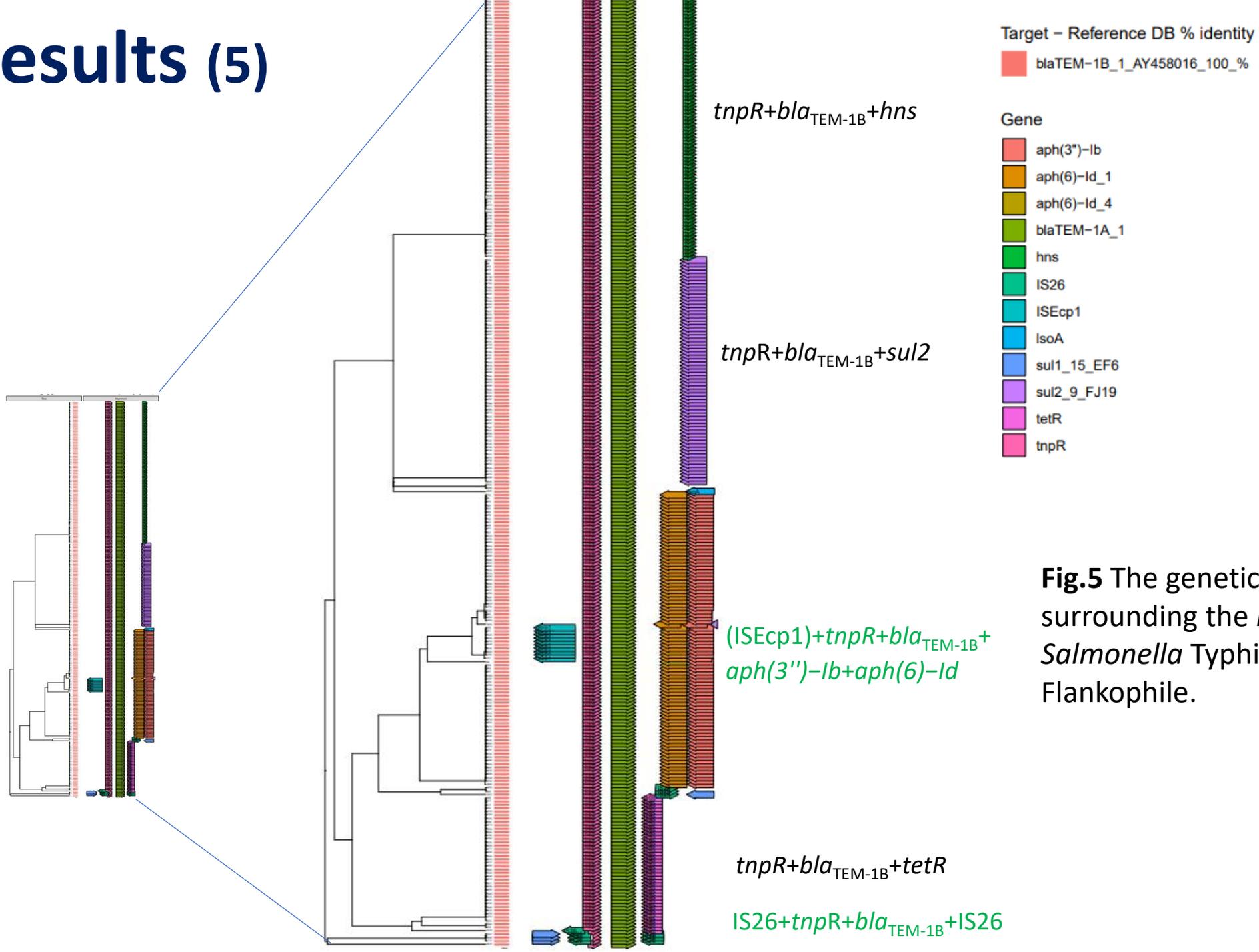


Fig.5 The genetic environment surrounding the *bla_{TEM-1B}* gene in global *Salmonella* Typhi visualized by Flankophile.

Metagenomic Analysis of Toilet Waste from Three Different Income Areas in Bangkok, Thailand



Burden of disease -> Enteric Infection

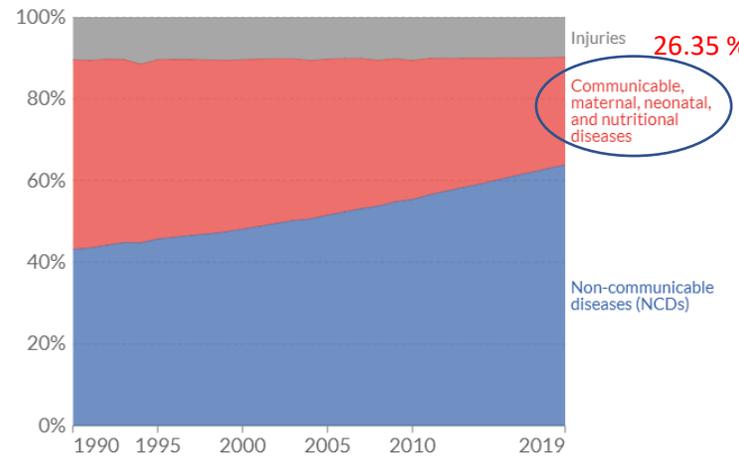
COVID-19 vaccinations, cases, excess mortality, and much more [Explore our COVID-19 data](#)

Total disease burden by cause, World, 1990 to 2019



Total disease burden measured as Disability-Adjusted Life Years (DALYs) per year. DALYs measure the total burden of disease - both from years of life lost due to premature death and years lived with a disability. One DALY equals one lost year of healthy life.

Change country Relative



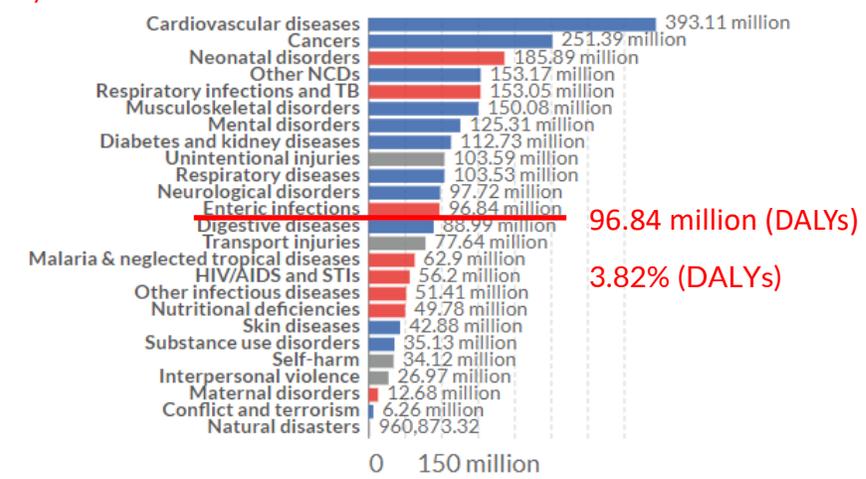
Source: IHME, Global Burden of Disease (2019) OurWorldInData.org/burden-of-disease • CC BY

Burden of disease by cause, World, 2019



Total disease burden, measured in Disability-Adjusted Life Years (DALYs) by sub-category of disease or injury. DALYs measure the total burden of disease - both from years of life lost due to premature death and years lived with a disability. One DALY equals one lost year of healthy life.

Change country



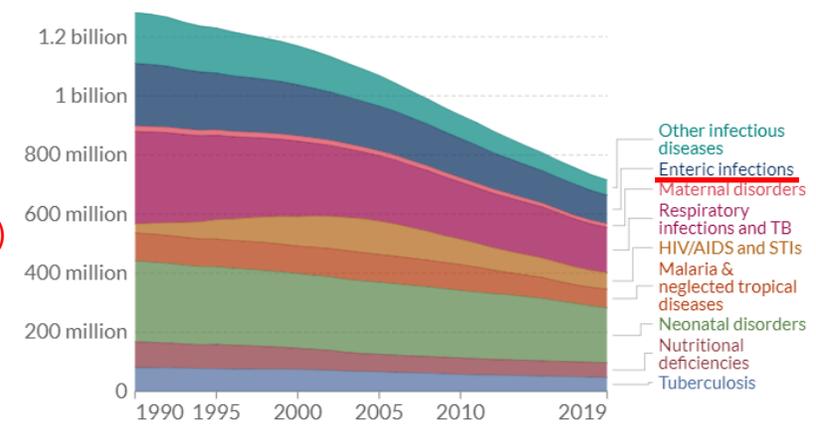
Source: IHME, Global Burden of Disease (2019)
 Note: Non-communicable diseases are shown in blue; communicable, maternal, neonatal and nutritional diseases in red; injuries in grey.
 OurWorldInData.org/burden-of-disease • CC BY

Disease burden from communicable, maternal, neonatal and nutritional diseases, World, 1990 to 2019



Total disease burden from communicable, maternal, neonatal and nutritional diseases, measured in DALYs (Disability-Adjusted Life Years) per year. DALYs are used to measure total burden of disease - both from years of life lost and years lived with a disability. One DALY equals one lost year of healthy life.

Change country Relative



Source: IHME, Global Burden of Disease (2019) OurWorldInData.org/burden-of-disease • CC BY

1990: 210.73 million (DALYs)
 2018: 100.33 million (DALYs)
 2019: 96.84 million (DALYs)

DALYs (Disability-Adjusted Life Years)

Updated communicable diseases

Disease topics

1. Middle East respiratory syndrome coronavirus (MERS-CoV) - Multi-country
2. COVID-19 associated with SARS-CoV-2 - Multi-country (EU/EEA) - 2019 - 2022
3. Increase in hepatitis cases in children – Multi-country – 2022
4. Monkeypox - Multi-country - 2022
5. West Nile virus - Multi-country (World) - Monitoring season 2022
6. Locally-acquired dengue cases - France - 2022
7. Ebola virus disease due to Sudan ebolavirus – Uganda – 2022
8. Human case with avian influenza A(H5N1) infection - Spain - 2022
9. *Aedes aegypti* detected in Cyprus
10. Invasive meningococcal disease - Ireland - 2022

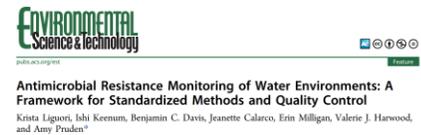


Week 40, 2 - 8 October 2022

MERS-CoV
SARS-CoV2
Monkeypox

Wastewater Surveillance System concept

- as **sentinel system**
- as **representative monitoring** (comprehensive view) for infectious disease that covers almost everyone (entire community), nearly every day, in almost every household and business.
- results can **warn public health officials** of a coming rise in cases before they show up as clinical results.
- evidence is increasing that **untreated wastewater** is a good indicator of the presence of the virus in a population.



AMR and Sustainable Development Goals (SDGs)

The SDGs were **published in 2015** by the United Nations to serve as a global blueprint for a better, more equitable, more sustainable life on our planet.

Infections caused by multidrug-resistant pathogens are directly associated with worse clinical outcomes, longer hospital stays, excess mortality in the affected patients and an increasing burden and costs on the healthcare infrastructure.



Perspective

Antimicrobial Resistance in the Context of the Sustainable Development Goals: A Brief Review

Márió Gajdác^{1,2,*}, Edit Urbán^{3,4}, Anette Stájer⁵ and Zoltán Baráth⁶

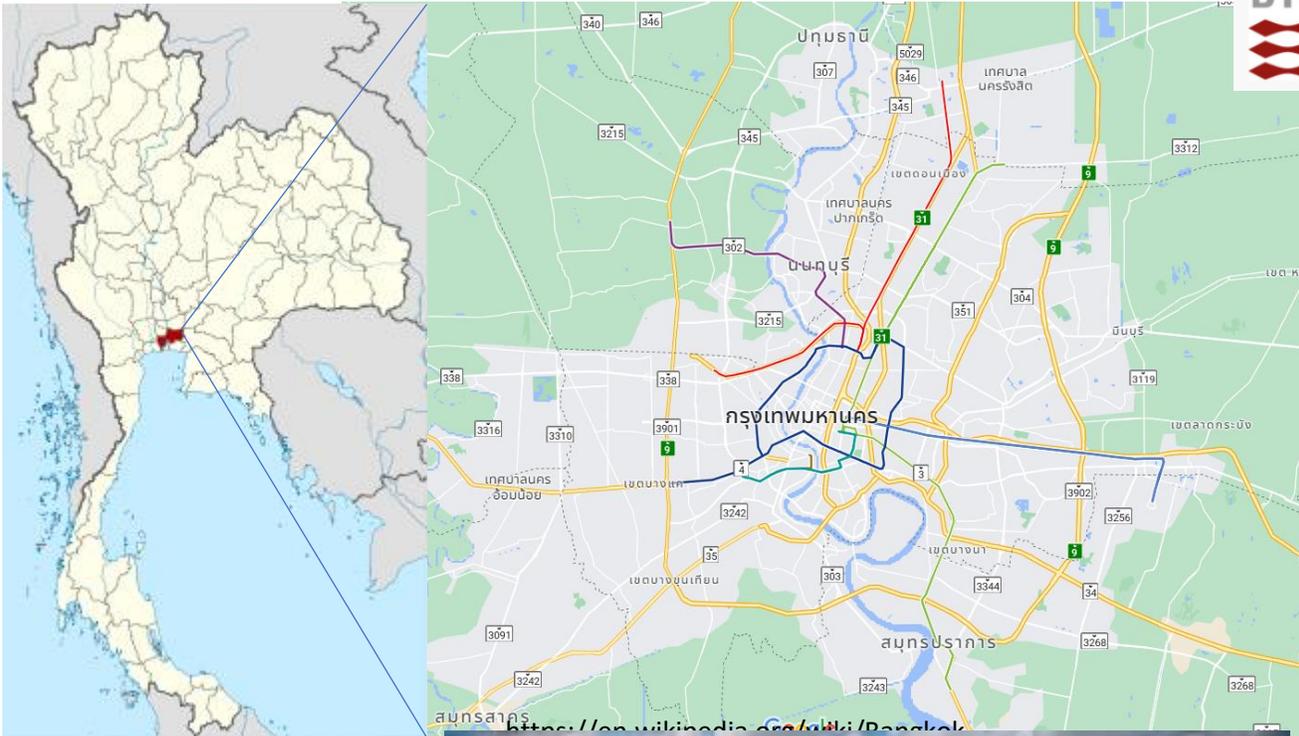
Table 3. The list of UN Sustainable Development Goals (2015–2030) *.



* The goals deemed relevant by the authors and discussed in the context of AMR are presented in **boldface**.

Bangkok

- Area: 1,568.7 km²
- Population: 10.72 million people (est. 2022)
- Density: 5,300 people/km²
- Income: several
- Natural disaster: flood
- Model for local surveillance of microbes and AMR



<https://qr.ae/pvmH2y>



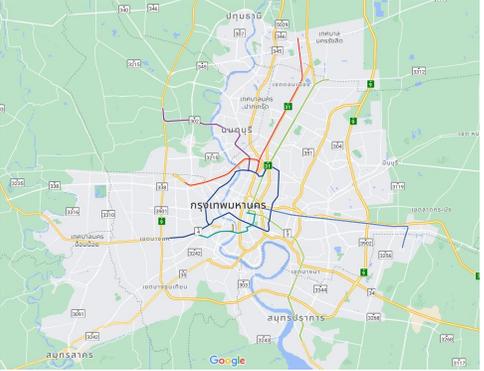
<https://qr.ae/pvJv8>

Objective

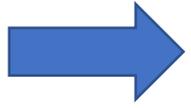
- To investigate and compare the abundance and diversity of bacterial pathogens and antimicrobial resistance from toilet wastes of three different income areas in Bangkok.
- To assess the quality of the wastewater before and after the treatment system.

Research workflow

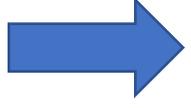
Ethical document will be submitted and approved



Site selection
? areas



Sampling strategy and transportation
?mL, duplication



Laboratory works
Toilet waste physical and chemical measurement, Genomic extraction and Sequencing (metagenomics)



Data management, analysis and visualization

<https://www.cdc.gov/healthywater/surveillance/wastewater-surveillance/wastewater-surveillance.html>

<https://www.labmanager.com/insights/the-importance-of-laboratory-quality-and-how-to-achieve-it-27442>

https://www.cdc.gov/healthywater/surveillance/pdf/328288_National_Wastewater_Surveillance_System_508.pdf

<https://healthserv.net/Bioinformatics-%E0%B8%8A%E0%B8%B5%E0%B8%A7%E0%B8%AA%E0%B8%B2%E0%B8%A3%E0%B8%AA%E0%B8%99%E0%B9%80%E0%B8%97%E0%B8%A8-12068>

Expected Outcome

- Surveillance information on pathogens and AMR including differences among income areas in Bangkok (model for local surveillance)
- The efficiency of treating the system of toilet waste on abundance and diversity of pathogens and AMR.