GenomicsDAM - Bangladesh

Country profile (2022)

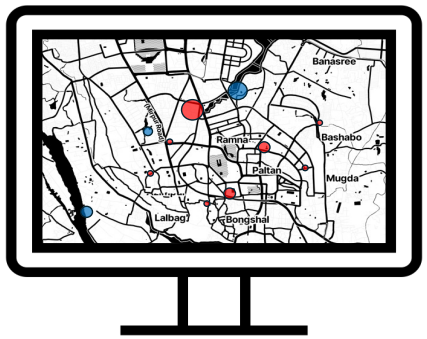
- >250K diarrheal disease hospitalisations & >20M cases
- >35K people died of diarrheal diseases
- Causes 7% of all deaths in children less than 5 years old
- 99K AMR associated deaths
- Documented presence of multidrug-resistant pathogens (resistant to >2 antibiotic groups) in clinical, public- and one-health settings.

Approach

Community sampling
- Isolates from water and other contaminated sources (e.g. food)
- Involving public health stakeholders and citizen science

Whole genome (WGS) & targeted amplicon (Amp-Seq) sequencing
- Using Illumina and Oxford Nanopore (ONT) platforms
- Prediction of AMR profiles

GIS mapping
Geographic epidemiology will inform infection hotspots and control measures



Clinical setting
- Isolates from icddr,b affiliated hospitals
- WGS/Amp-Seq data will inform treatment decisions

GenomicsDAM - Leadership Team

icddr,b (Bangladesh)

Dr. Dinesh Mondal
Clinical microbiology and parasitology. Leads research projects in infectious diseases, involving multidisciplinary teams. Uses WGS to understand pathogen AMR.

Dr. Mustafizur Rahman
Head of the Genomics Centre. Microbiologist with vast experience in WGS of bacteria and viruses from clinical and environmental samples.

Faria Hussein
Research investigator with expertise in microbiology and molecular biology, applied to the area of maternal and child nutrition.

LSHTM (UK)

Professor Taane G. Clark
Genomic epidemiology of infectious diseases using cutting-edge WGS, bioinformatics, phylogenetics, and AI. >325 publications, >£30M funding.

Professor Susana Campino
Genomics of infectious diseases, including the development of methods to sequence micro-organisms from clinical / environmental samples (WGS/Amp-Seq).

Dr. Jody Phelan
Computational biology, bioinformatics, and software development, including tools to profile pathogens using sequence data (e.g., TB-Profiler)

Working groups

Clinical & microbiology, Genomics & Informatics, and Community & Stakeholder engagement

External advisory group (to be established)

Experts in genomics, IT, infectious diseases, business and policy development

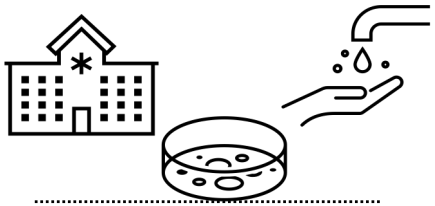
The GenomicsDAM partnership

icddr,b

LONDON SCHOOL of HYGIENE &TROPICAL MEDICINE

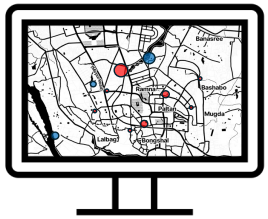
Objective 1

Collection of clinical and community samples for AMR personalised medicine and surveillance.



Objective 2

Development and deployment of whole genome (WGS) and targeted amplicon (Amp-Seq) sequencing and analysis pipelines.

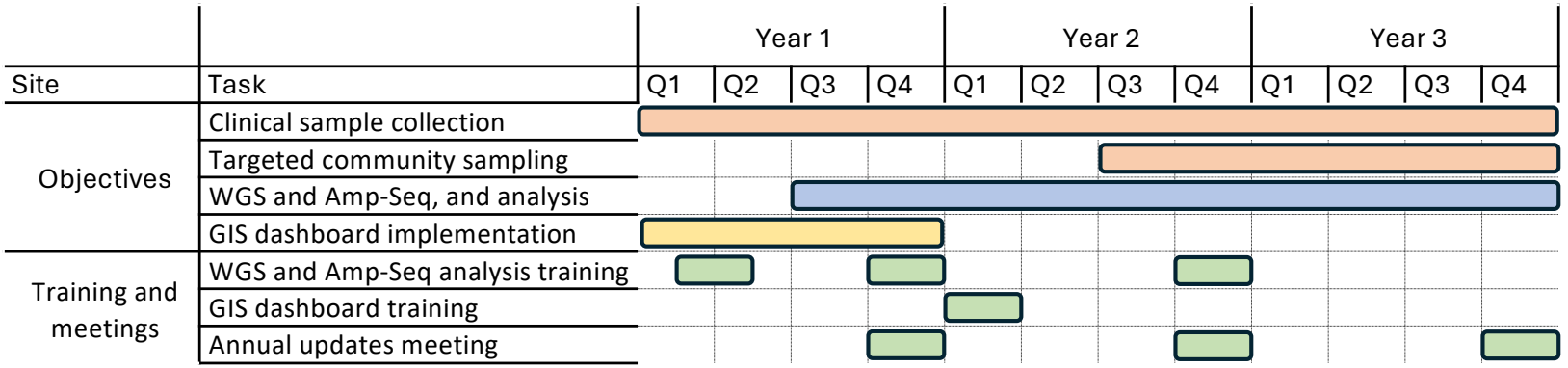


Objective 4

Capacity strengthening and training in genomics investigations, bioinformatics and data analysis.

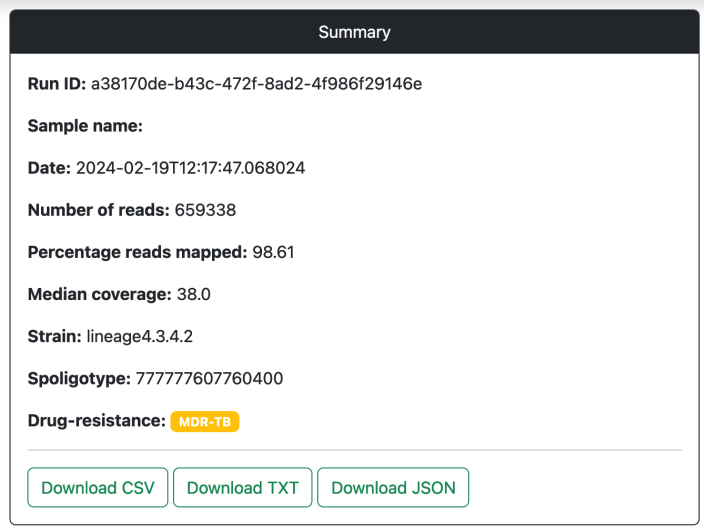
Objective 3

Implementation of GIS dashboard for real-time AMR tracking, including to inform public health interventions and citizen science activities.



TB-Profiler: Sequence-based profiling of *Mycobacterium tuberculosis*

Features such as **strain type**, **AMR class** and **sequence quality control** metrics are calculated for each submitted sample.



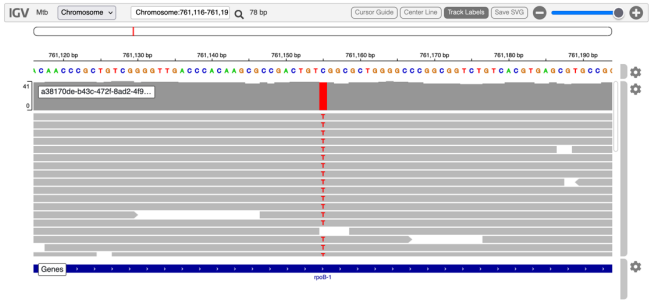
AMR profiles are predicted based on the detection of resistance mutations allowing the determination of an effective treatment regimen.

Drug resistance-Associated Mutations: This table reports mutations found in candidate resistance genes which have been associated with drug resistance

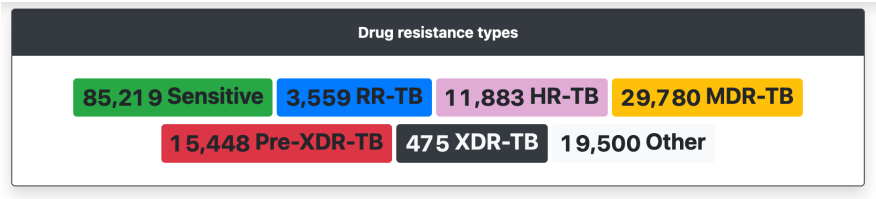
Gene	Chromosome position	Mutation	Type	Estimated fraction	Drugs	Confidence	Comment
rpoB	761155	p.Ser450Leu	missense_variant	1.0	rifampicin	Assoc w R	
inhA	1673425	c.-777C>T	upstream_gene_variant	1.0	ethionamide	Assoc w R	Alias fabG1_c.-15C>T
						Assoc w R	Alias fabG1_c.-15C>T. Low-level resistance (multiple, genetically linked low-level resistance mutations are additive and confer high-level resistance)
pncA	2288868	p.Val125Gly	missense_variant	1.0	pyrazinamide	Assoc w R	
embB	4247429	p.Met306Val	missense_variant	1.0	ethambutol	Assoc w R	

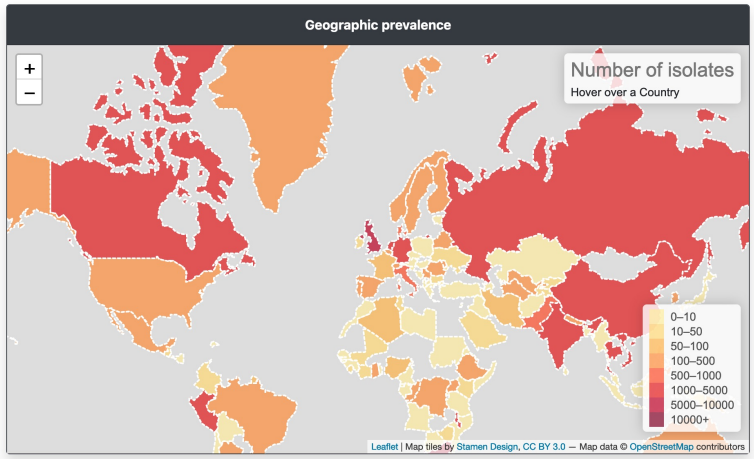
https://tbdr.lshtm.ac.uk

Interactive visualisation and analysis of WGS data is prioritised, giving the user control.



Results are integrated into a large global database of >100,000 TB isolates; allowing **mapping and tracking of AMR pathogens across the world**.



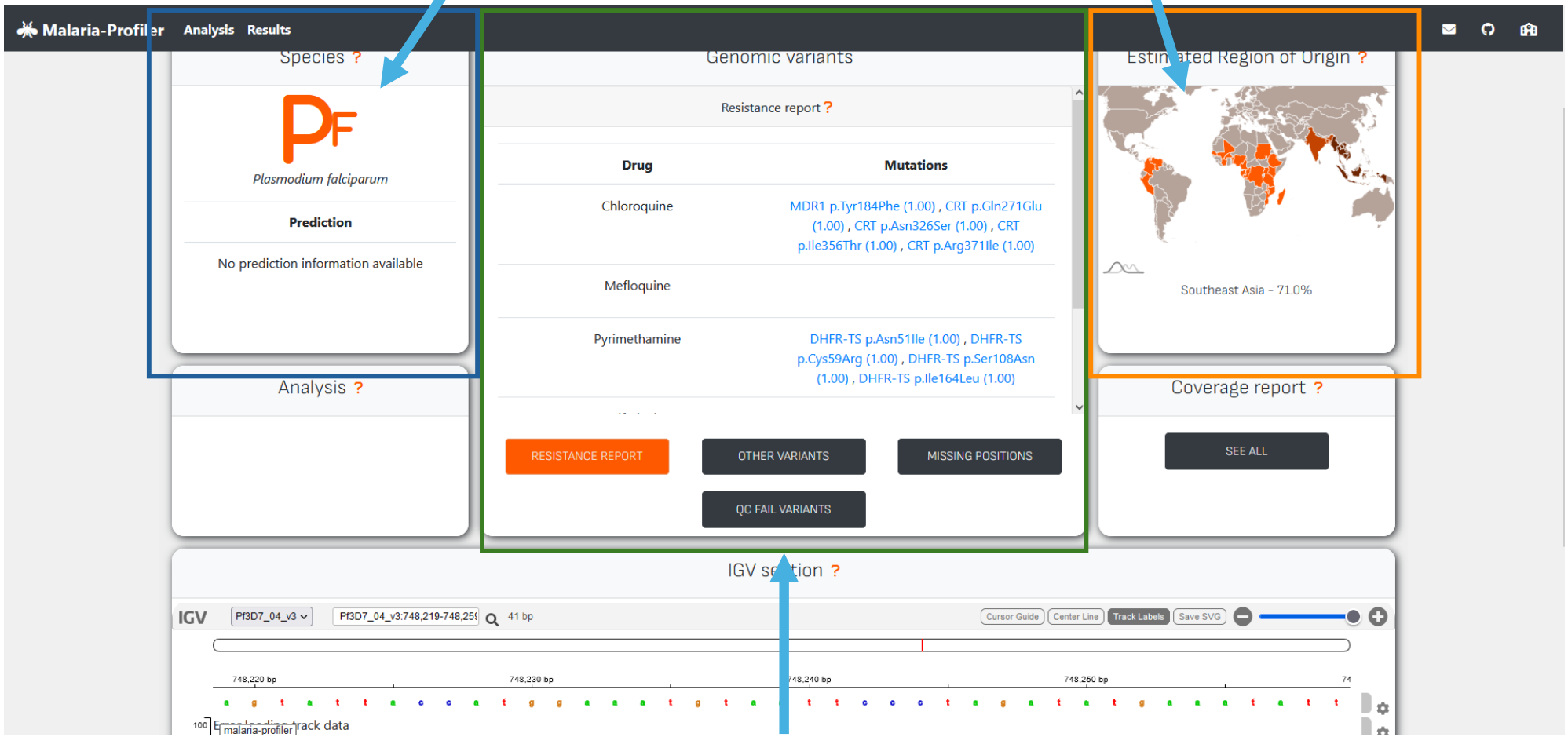


Phelan J, et al. Genome Med. 2019

Malaria-Profiler

Species prediction
Plasmodium malaria species is predicted based on a barcode of markers in the mitochondria genome.

Geographic source prediction
The geographic source is predicted using a machine learning model trained on genome-wide mutation data.



Drug resistance mutations
Mutations conferring resistance to anti-malarial drugs are detected using WGS and Amp-Seq data, and then used to determine available effective drugs for treatment.

https://bioinformatics.lshtm.ac.uk/malaria-profiler/

Phelan J et al.
Genome Med. 2023