
DTU

Vibrio Cholerae data from Great Lakes region

Octopus Project

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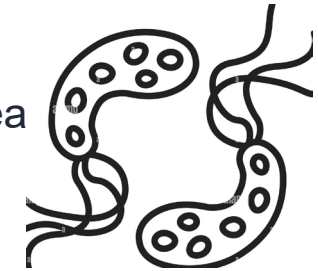
Vibrio Cholerae in Great Lakes Region

Greatlife project - Linking infectious disease front-liners' control efforts with central public health authorities in The African Great Lakes Region

Vibrio Cholerae



Cholera - an acute diarrhoeal infection caused by toxigenic Vibrio cholerae; severe disea within hours if treatment is delayed.

A species of Gram-negative, facultative anaerobe and comma-shaped bacteria

WHO estimates 1.3–4.0 million cases and 21,000–143,000 deaths globally each year

Only O1 and O139 cause epidemic cholera; O1 El Tor drives the ongoing seventh pandemic.

Control depends on fast surveillance, case management, oral cholera vaccine, and sustained WASH investment.

Vibrio Cholerae

17 different introductions (T1-T17) of 7PET into Africa through 3 big historical waves

Intermittent and often seasonally outbreaks in east Africa

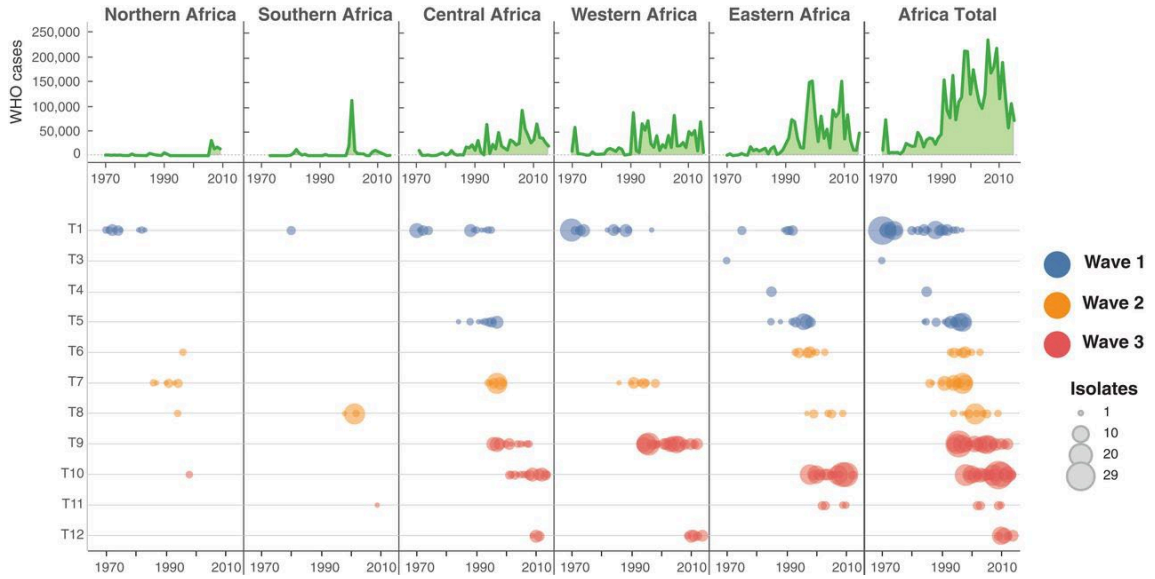
Countries most affected: DRC, Mozambique, Malawi, Zambia, Malawi

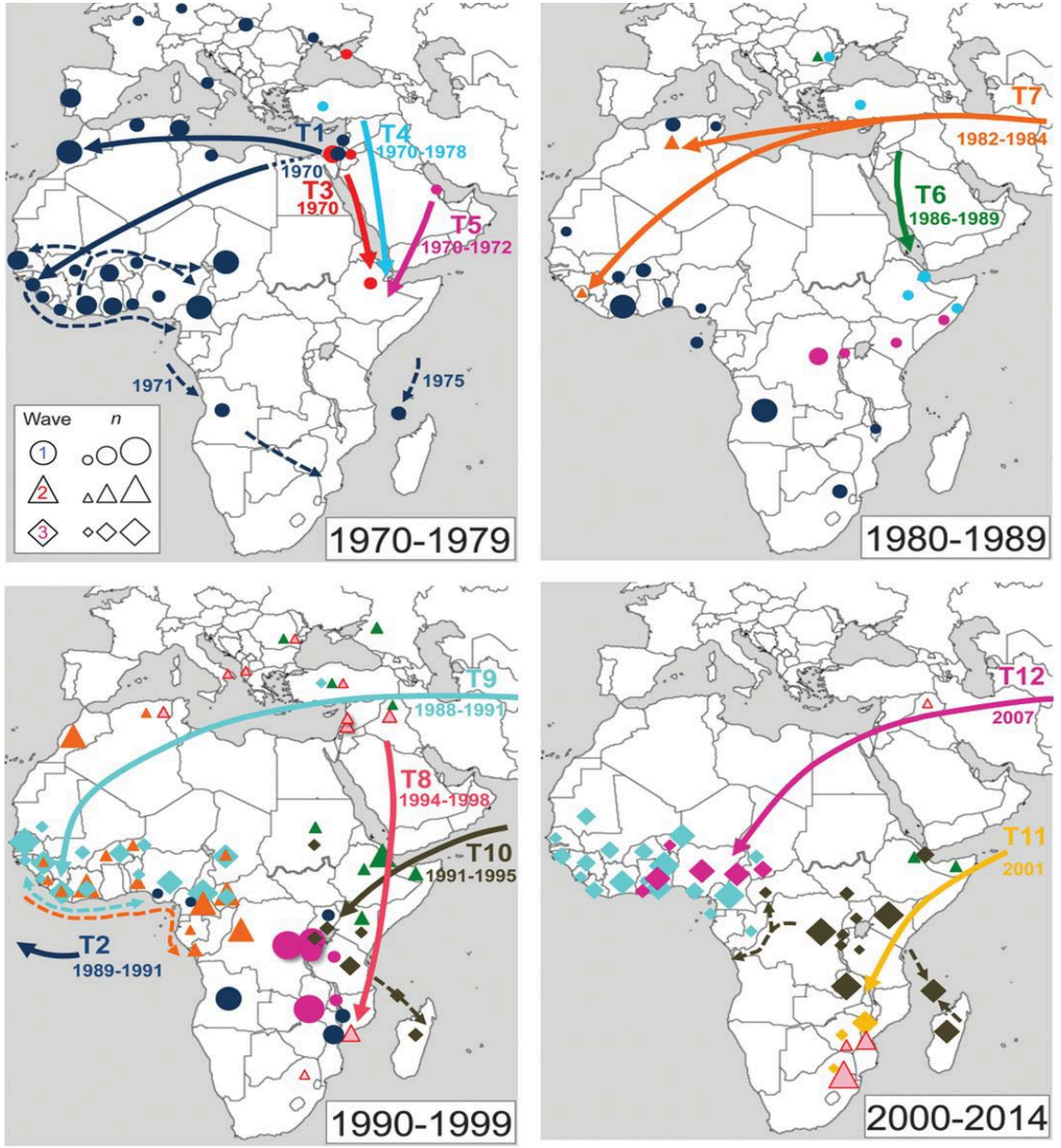
Vibrio Cholerae

17 different introductions (T1-T17) of 7PET into Africa through 3 big historical waves

Intermittent and often seasonally outbreaks in east Africa

Over 178,000 cases in 16 countries in Eastern and Southern Africa from January 2024 until March 2025 – WHO Dashboard





Genomic history of the seventh pandemic of cholera in Africa

T1-T12 Africa
François-Xavier Weill *et al.*,

Science 358,785-789(2017).DOI:10.1126/science.aad5901

Into East Africa

T3 – 1970

T4 – 1970-1978

T5 – 1970-1972
T10 – 1991 – 1995

T11 - 2001

East Africa Great Lakes region

Lake-shore settlements, fishing ports, refugees, markets, and border crossings create **intense cross-border connectivity**.

Same lakes and corridor systems, making it ideal for dated transmission modelling.

Outbreak control is complicated by displacement, insecurity, flooding, fragile WASH infrastructure, and unequal health-system access.

Previous studies …..

Lineages and sub-lineage introductions vs persistence;
Established crossborder and local transmission;
Value of sequencing

Gap

How are genomic transmission explained by **epidemiological trends**

Great-Life Data

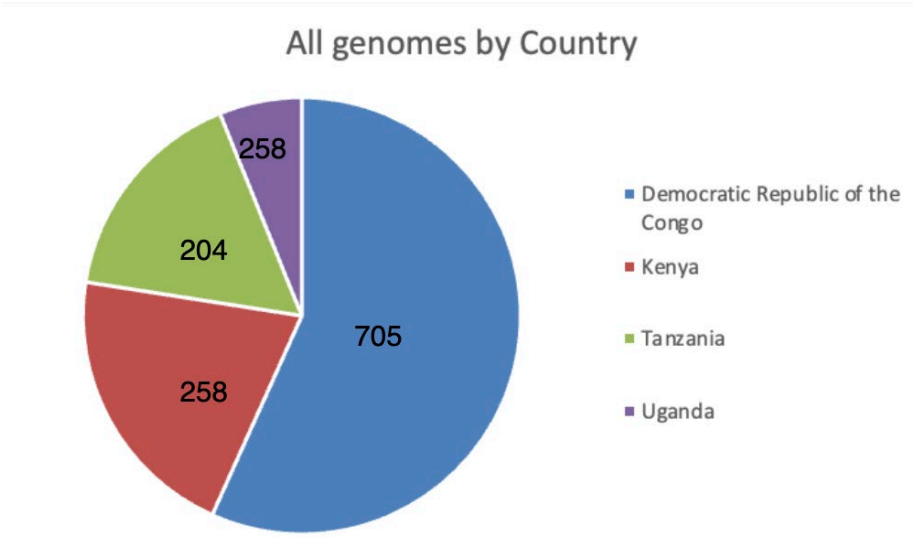
~ 220 single isolate genomes (Greatlife ONT Sequencing 2024-2025)

QC (-metadata, QUAST, Kmerfinder)

↓

113 Good quality genomes + 1243 public = 1,356

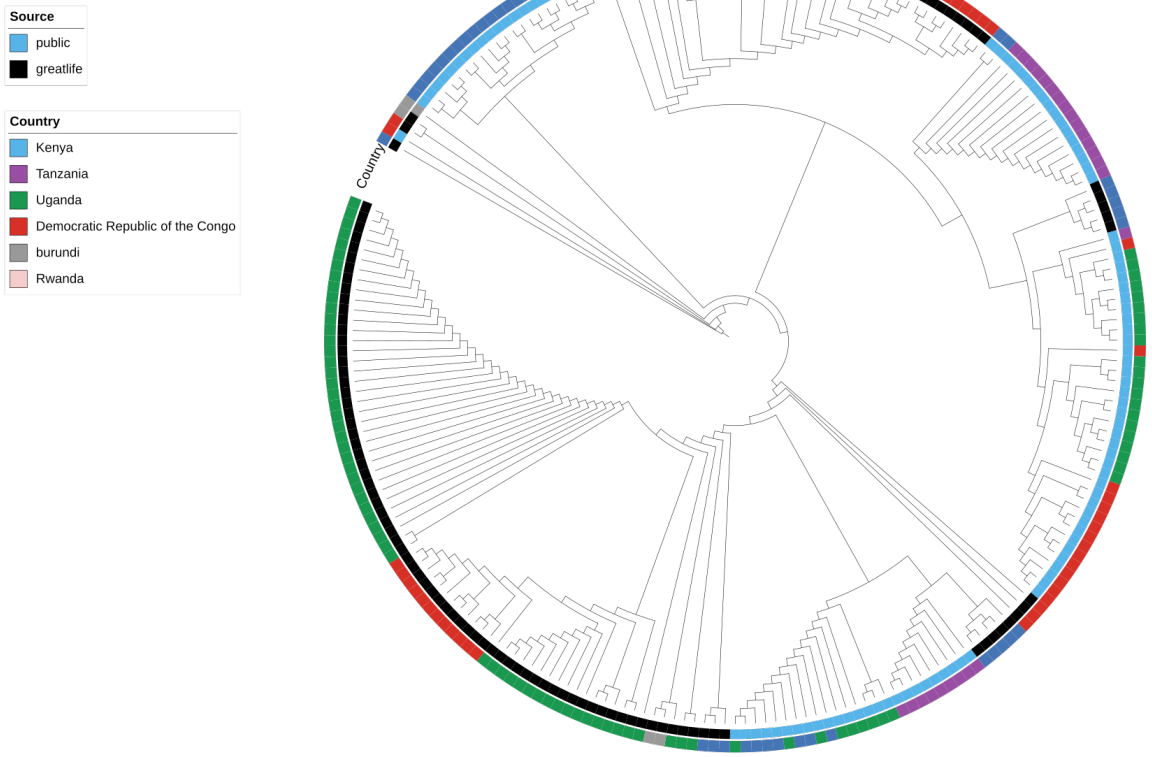
Country	QC Pass	Public	Total
DRC	40	705	745
Uganda	56	76	132
Kenya	14	258	273
Tanzania	00	204	204
Burundi	03	00	03
Rwanda	00	00	00
Total	113	1243	1356



Broader regional context phylogeny

Geographical structure

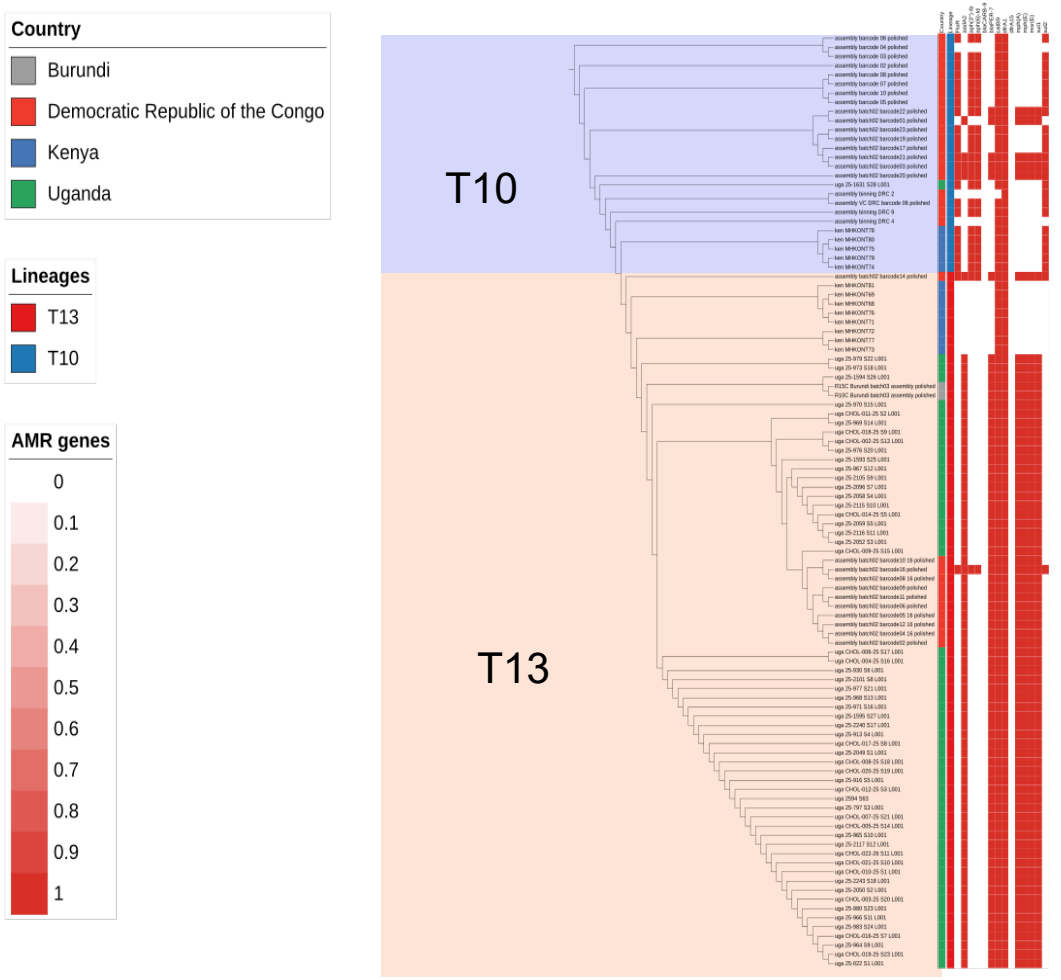
Greatlife sequenced genomes
not forming a single monophyletic cluster



Lineages x AMR

Composed mainly of;

1. canonical African O1 lineage T13
2. smaller but clear T10
3. Share MDR
4. Unique AMR signatures



Next - Transmission rates between countries

Time-scale using Bayesian phylogenetics (BEAST) using sampling dates.

Discrete-trait models in BEAST to estimate where transitions are occurring between and within countries, provinces, border corridors.

Machine Learning Integration of genomic patterns with epidemiological, environmental, mobility proxies, WASH, conflict and displacement variables

Greatlife Naivasha workshop in February 2025

Capacity gaps

Global Health EDCTP3

ONE COLLABORATIVE TRAINING PROGRAM FOR OUTBREAK PREPAREDNESS AND UNIVERSAL SURVEILLANCE – OCTOPUS

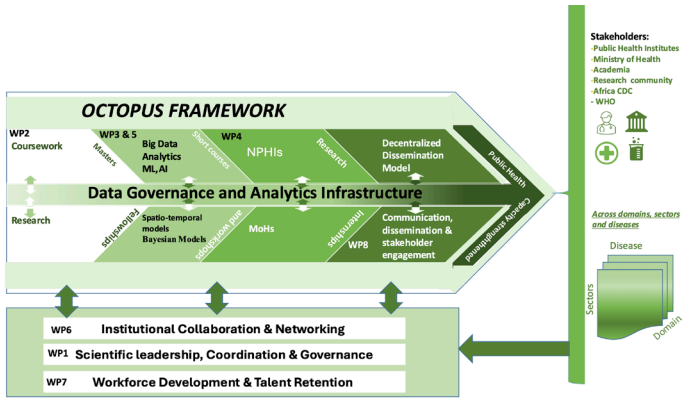
1.3M Euros Global Health EDCTP3 Training fellows in Public Health covering Biostatistics, Epidemiology and Modelling

~ 6 training workshops

Online course materials

Scholarships to over **45 MSc students**

May 2026 - 2028



Thank you