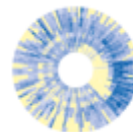


Combining epidemiologic and genomic data to define epidemiologically relevant units of cholera transmission in Africa

Bethany L. DiPrete, PhD
Gillings School of Global Public Health
University of North Carolina at Chapel Hill

Meeting of the Global Task Force on Cholera Control (GTFCC)
Epidemiology Working Group
Using data to better understand and control cholera
Cairo, Egypt
May 23, 2024



Bethany L. DiPrete;¹ Javier Perez-Saez;^{2,3} Andrew Azman;^{2,3,4} Shirlee Wohl;⁵ Justin Lessler^{1,6}

¹Department of Epidemiology, Gillings School of Global Public Health, University of North Carolina, Chapel Hill, North Carolina, USA.

²Department of Epidemiology, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, Maryland, USA.

³Institute of Global Health, University of Geneva, Geneva, Switzerland.

⁴Unit of Population Epidemiology, Division of Primary Care Medicine, Geneva University Hospitals, Geneva, Switzerland

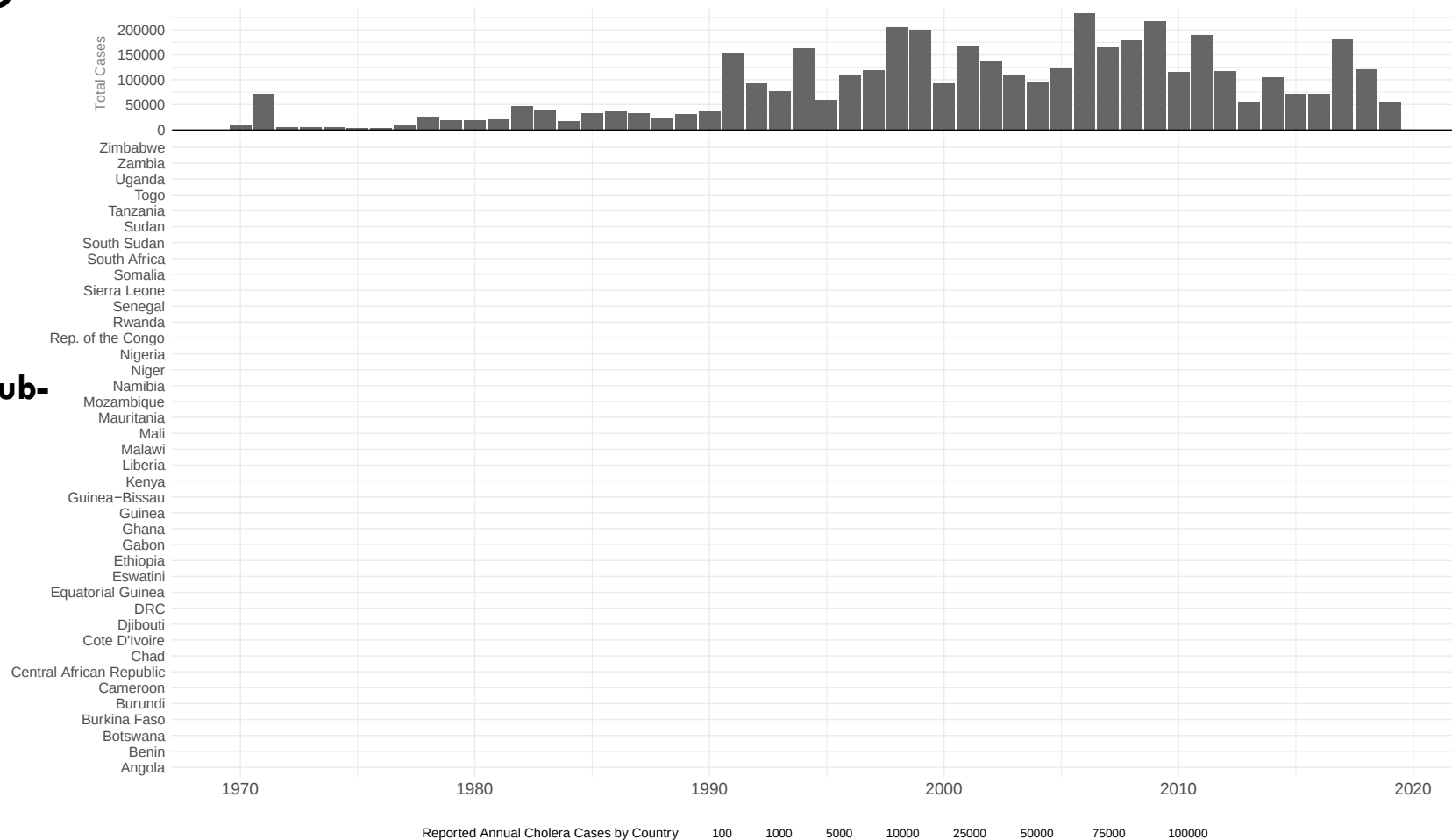
⁵Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts, USA.

⁶Carolina Population Center, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA.



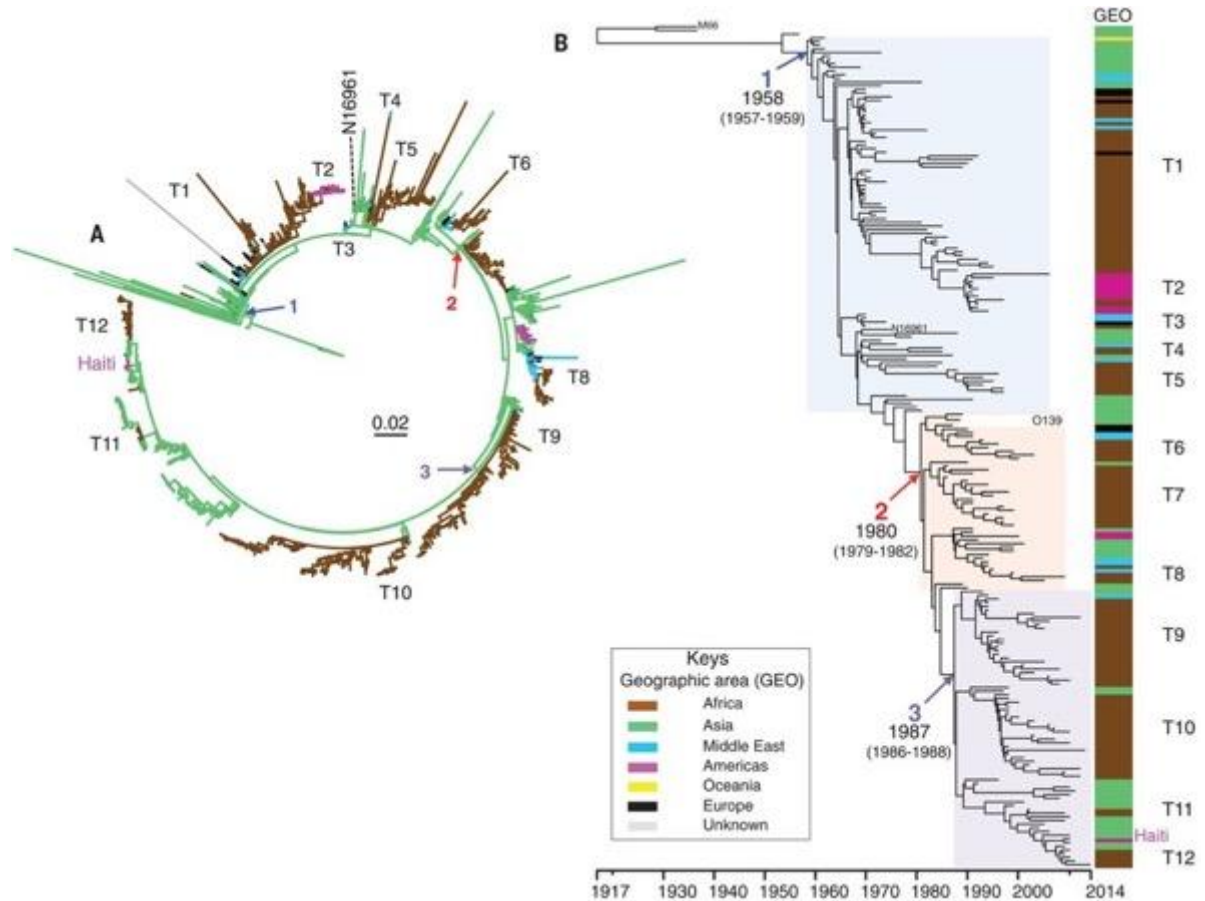
Background

Cholera burden in sub- Saharan Africa

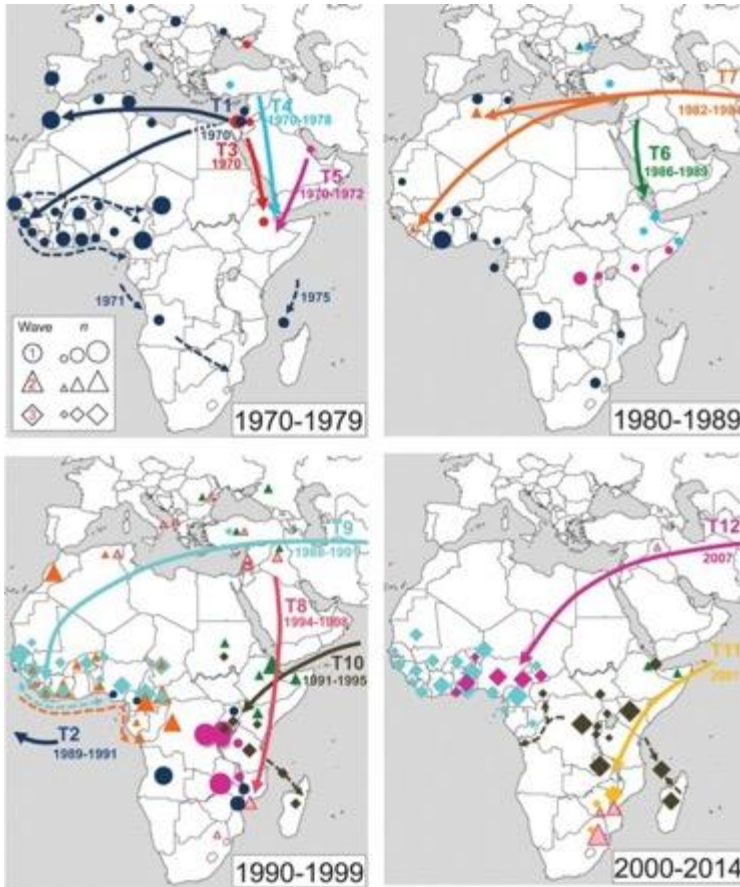


Background

Recent phylogenetic analysis found distinct introduction events into Africa



Background



Based on these findings, authors inferred propagation routes of seventh pandemic *V. cholerae* O1 El Tor in the African continent

Motivation

- Despite recent evidence, much remains unknown about cholera transmission dynamics within Africa.



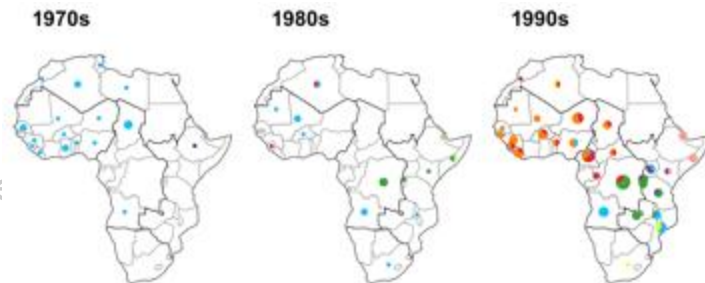
Motivation

- Despite recent evidence, much remains unknown about cholera transmission dynamics within Africa.
- While there is clear evidence of multiple introductions to the continent that have helped sustain the seventh cholera pandemic in Africa, epidemiologic data suggests that there are also areas that maintain endemic cholera.



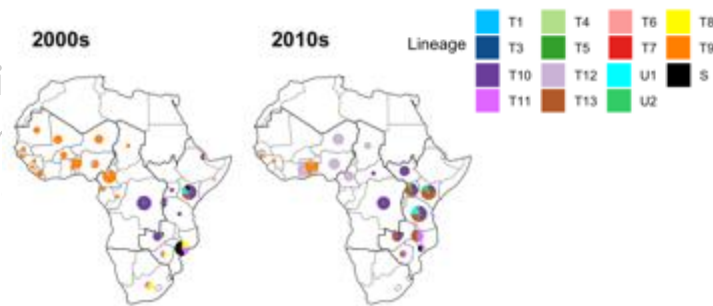
Motivation

- Despite recent evidence of sustained transmission dynamics within Africa.



era transmission

- While there is clear evidence of sustained transmission dynamics within Africa, there are also areas that



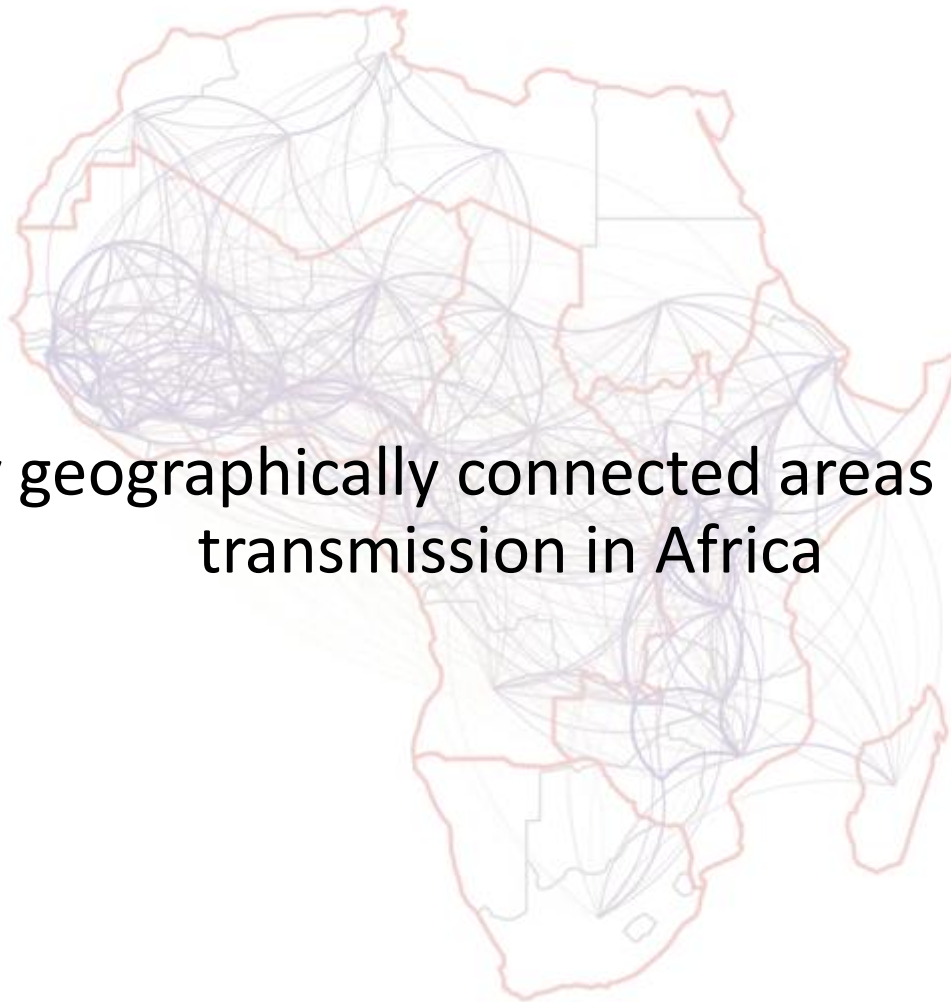
e continent that have
ologic data suggests that

- Connected areas likely have correlated transmission dynamics. These basic epidemiologic units of transmission may:
 - Propagate outbreaks from intercontinental introductions
 - Maintain endemic circulation that seed outbreaks elsewhere on the continent



Objective

Identify geographically connected areas of cholera transmission in Africa



Data sources

Combine molecular data with epidemiologic and ecologic data of cholera incidence.

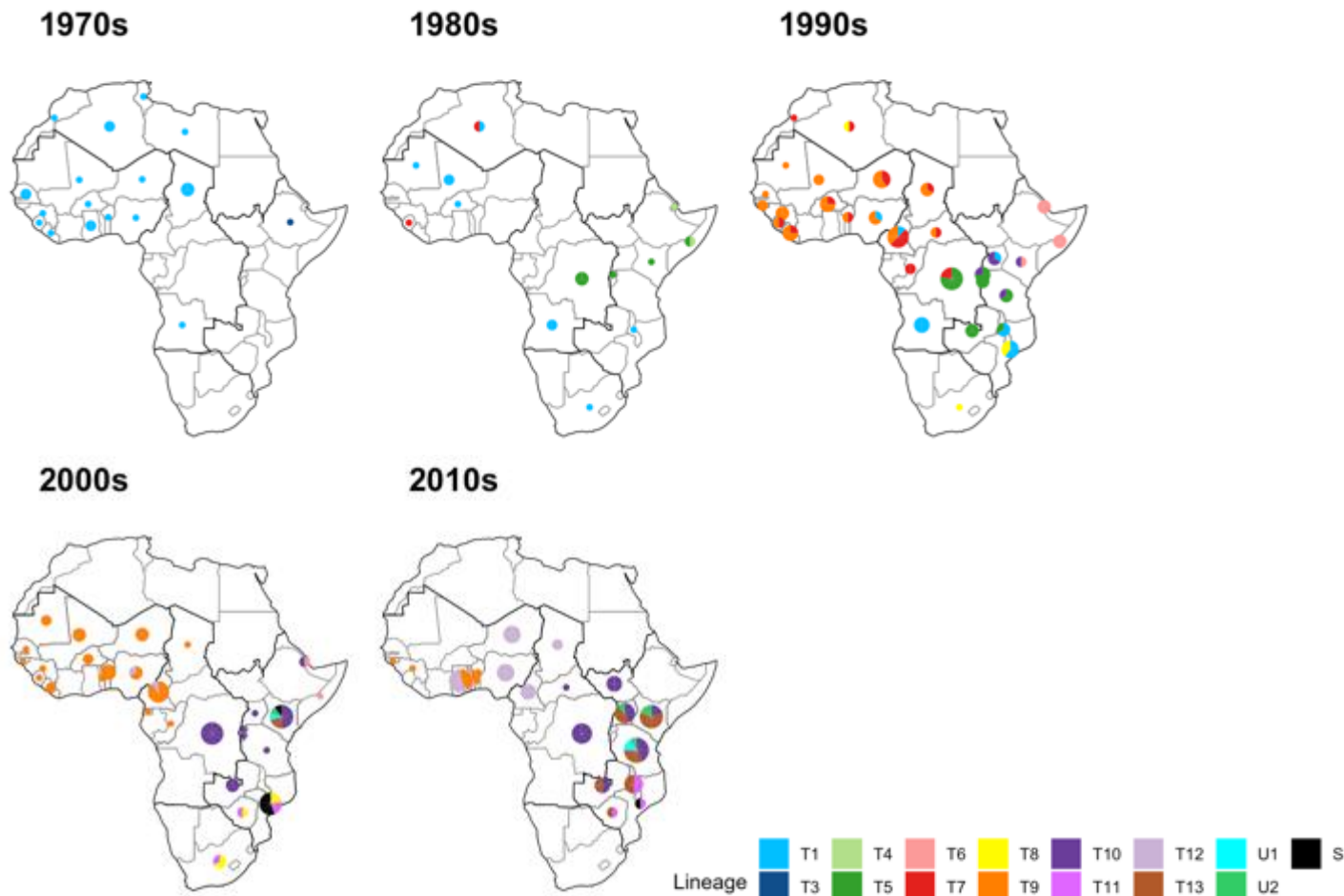
- Molecular data:
 - Cholera sequencing data from public repositories
- Epidemiologic data
 - WHO reported cholera case counts by year and country



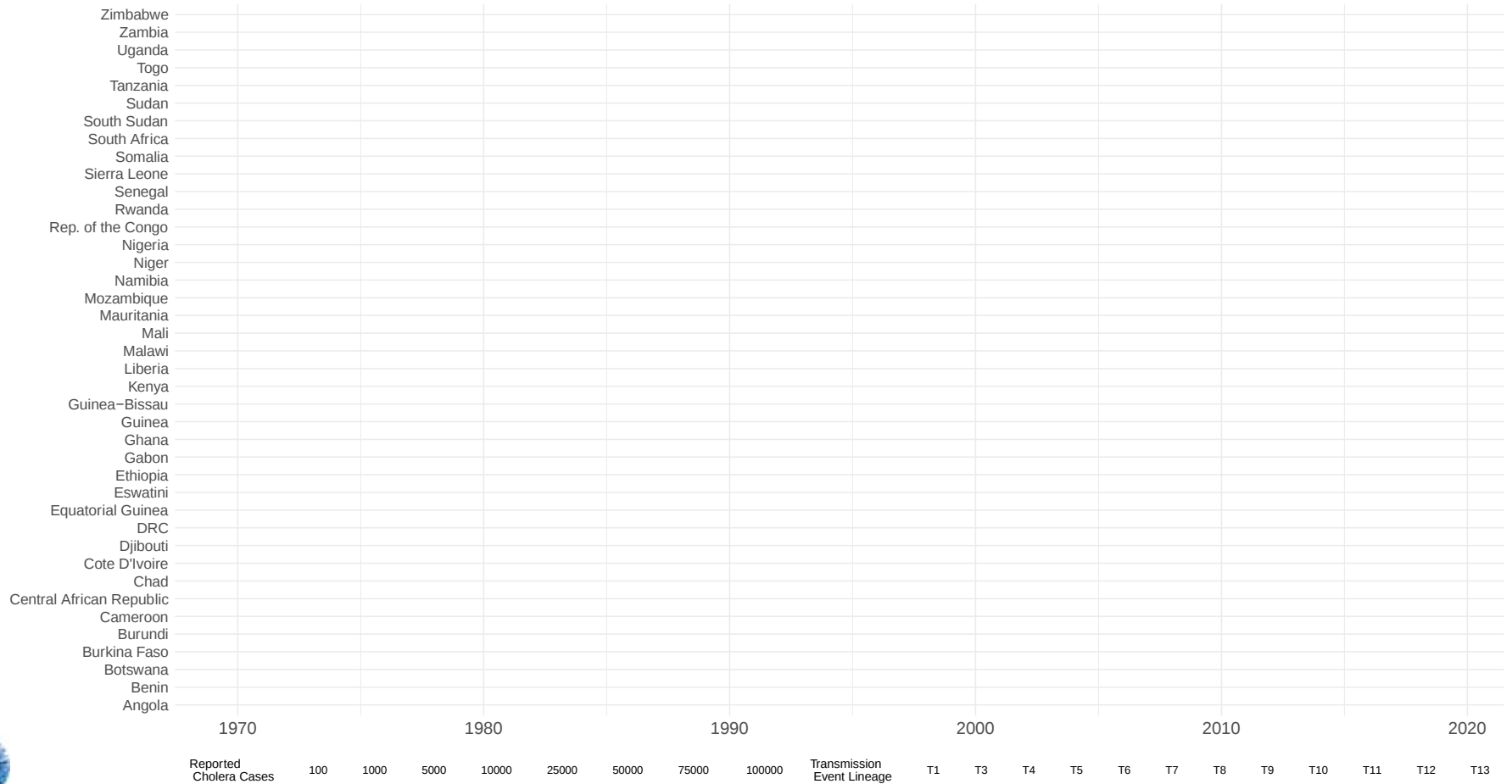
Gaps in observed data



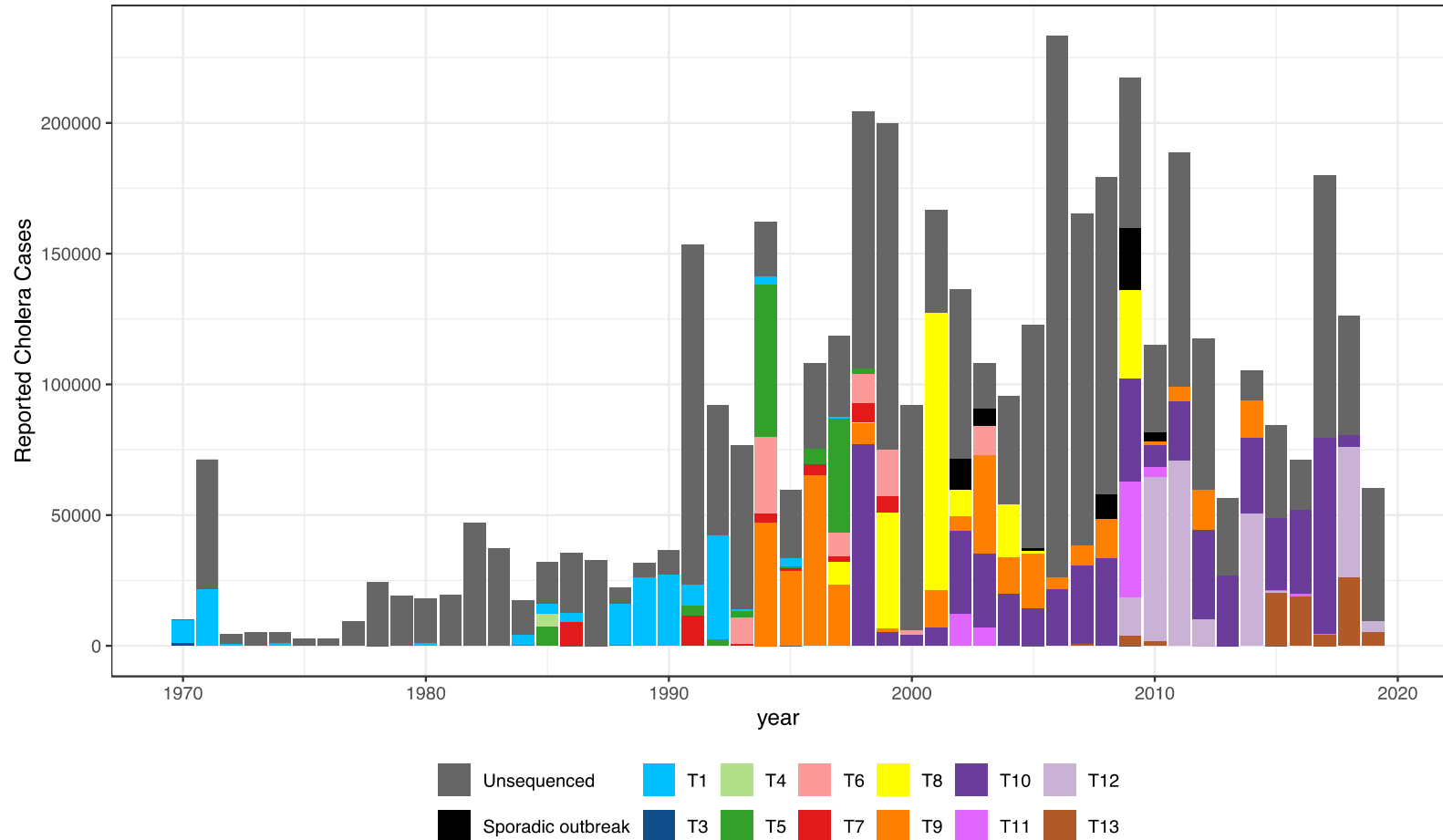
Gaps in observed data



Gaps in observed data



Gaps in observed data



**Inferring occurrence & prevalence of
cholera sub-lineages to define
epidemiologically relevant transmission
units**

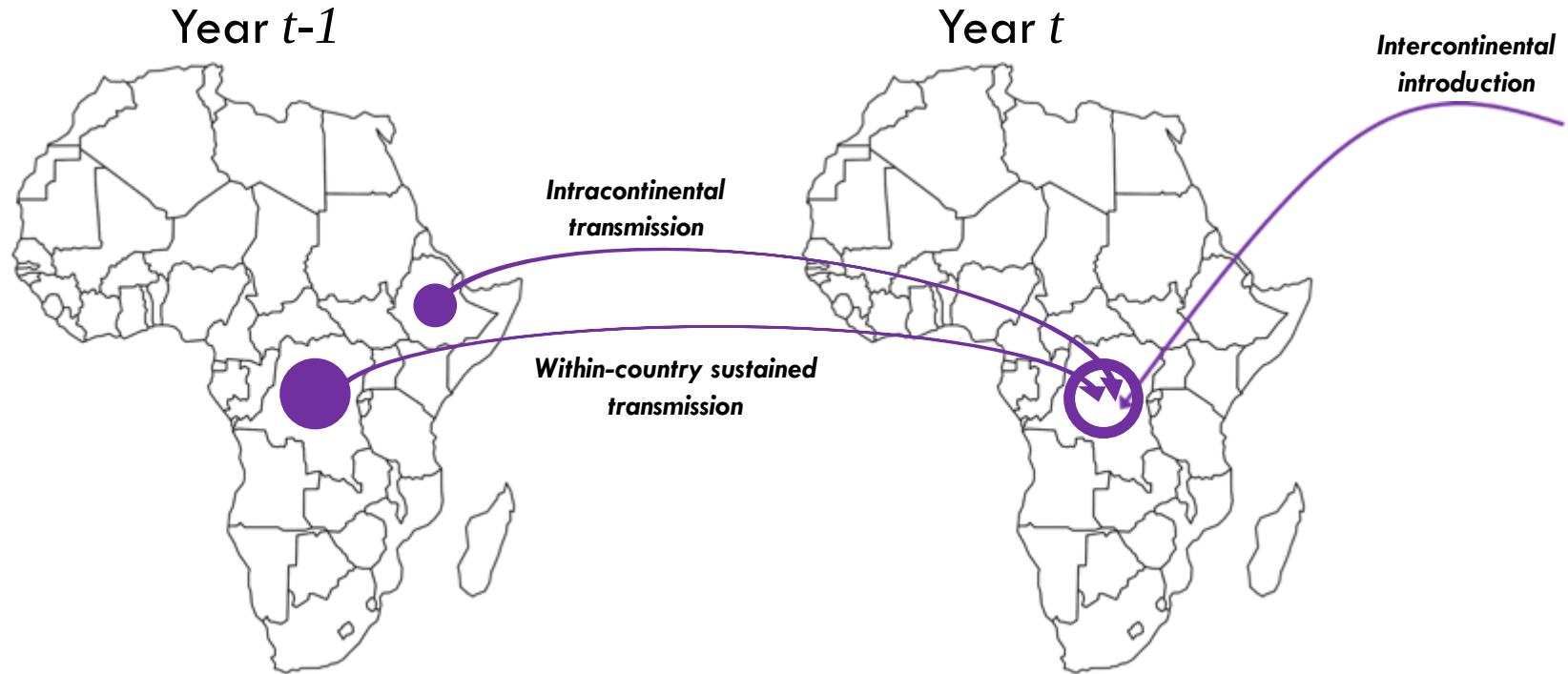


Approach

- Model occurrence and prevalence of distinct cholera sub-lineages in countries through time using a Hidden Markov Model.
 - Accounting for historical information of cholera presence
- Targets of inference:
 - strength of connectivity driving transmission between locations
 - underlying occurrence and prevalence of cholera sub-lineages in each country in all years



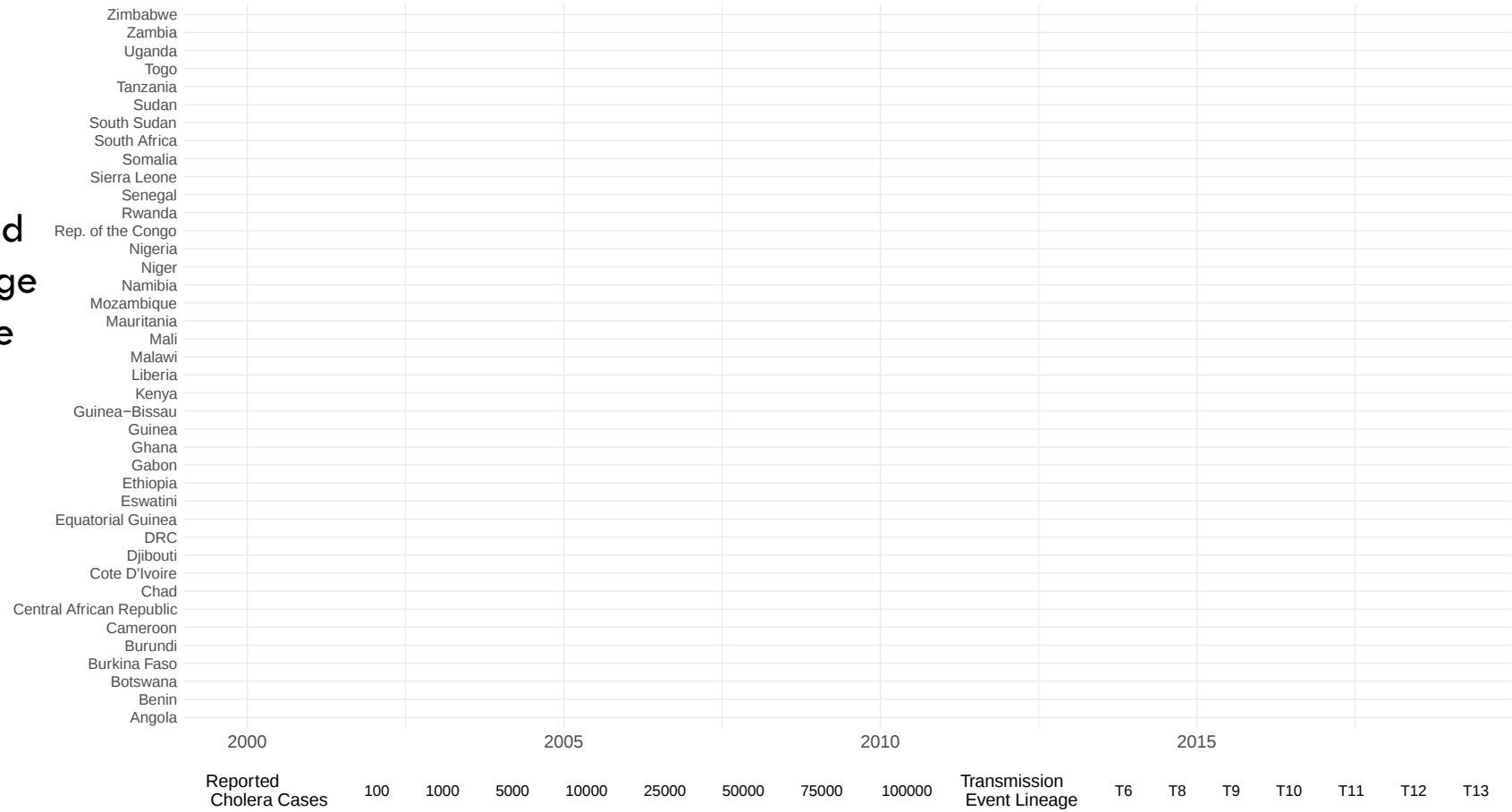
Transition Process



Model Results

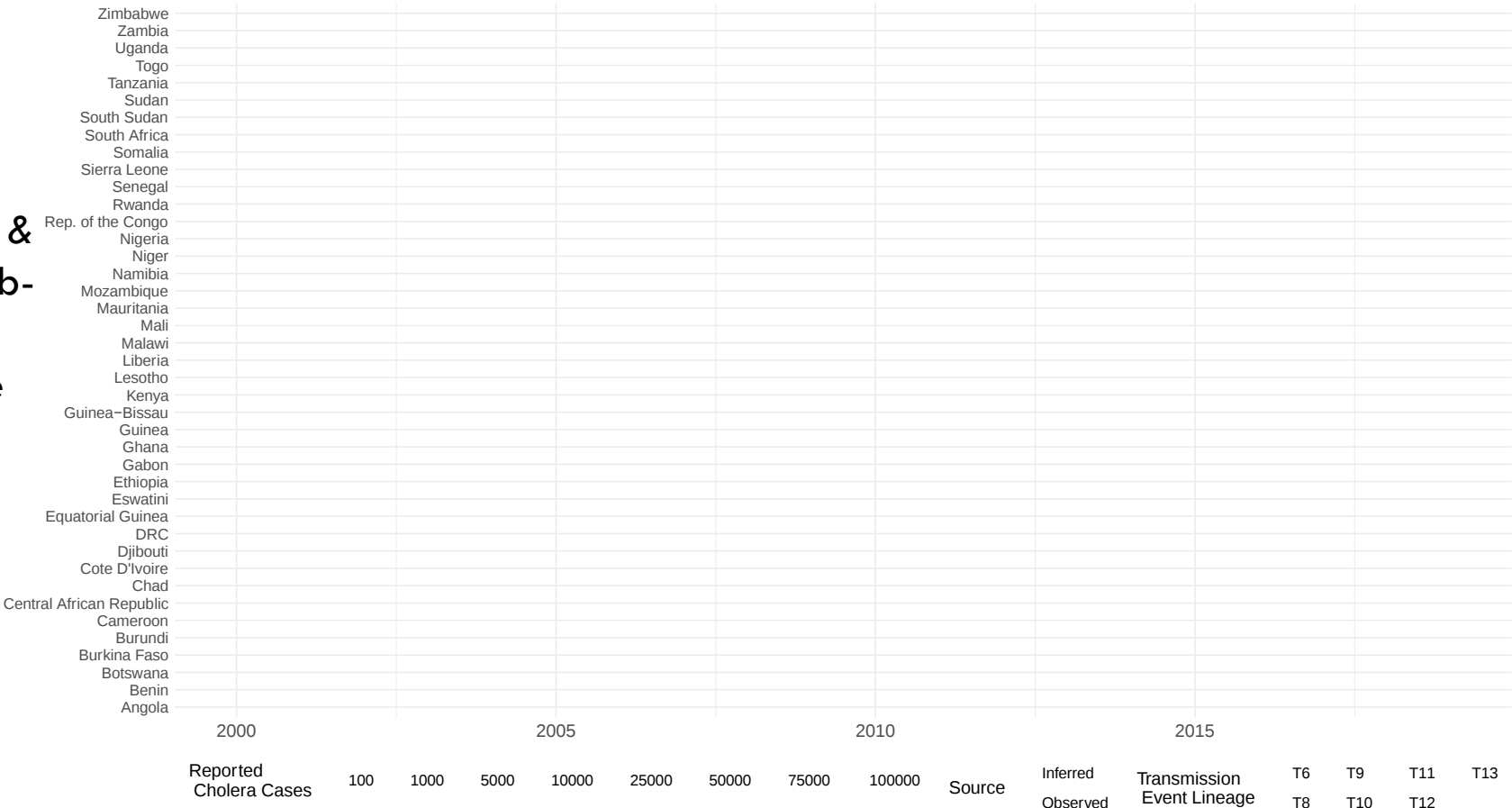
Observed
sub-lineage
presence

~Since 2000~



Model Results

Observed &
inferred sub-
lineage
presence
~Since 2000~

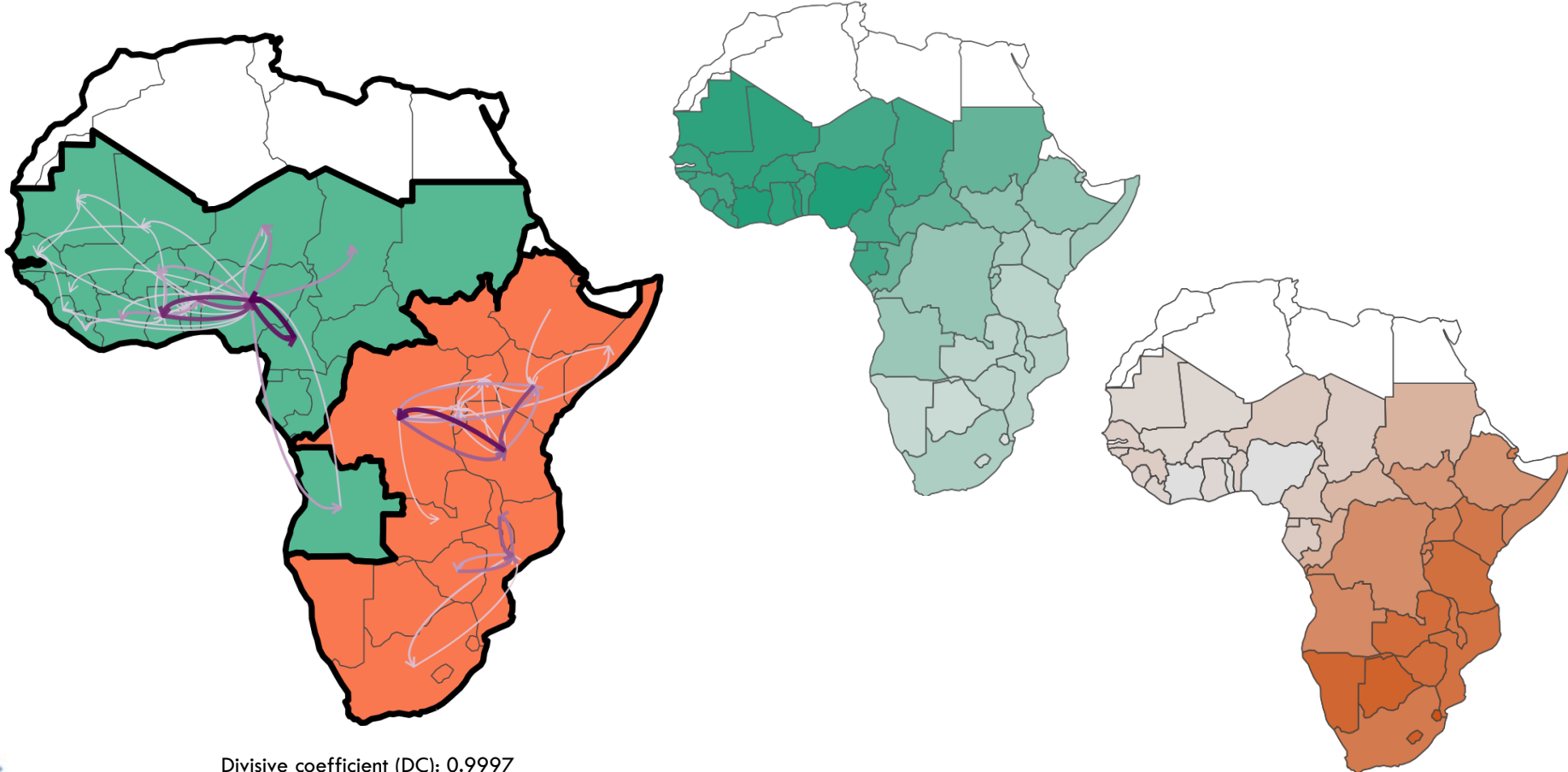


Model Results

Inferred prevalence
~Since 2000~



Inferred Connectivity



Divisive coefficient (DC): 0.9997



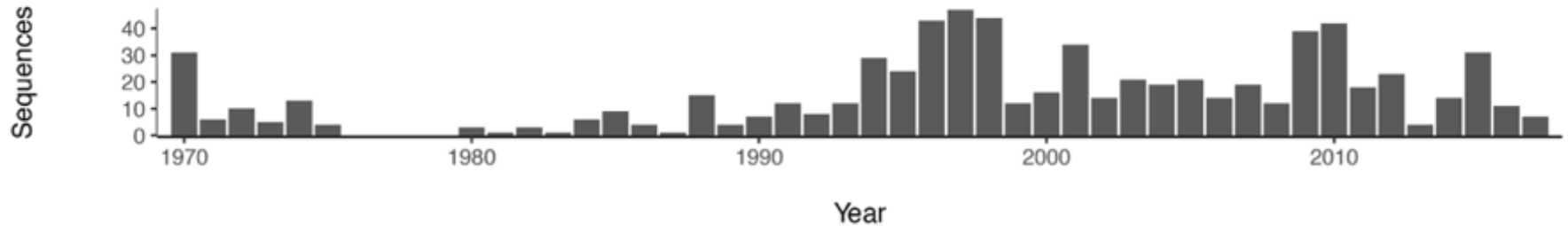
Ongoing Analysis

- Continue to refine and validate our model, incorporating additional elements to capture transmission dynamics and connectivity between locations.
- Simulate transmission between countries based on inferred connectivity from our model.



Limitations

- Ultimately, sequencing remains sparse and cholera cases are often under-reported.
 - Areas with extremely sparse data can impact the ability of our model to infer underlying presence of distinct sub-lineages.



- Additional sequencing efforts can help improve our understanding of phylodynamic processes driving cholera transmission in Africa.



Implications & Future Directions

- Transmission units informing cholera control:
 - Proactive intervention:
 - identify areas where increases in cases → increase in local cholera risk in connected areas
 - Maximize indirect effects:
 - targeted vaccination and water/sanitation campaigns
- Assess drivers of cholera endemicity to determine the influence of new and re-introductions versus local undetected persistence



ACKNOWLEDGEMENTS

Javier Perez-Saez

Shirlee Wohl

Andrew Azman

Justin Lessler

Nathaniel Matteson

BILL & MELINDA
GATES *foundation*



Bethany L. DiPrete, PhD • diprete@email.unc.edu
@bethanydiprete • LinkedIn: bethany-diprete

Thank You

