



Continental analysis of Arbovirus transmission dynamics in Africa using genomic and epidemiological data

Preliminary Results

CLIMADE Africa – 14th March 2023

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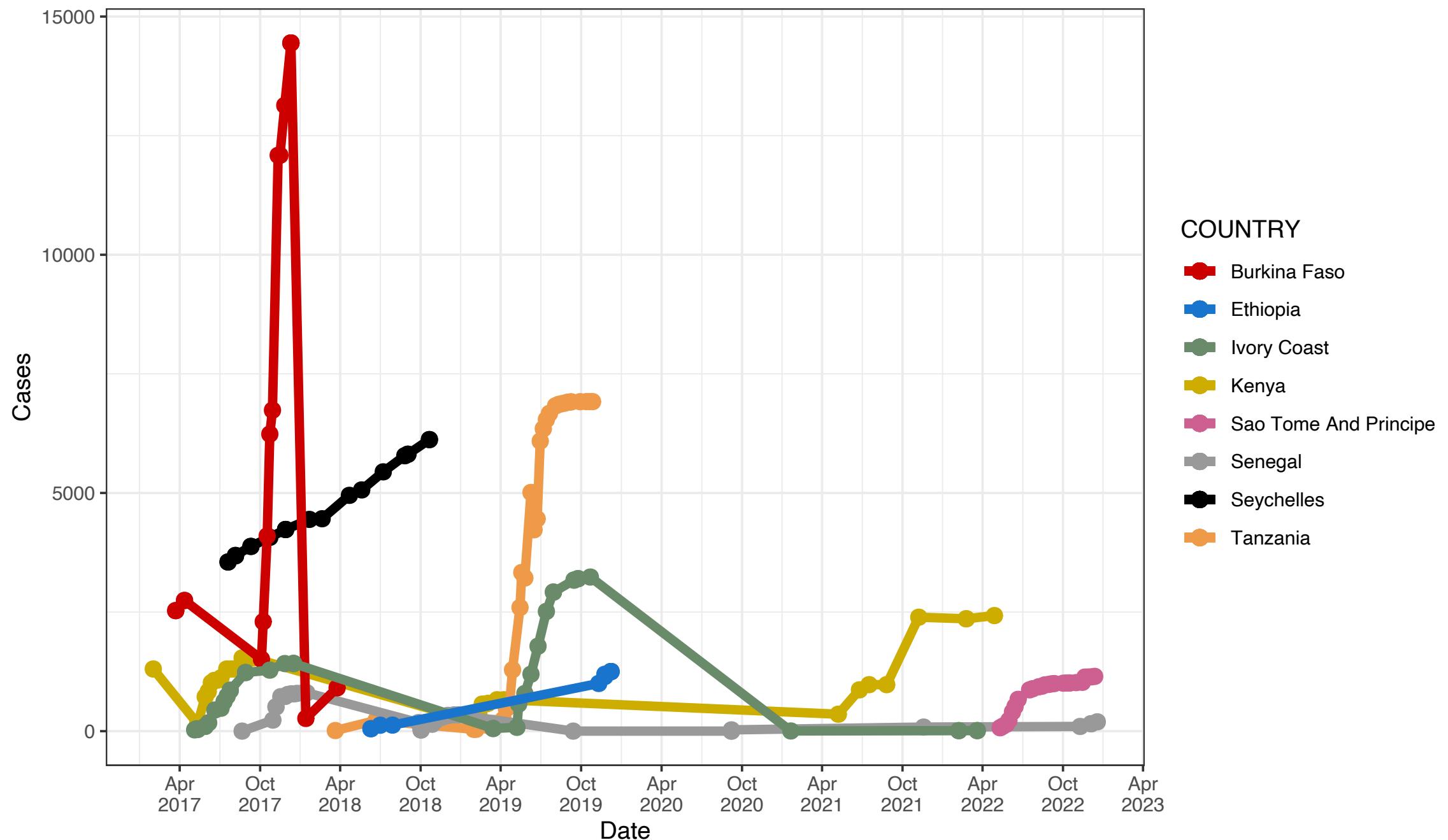
Questions to Answer

- What is the status of surveillance for Arboviruses in Africa in the face of recorded outbreaks?
- What are the levels of importations vs endemicity in Africa?
- Are the effective population sizes of the relevant pathogens increasing in Africa? (indicates endemic circulation)
- What are the risks of importations of Arboviruses from Asia and Americas?
- What are the risks of local transmission/outbreaks/epidemics upon importation?
- Do transmission dynamics correlate with environmental factors?

Dengue (I to IV) Phylogenetics & Transmission Dynamics in Africa

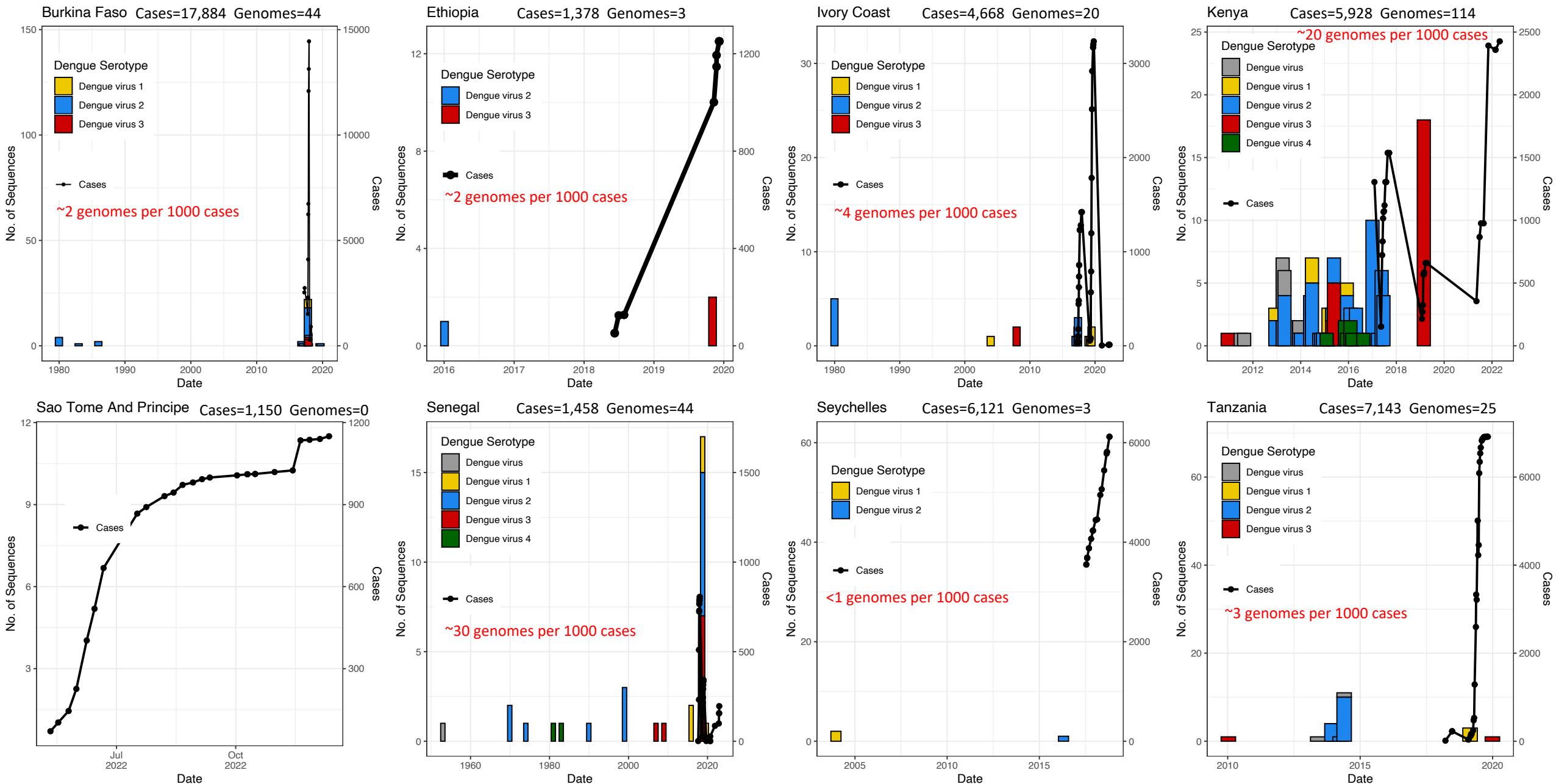
Dengue (I to IV) outbreaks in Africa from 2017 to 2023 – Countries with top 8 incidence

(Source: <https://www.afro.who.int/health-topics/disease-outbreaks/outbreaks-and-other-emergencies-updates>)



Dengue (I to IV) outbreaks in Africa from 2017 to 2023 – Countries with top 8 incidence

(Source: <https://www.afro.who.int/health-topics/disease-outbreaks/outbreaks-and-other-emergencies-updates>)



The landscape of genomic surveillance of Dengue (I to IV) in Africa

Dengue

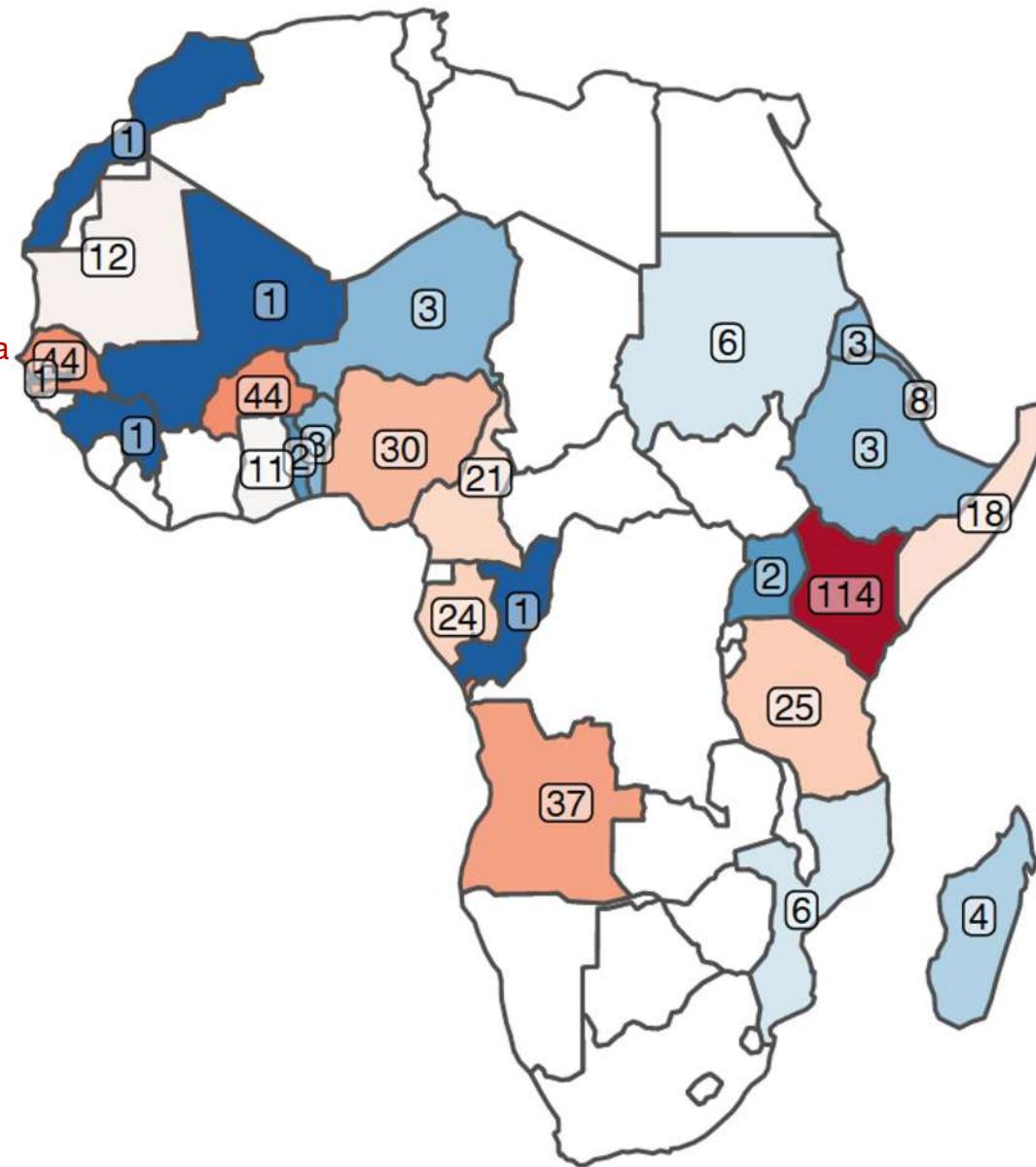
Africa:

genomes = 457
countries = 30
1953-2021

253 genomes from countries with top 8 incidence in Africa
204 genomes from rest 22 countries

Quality:

Coverage >90% = 215
Genotyped = 208



The landscape of genomic surveillance of Dengue (I to IV) in Africa

Dengue

Africa:

genomes = 457

countries = 30

1953-2021

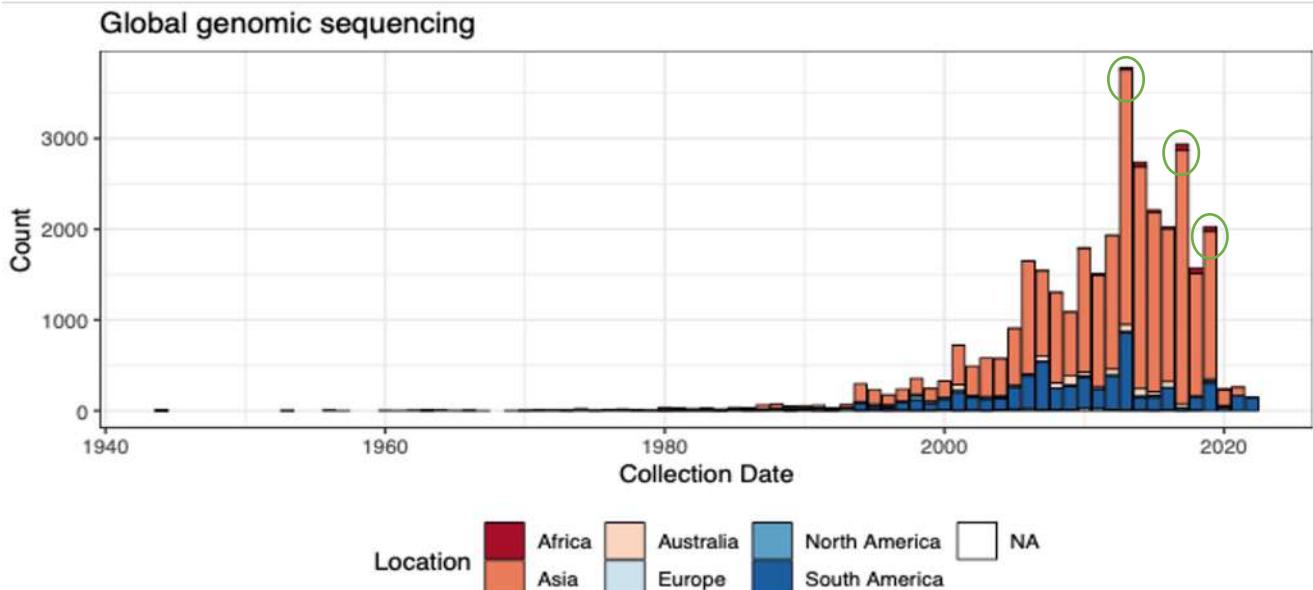
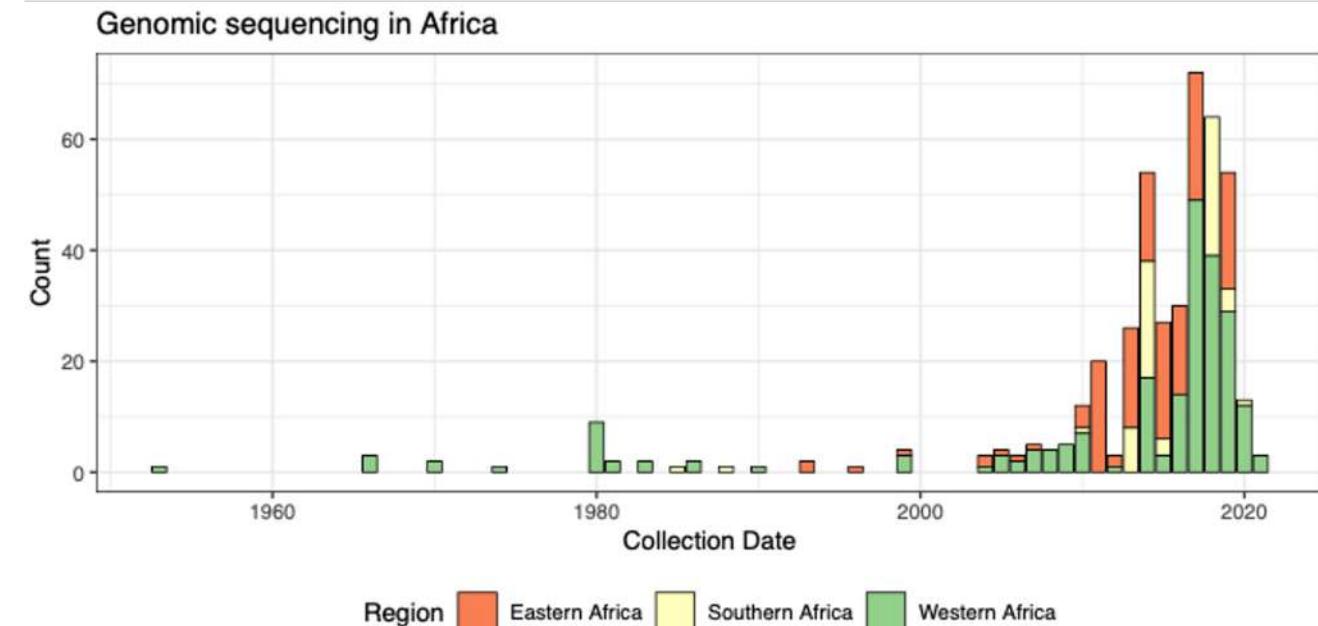
Quality:

Coverage >90% = 215

Genotyped = 208

Global Genomic sequencing:

Genomes > 40,000



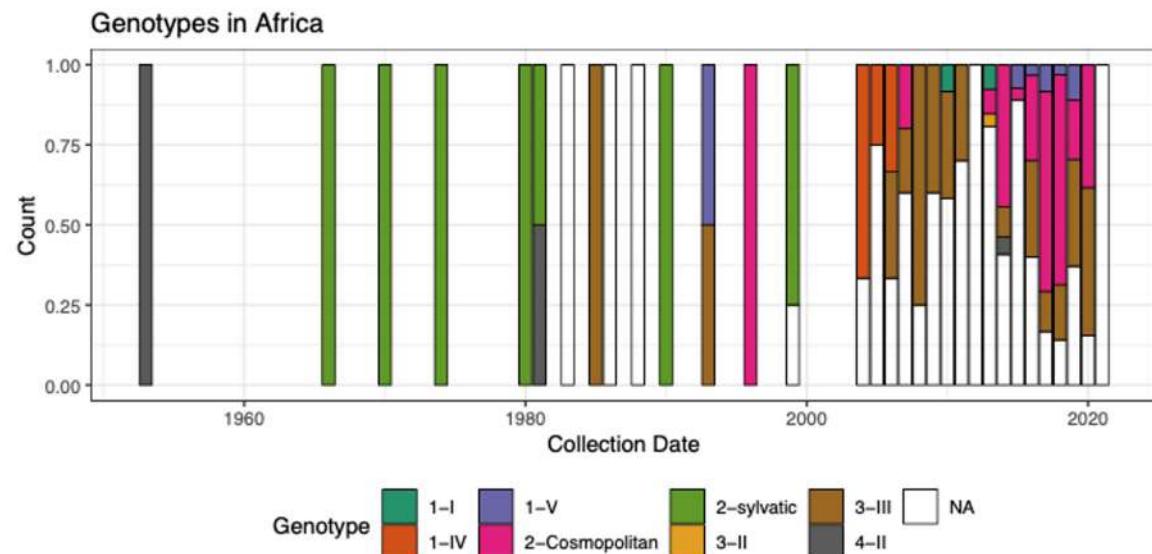
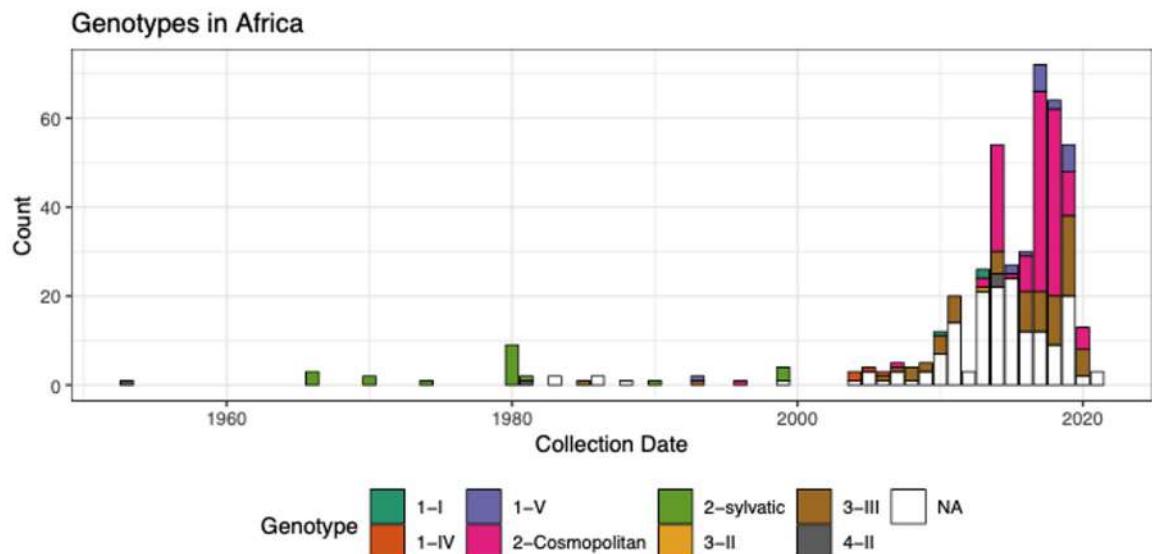
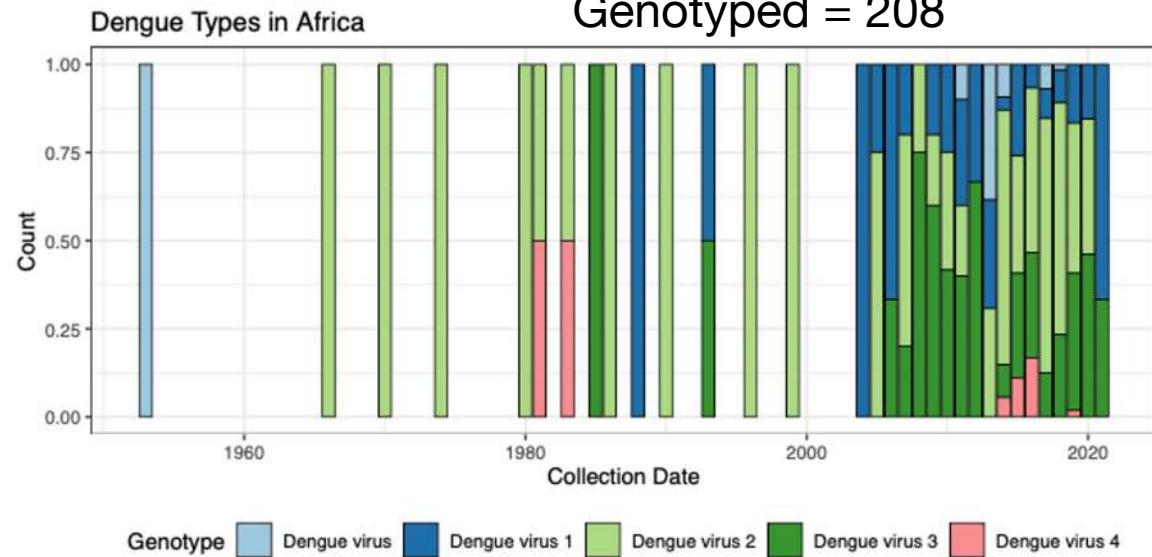
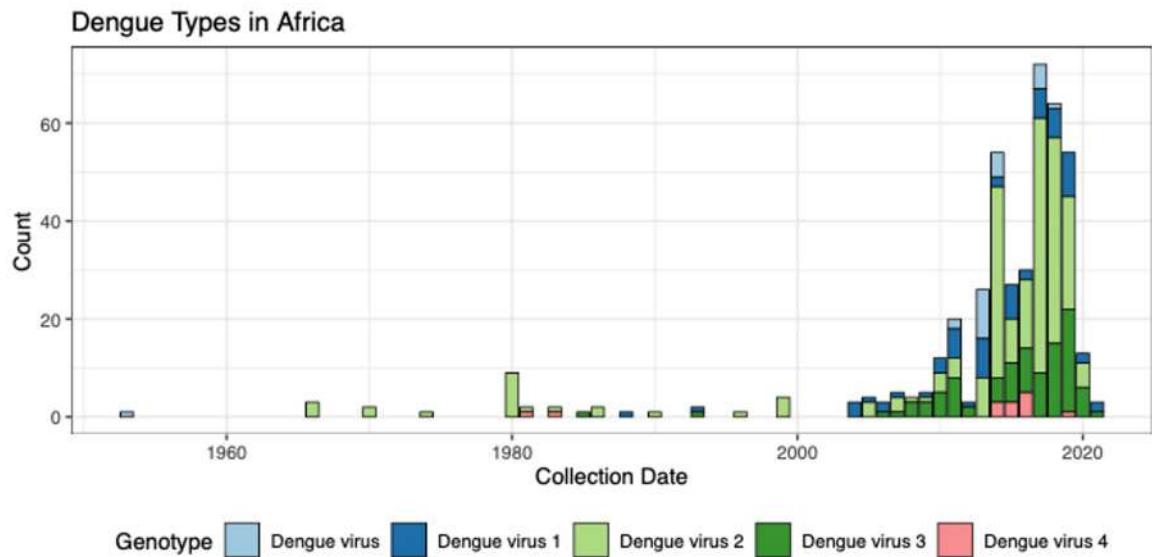
The landscape of genomic surveillance of Dengue (I to IV) in Africa

Genomes = 457

Quality:

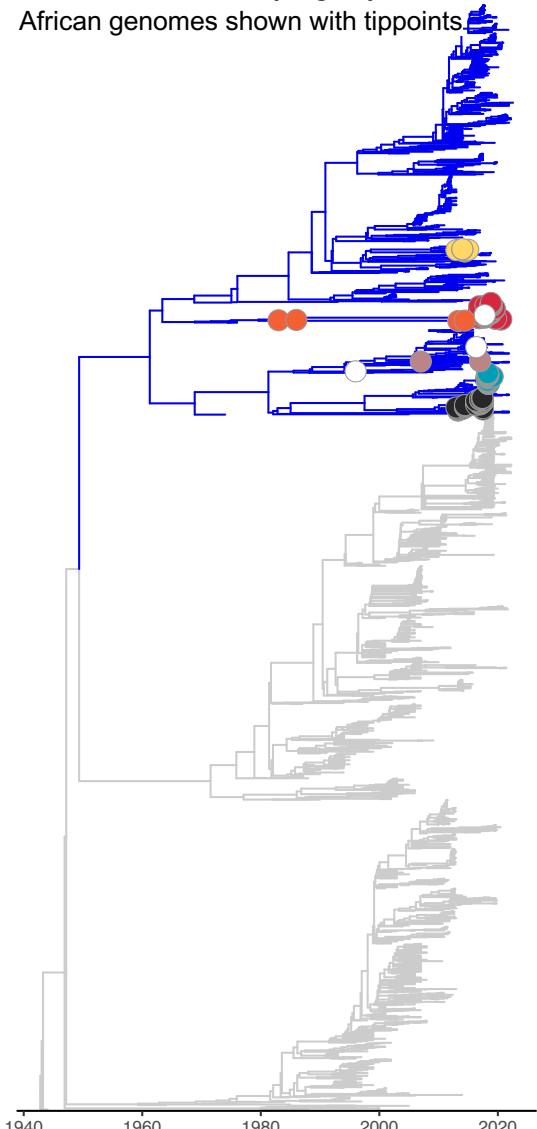
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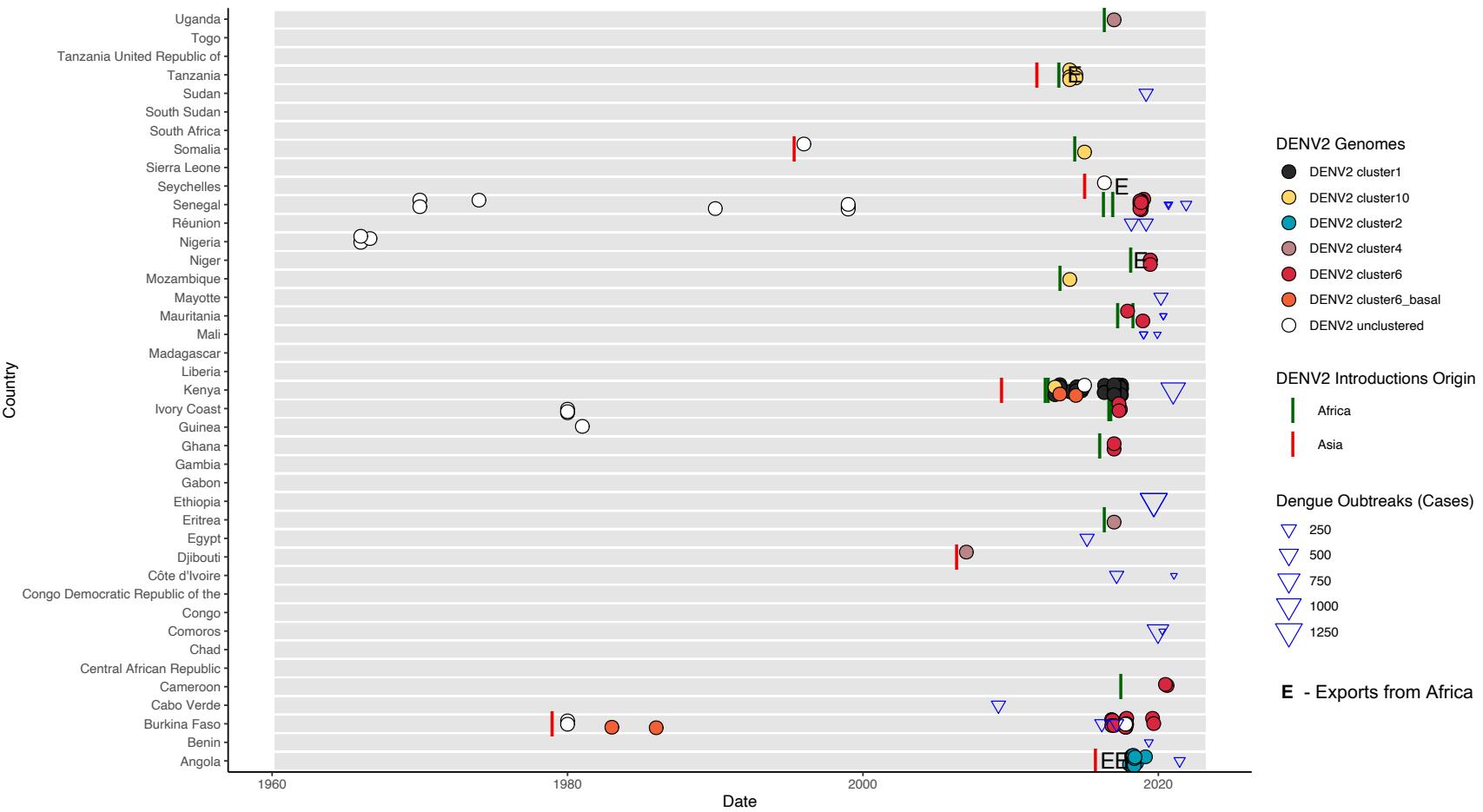


DENV2 Global Phylogeny

African genomes shown with tippoints

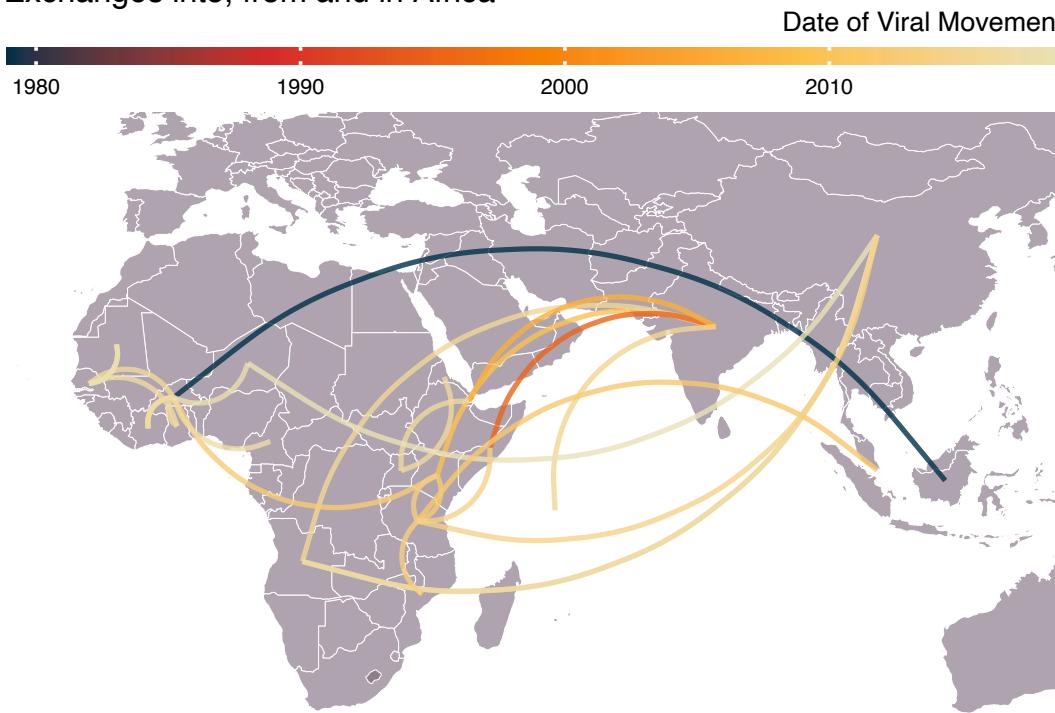


DENV2 Transmission Dynamics in Africa

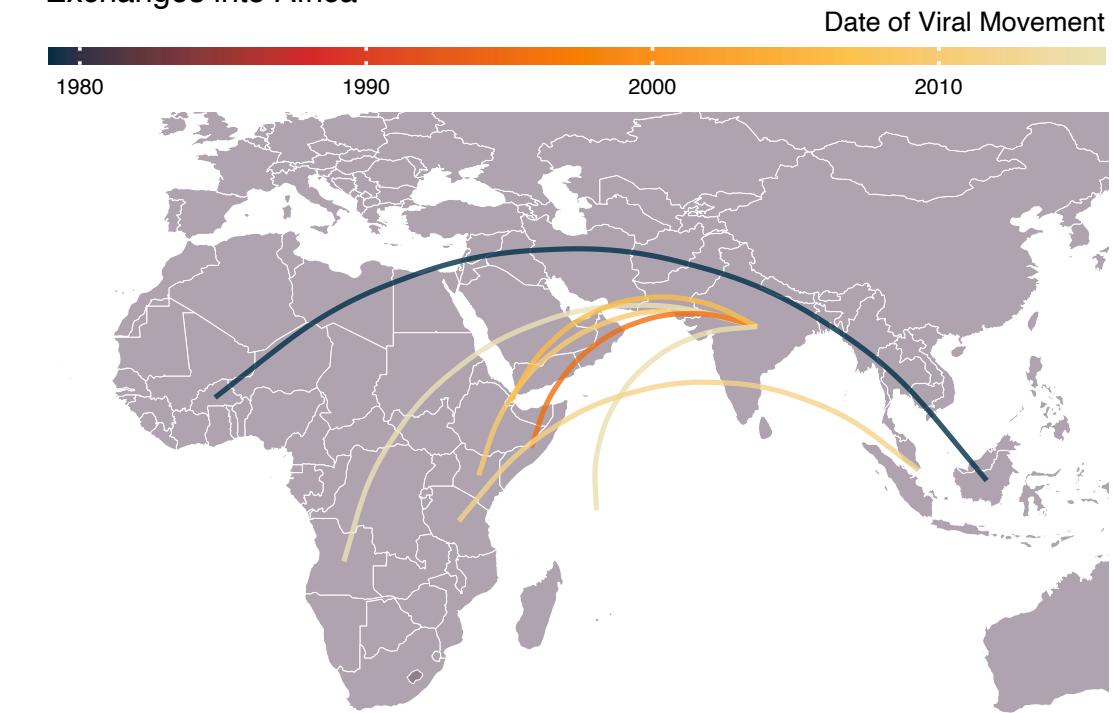


DENV2 Viral Movement Maps
Focused on Africa

Exchanges into, from and in Africa



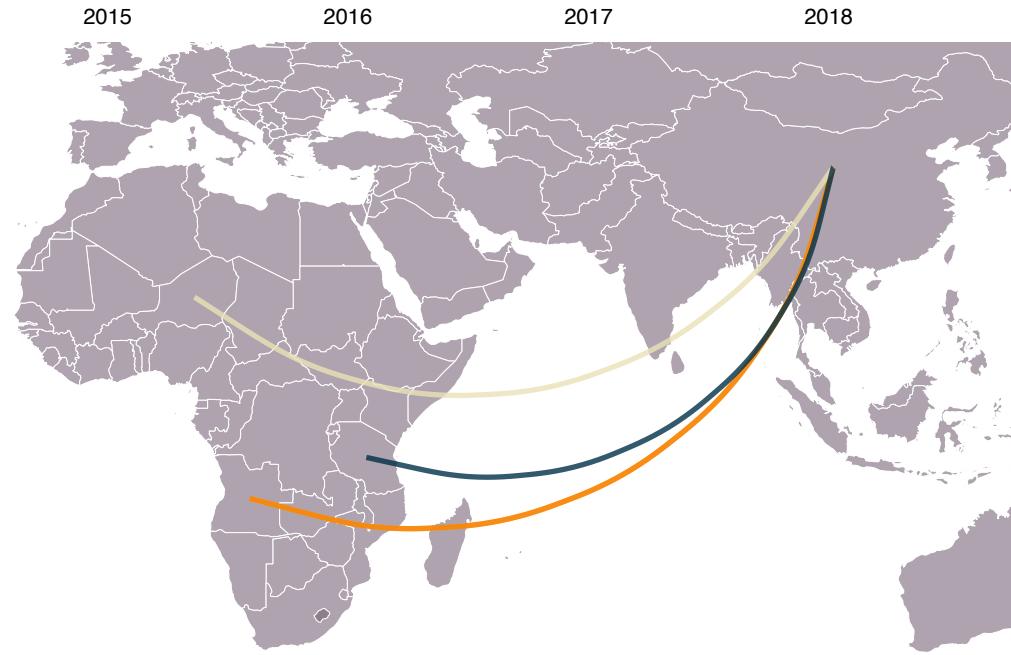
Exchanges into Africa



DENV2 Viral Movement Maps
Focused on Africa

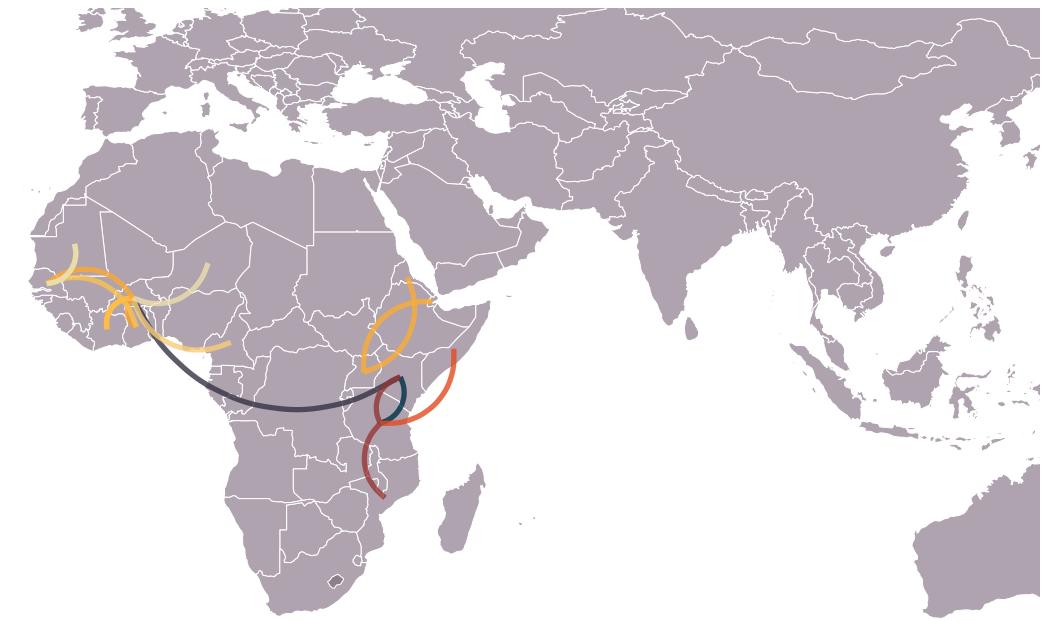
Exchanges from Africa

Date of Viral Movement



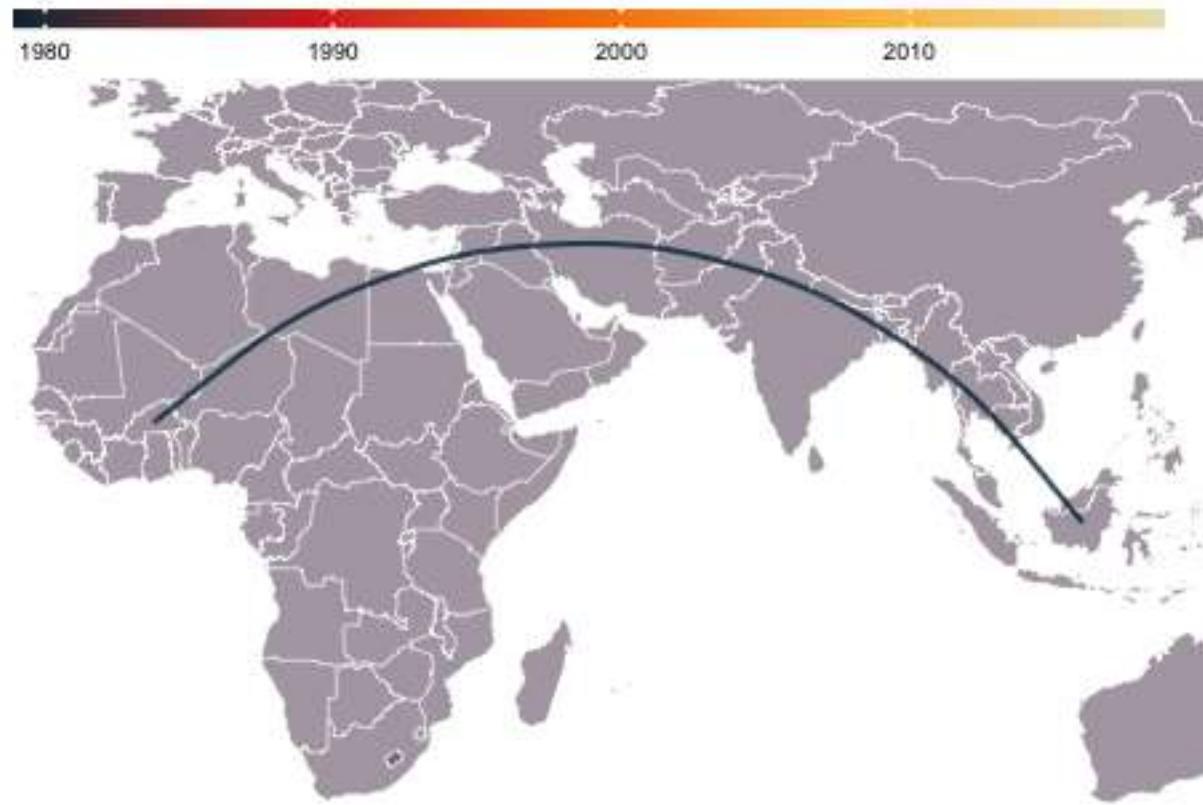
Exchanges in Africa

Date of Viral Movement



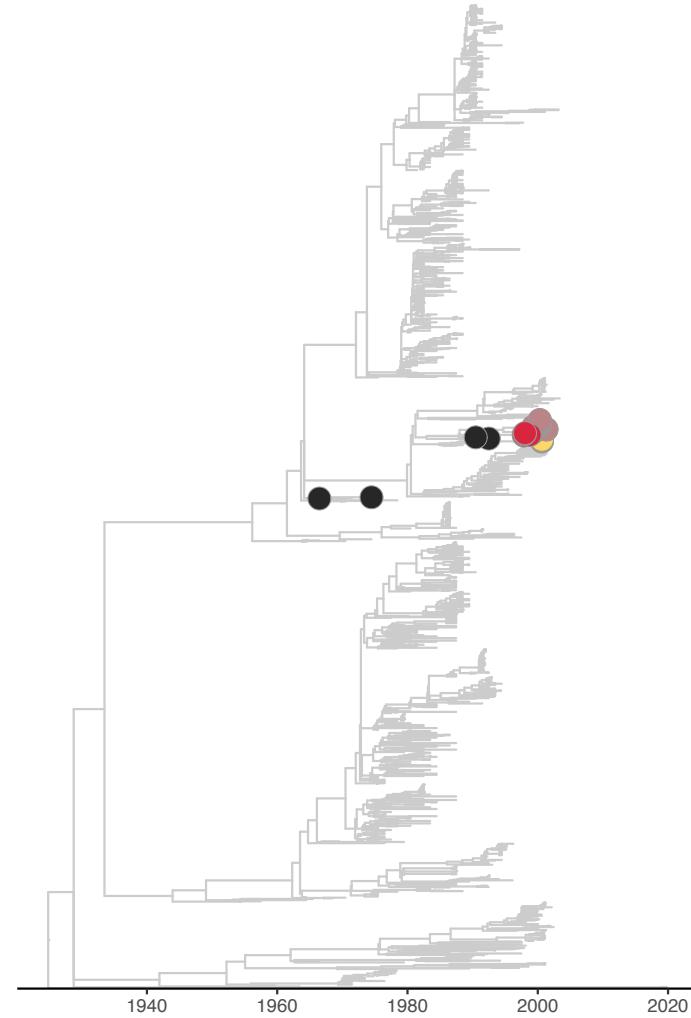
Exchanges into, from and in Africa 1978-12-15

Date of Viral Movement

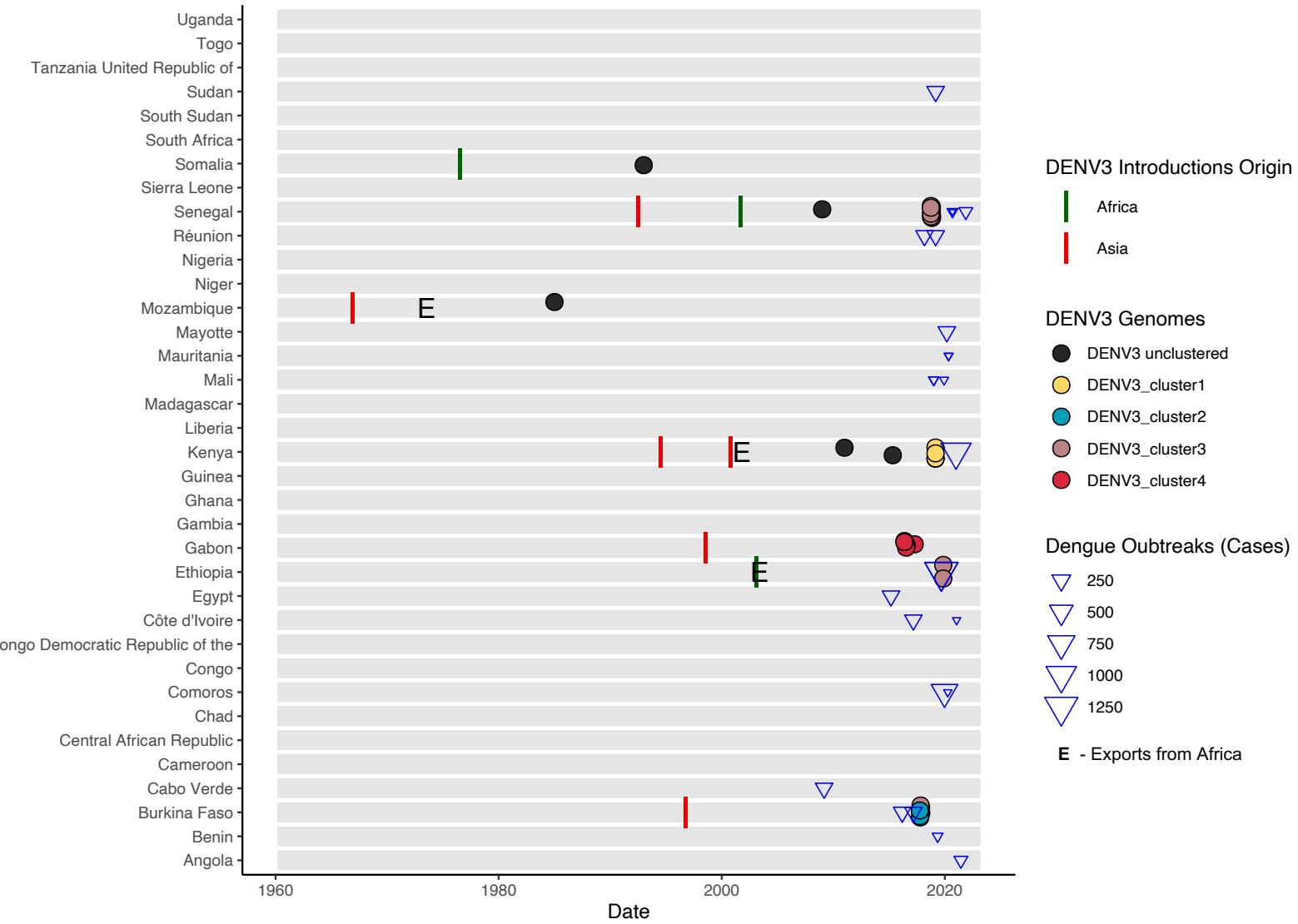


DENV3 Global Phylogeny

African genomes shown with tippoints



DENV3 Transmission Dynamics in Africa

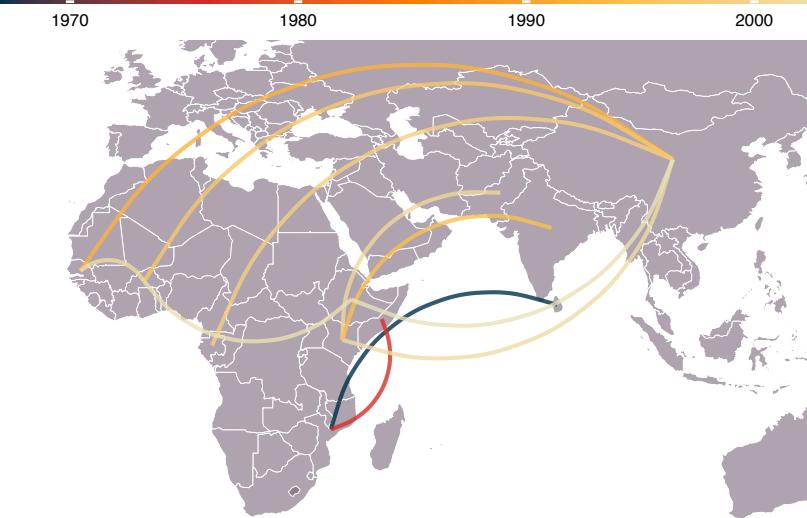


DENV3 Viral Movement Maps

Focused on Africa

Exchanges into, from and in Africa

Date of Viral Movement



Exchanges into Africa

Date of Viral Movement



Exchanges from Africa

Date of Viral Movement



Exchanges in Africa

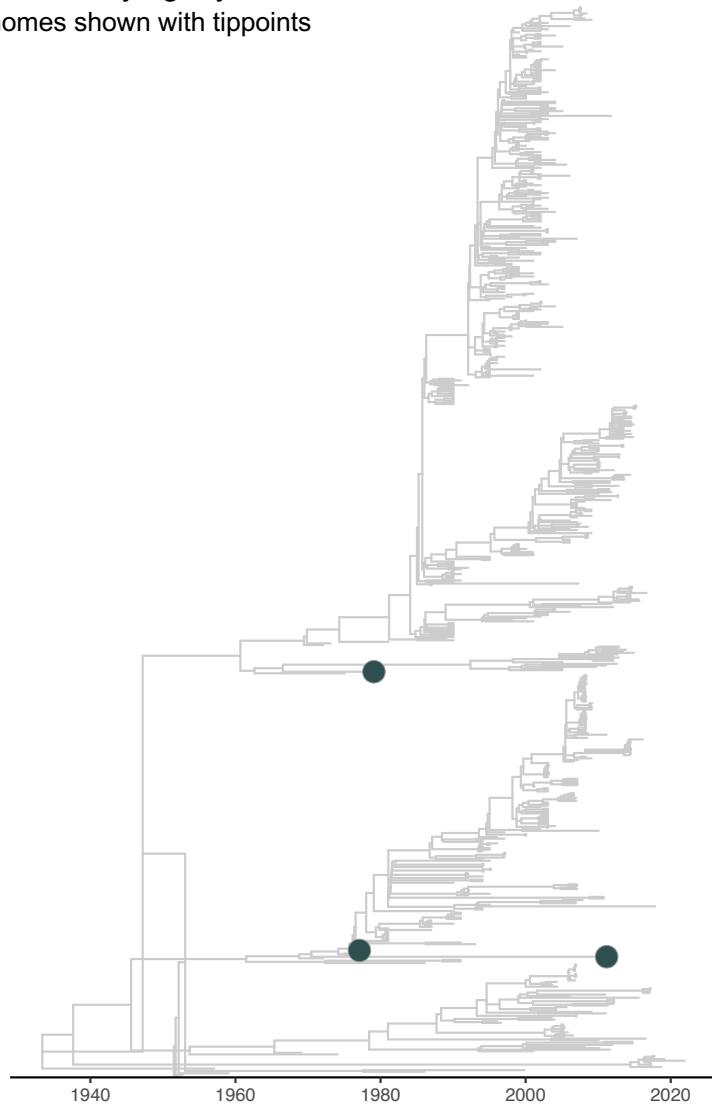
Date of Viral Movement



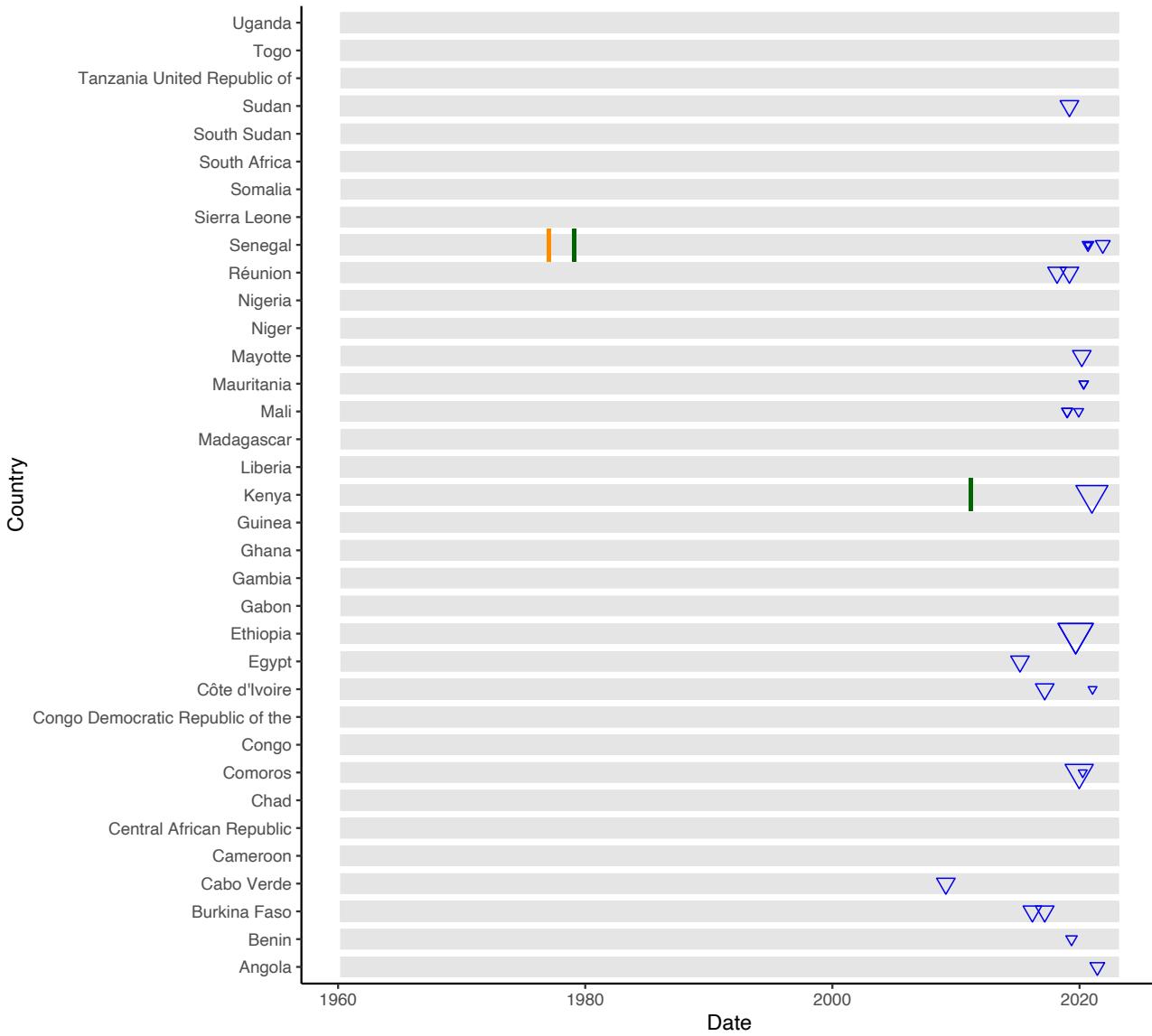


DENV4 Global Phylogeny

African genomes shown with tippoints

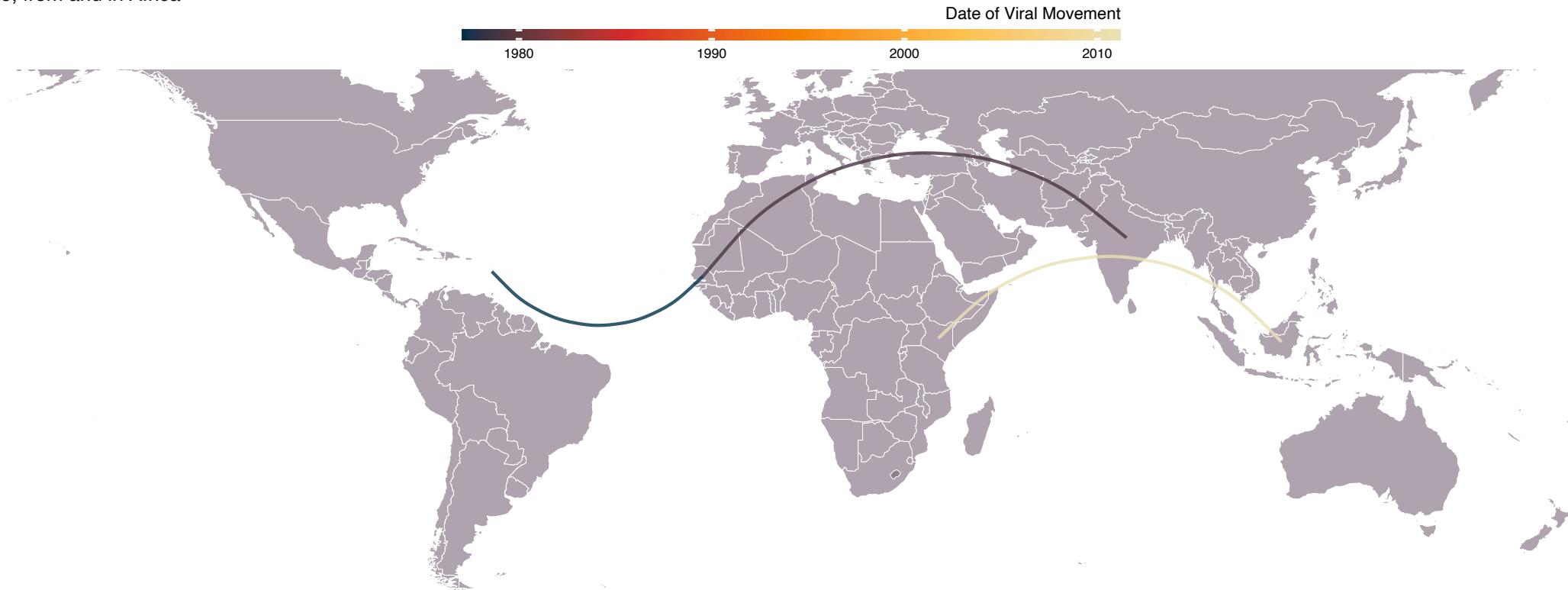


DENV4 Transmission Dynamics in Africa



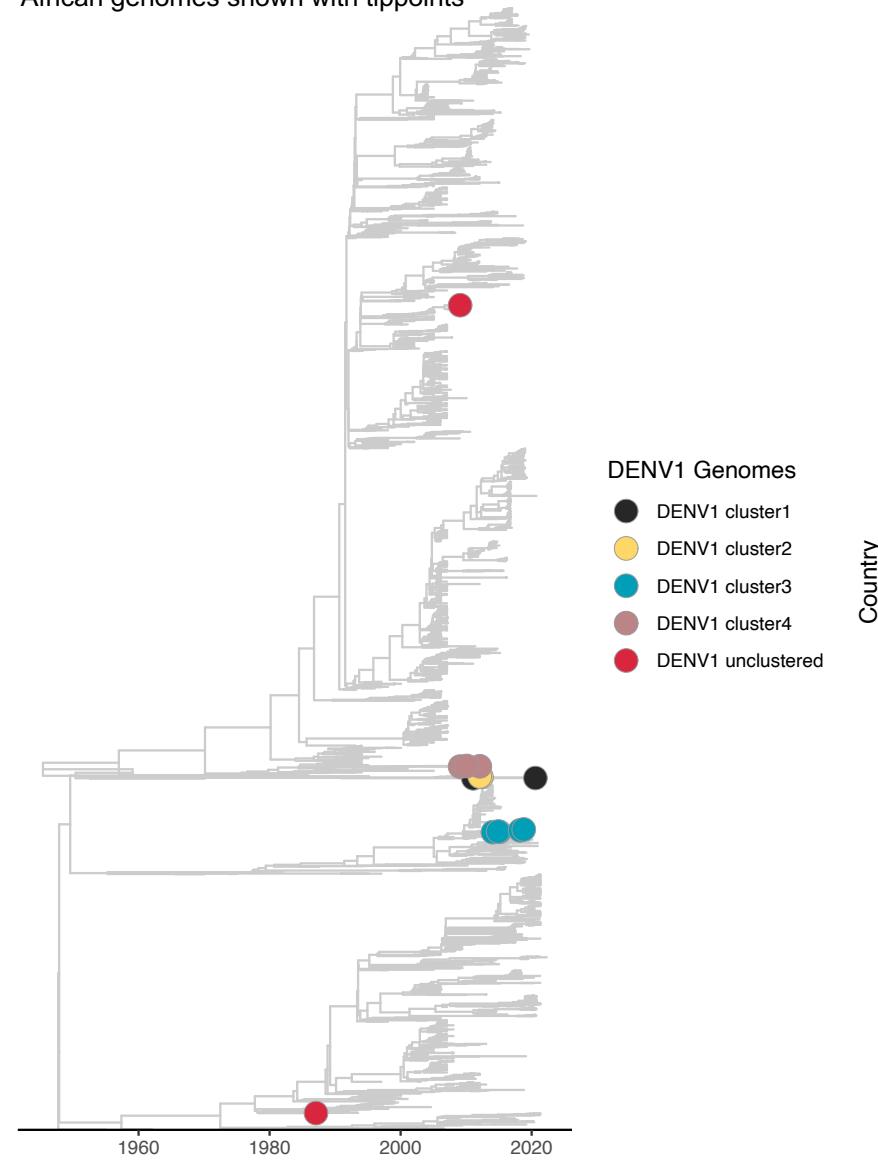
DENV4 Viral Movement Maps
Focused on Africa

Exchanges into, from and in Africa

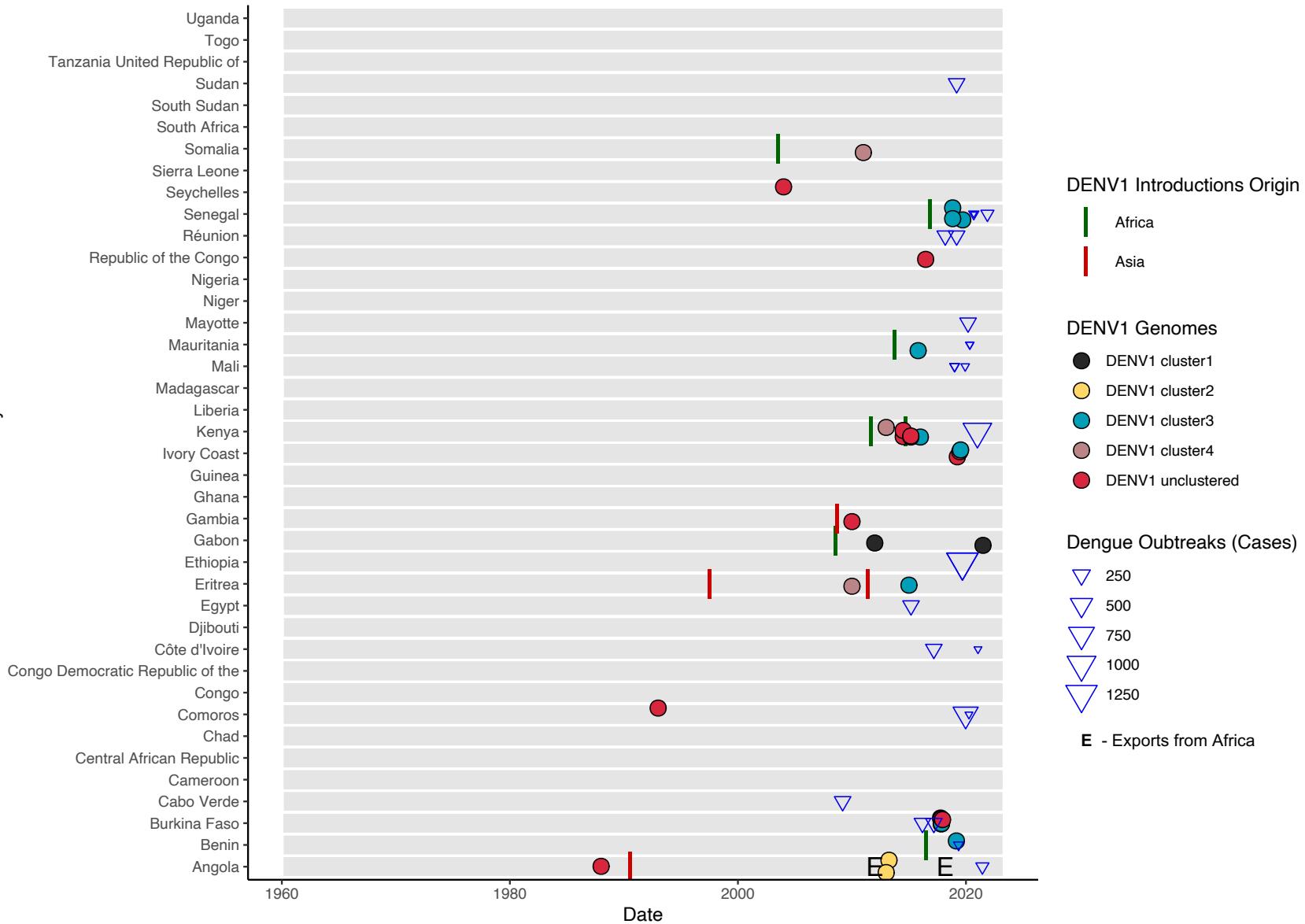


DENV1 Global Phylogeny

African genomes shown with tippoints



DENV1 Transmission Dynamics in Africa

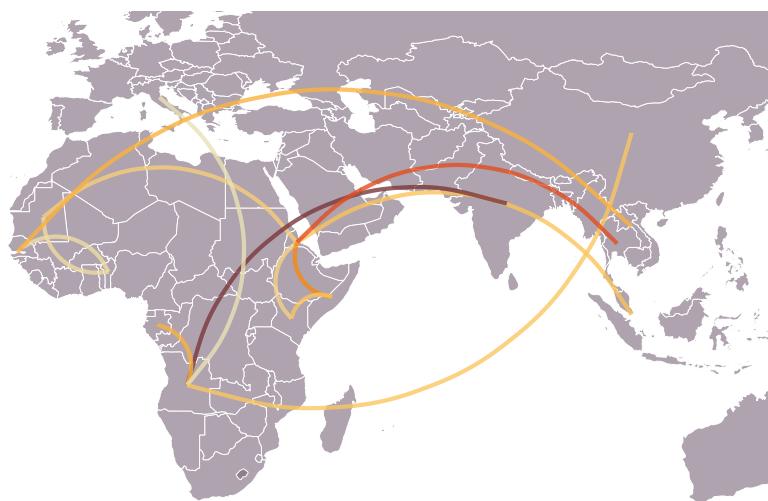


DENV1 Viral Movement Maps

Focused on Africa

Exchanges into, from and in Africa

Date of Viral Movement



Exchanges into Africa

Date of Viral Movement



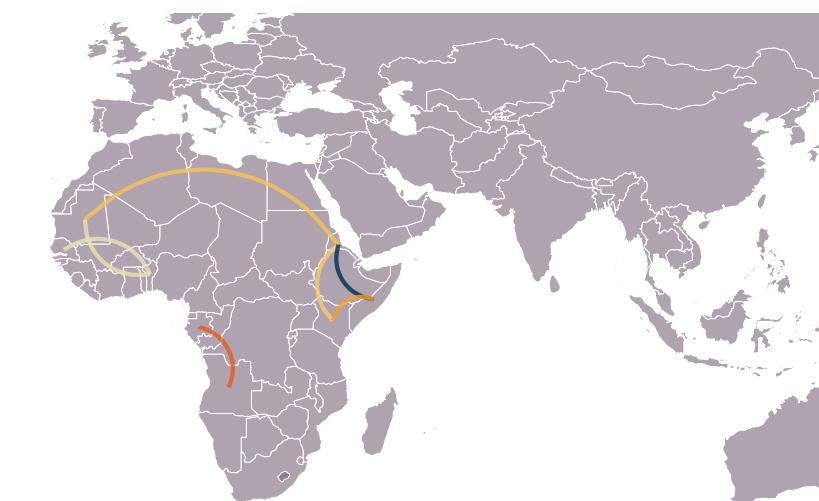
Exchanges from Africa

Date of Viral Movement



Exchanges in Africa

Date of Viral Movement

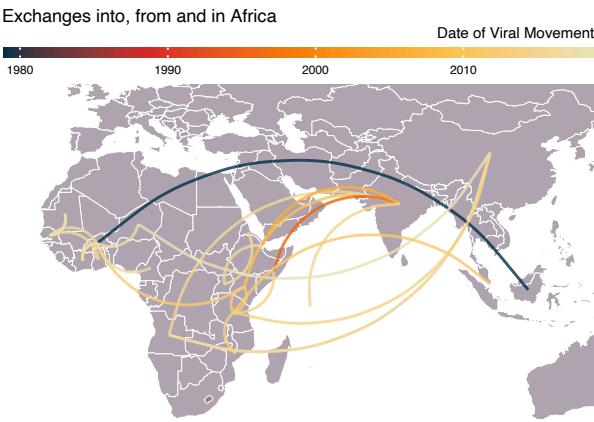


Dengue – All Serotypes transmission dynamics

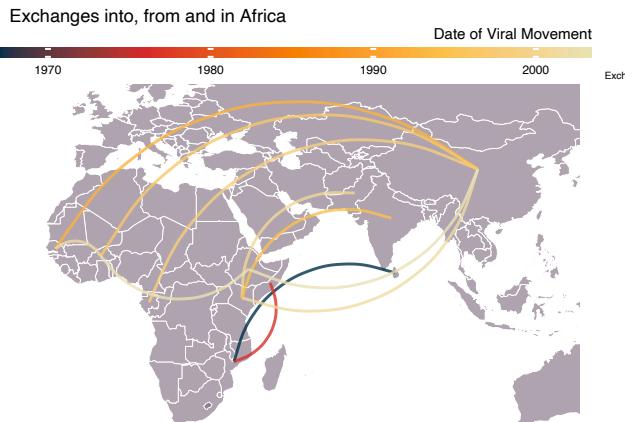
DENV1



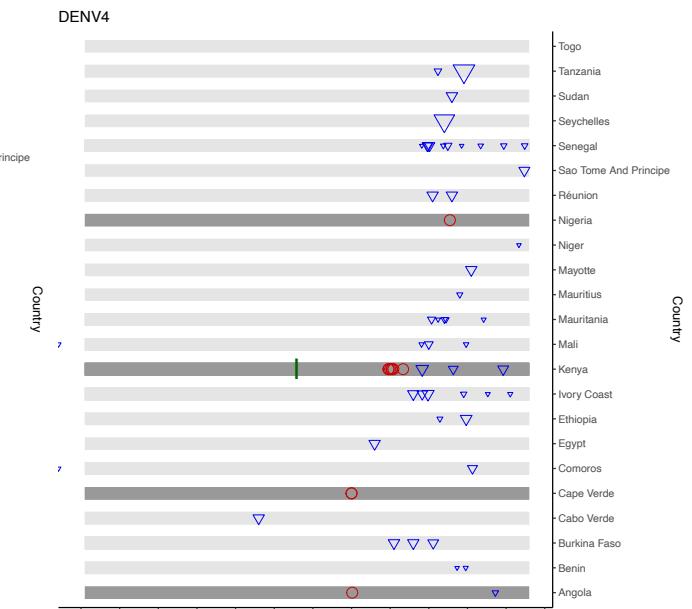
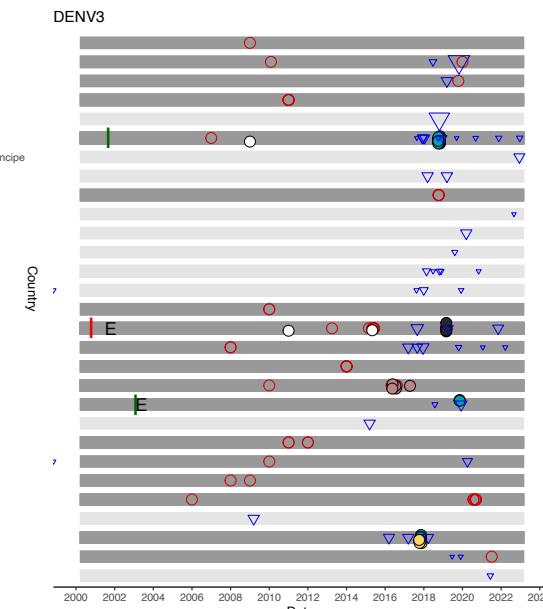
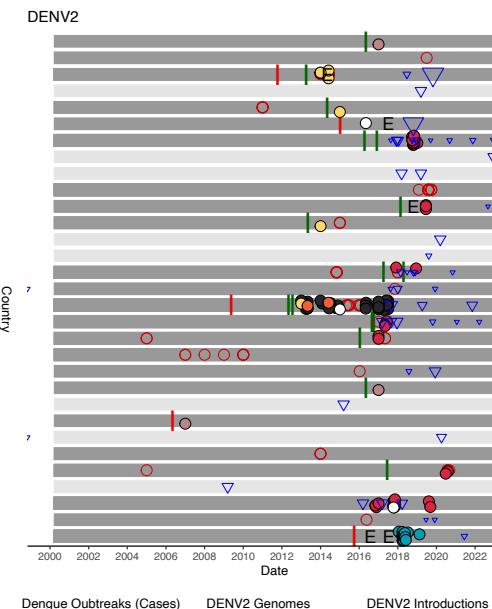
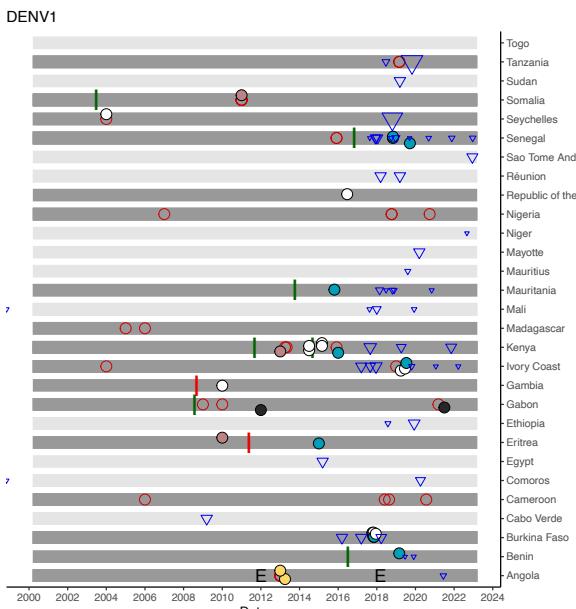
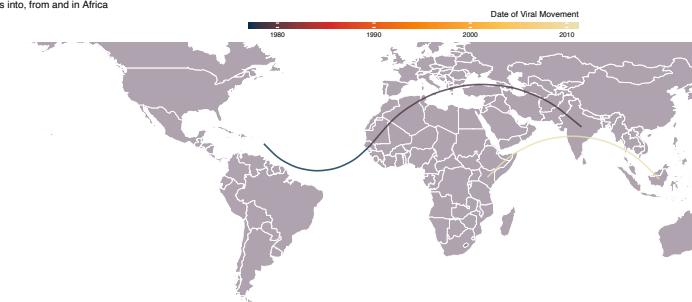
DENV2



DENV3



DENV4



Dengue Outbreaks (Cases)

- ▽ 100
- ▽ 1000
- ▽ 4000
- ▽ 6000

DENV1 Introductions Origin

- Africa
- Asia

E - Exports from Africa

○ Genomes <50% coverage

○ DENV1 unclustered

DENV1 Genomes

- DENV1_cluster1
- DENV1_cluster2
- DENV1_cluster3
- DENV1_cluster4
- DENV1_cluster6
- DENV1_cluster6_basal
- DENV1 unclustered

DENV2 Genomes

- DENV2_cluster10
- DENV2_cluster2
- DENV2_cluster4
- DENV2_cluster6
- DENV2_cluster6_basal
- DENV2 unclustered

DENV2 Introductions Origin

- Africa
- Asia

E - Exports from Africa

○ Genomes <50% coverage

Dengue Outbreaks (Cases)

- ▽ 100
- ▽ 1000
- ▽ 4000
- ▽ 6000

DENV3 Introductions Origin

- Africa
- Asia

E - Exports from Africa

○ Genomes <50% coverage

○ DENV3 unclustered

● DENV3_cluster1

● DENV3_cluster2

● DENV3_cluster3

● DENV3_cluster4

DENV3 Genomes

DENG4 Introductions Origin

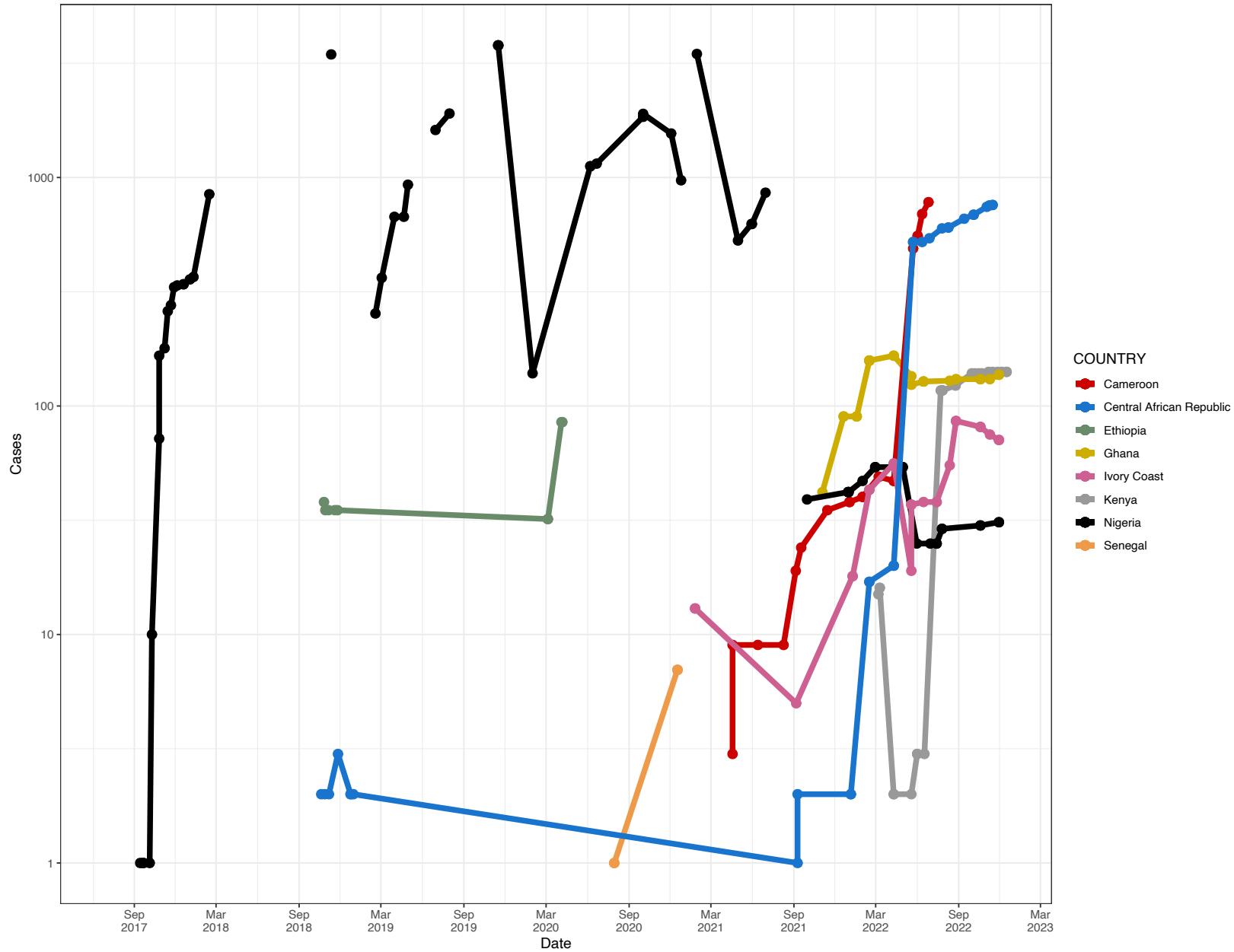
- Asia
- South America

E - Exports from Africa

○ Genomes <50% coverage

Yellow Fever Phylogenetics & Transmission Dynamics in Africa

Yellow Fever outbreaks in Africa



The landscape of genomic surveillance of Yellow Fever in Africa

Yellow Fever

Africa:

genomes = 185

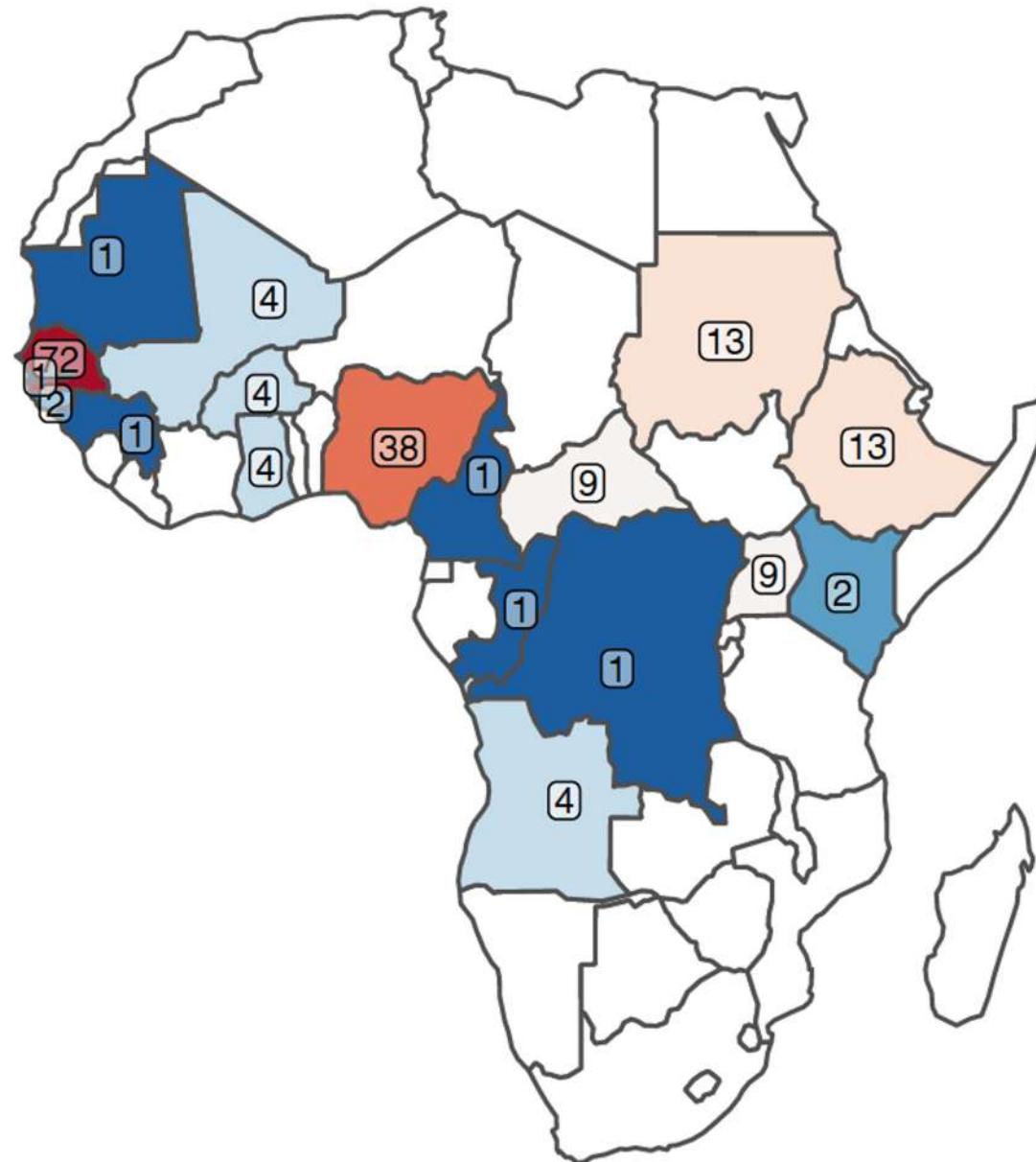
countries = 17

1927-2021

Quality:

Coverage >90% = 64

Genotyped = 177



The landscape of genomic surveillance of Yellow Fever in Africa

Yellow Fever

Africa:

genomes = 185

countries = 17

1927-2021

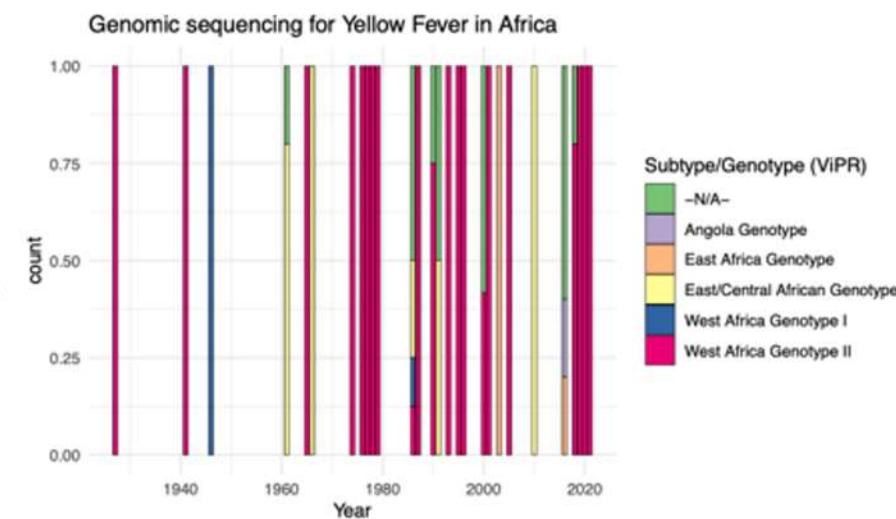
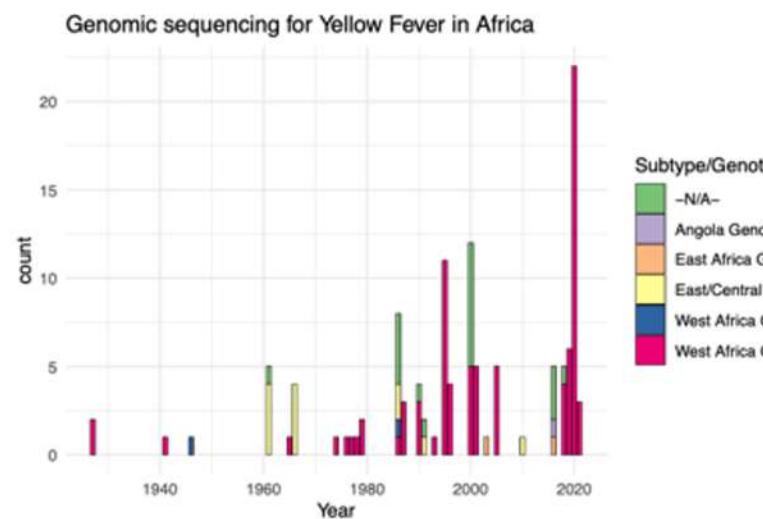
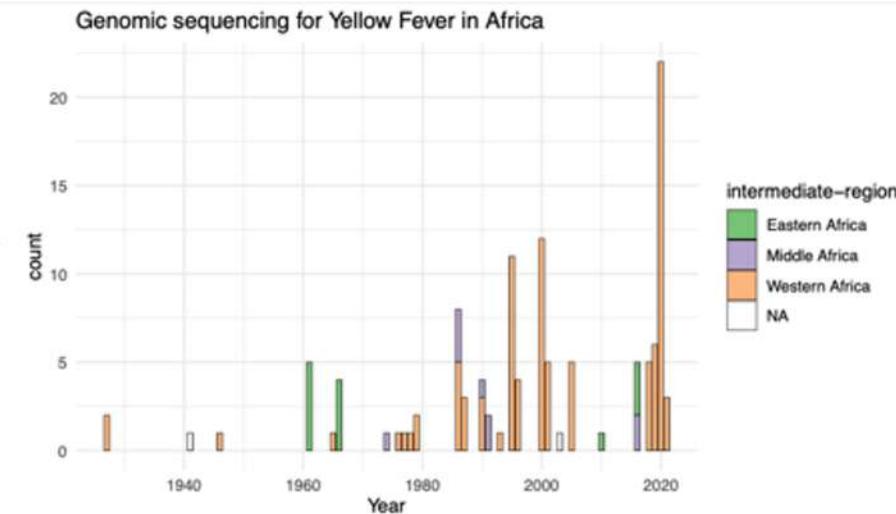
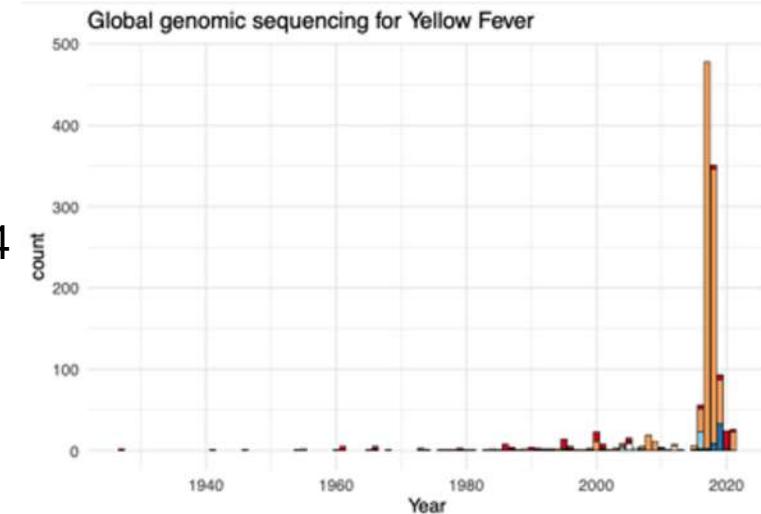
Quality:

Coverage >90% = 64

Genotyped = 177

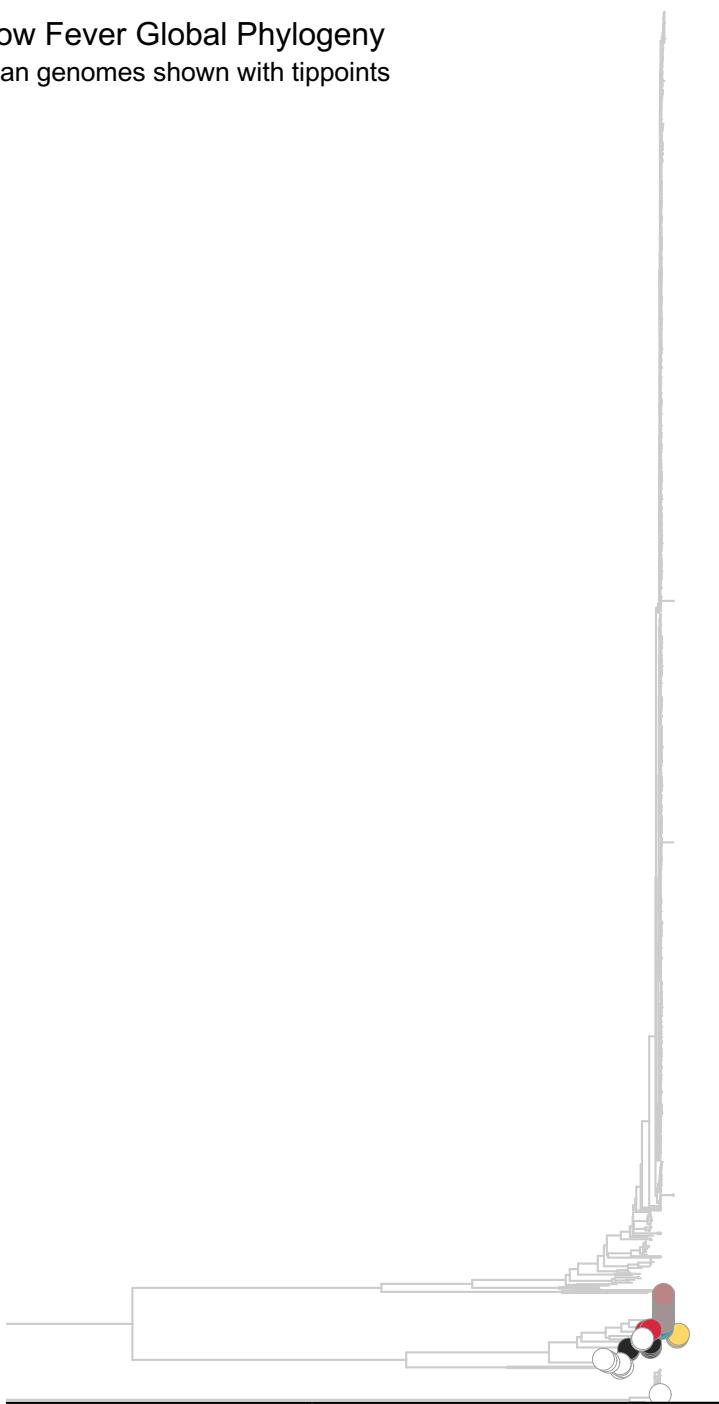
Global Genomic sequencing:

Genomes = 1823

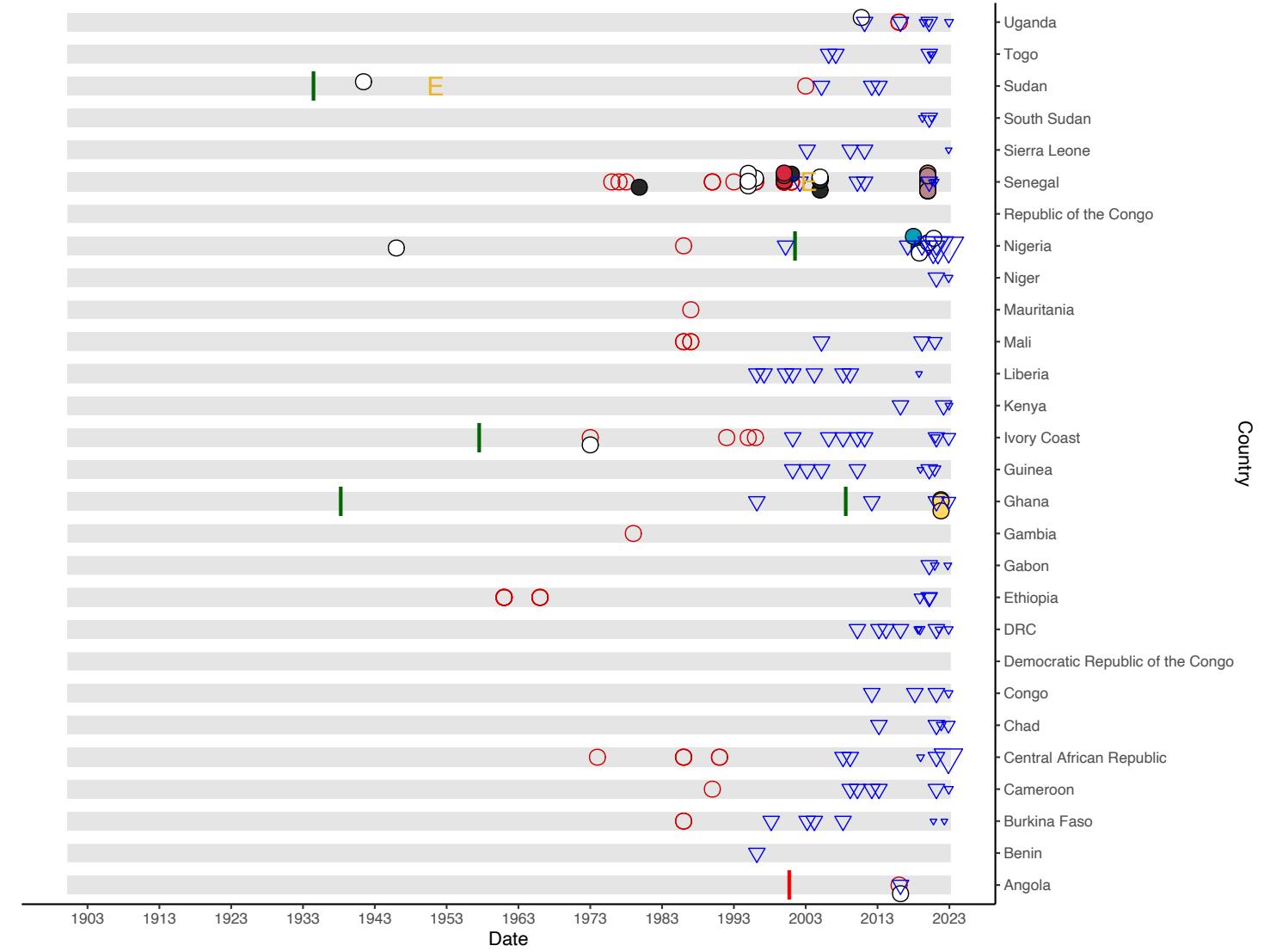


Yellow Fever Global Phylogeny

African genomes shown with tippoints



YFV Transmission Dynamics in Africa



YFV Introductions & Exports

- Africa
- Asia
- Europe
- South America

Yellow Fever Outbreaks (Cases)

- 50
- 250
- 500
- 750

YFV Genomes

- YFV_cluster1
- YFV_cluster2
- YFV_Cluster3
- YFV_cluster4
- YFV_cluster5
- YFV_unclustered

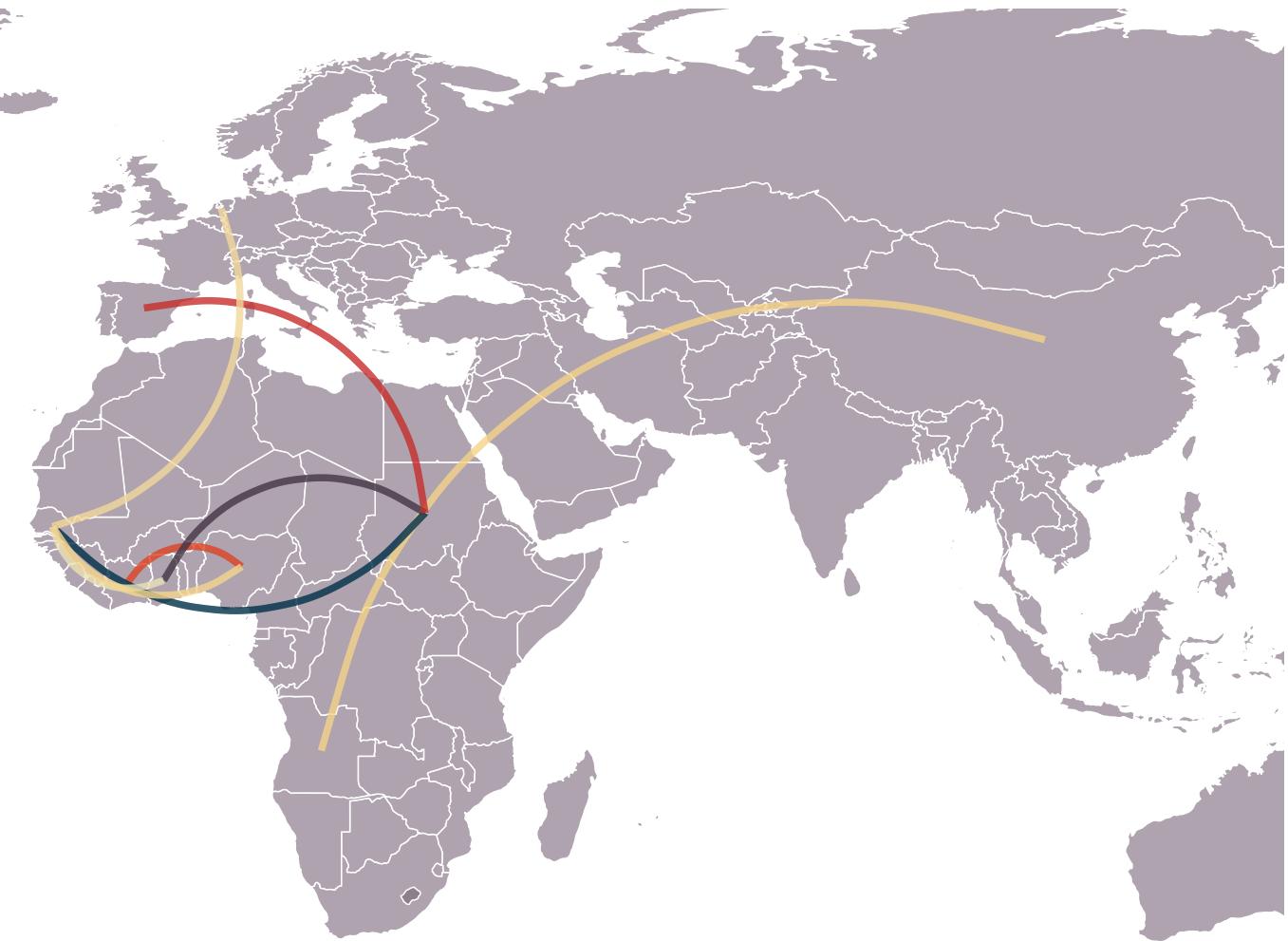
○ Genomes <50% coverage

Country

Exchanges into, from and in Africa

Date of Viral Movement

Yellow Fever Viral Movement Maps
Focused on Africa
>1900s



Next steps

- Complete phylogenetics for selected pathogens (Dengue, Chikungunya, Zika, RVF, Yellow Fever, West Nile, CCHF)
- Define levels of importations vs endemicity by mapping outbreak info with phylogenetics clusters
- Gather and map all seroprevalence studies against outbreak and genomic data to identify gaps
- BEAST Phylodynamics in select countries to understand if effective population size is increasing (indicates endemic circulation)
- Quantify risk of importations of Arboviruses from Asia and Americas using mobility data and disease susceptibility data
- Correlate outbreaks/phylodynamics with environmental info
- Gather and map all published estimates of disease susceptibility modelling and correlate with outbreaks
- **Expand genome database for Arboviruses in Africa!**

Acknowledgements

- Groups in Africa that have made their genomic data available publicly on Genbank
- WHO-AFRO Outbreak Data Curation
 - Dr. Monika Moir
 - Dr. James E. San
 - Yajna Ramphal
 - Akhil Maharaj

