

The landscape of prevalence and surveillance of climate sensitive vector-borne diseases in Africa

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CLIMADE-Africa

(Preliminary)

Sourcing Prevalence Information (Disease Occurrence/Outbreaks)

1. WHO Afro outbreak reports

Outbreaks and Emergencies Bulletin, Week 47: 14 - 20 November 2022

The WHO Health Emergencies Programme is currently monitoring 153 events in the region. This week's articles cover:

- Ebola Disease caused by Sudan virus in Uganda
- Cholera in Kenya

 [Week 47: 14 - 20 November 2022](#)



 [Week 46: 7 - 13 November 2022](#)

 [Week 45: 31 October - 6 November 2022](#)

 [Week 44: 24 to 30 October 2022](#)

 [Week 43: 17 - 23 October 2022](#)

 [Week 42: 10 - 16 October 2022](#)

 [Week 41: 3 to 9 October 2022](#)

 [Week 40: 26 September to 2 October 2022](#)

Sourcing Prevalence Information (Disease Occurrence/Outbreaks)

1. WHO Afro outbreak reports

WHO Afro outbreak report data

File Edit View Insert Format Data Tools Extensions Help

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NAME

NAME	WEEK	DATE	EVENT_TYPE	ISO3	COUNTRY	EVENT_NAME	GRADE	DATE_NOTIF	DATE_START	DATE_END	CASES_TOTA	CASES_CONF	DEATHS	CFR	LOCATION
OEW10-041017		4 - 10 Mar 2017	Ongoing	DRC	Cholera		2	2015-01-01			35181	1020	2,9		Detailed update
OEW10-041017		4 - 10 Mar 2017	Ongoing	Tanzania	Cholera		2	2015-04-04			25,041	388	1,5		40% decrease in
OEW10-041017		4 - 10 Mar 2017	Ongoing	S��o Tom�� and Princ��p��	Necrotising cellulitis/ fasciitis		2	2017-01-10			1421	9	0,6		Detailed update
OEW10-041017		4 - 10 Mar 2017	Ongoing	Chad	Hepatitis E		1	2016-09-01			1182 (5)	13	1,1		Detailed update
OEW10-041017		4 - 10 Mar 2017	Ongoing	Angola	Cholera		1	2017-01-04			271	11	4,1		AFRO & HQ r
OEW10-041017		4 - 10 Mar 2017	Ongoing	Burundi	Cholera	-		2016-07-28			167 (5)	0	0		No reported cas under control, he
OEW10-041017		4 - 10 Mar 2017	Ongoing	Burkina Faso	Dengue fever	-		2016-10-29			2530	20	0,8		No update receiv
OEW10-041017		4 - 10 Mar 2017	Ongoing	Zimbabwe	Typhoid fever	-		2016-11-21			2200 (88)	8	0,4		Cases continue
OEW10-041017		4 - 10 Mar 2017	Ongoing	Nigeria	Lassa fever	-		2016-12-18			178 (73)	53 (37)	29,8 (50,7)		Outbreak in 13
OEW10-041017		4 - 10 Mar 2017	Ongoing	Cabo Verde	Dengue fever	-		2017-01-04			98 (19)	0	0		Investigations by
OEW10-041017		4 - 10 Mar 2017	Ongoing	Angola	Zika virus	-		2017-01-06			3	0	0		No new cases re
OEW10-041017		4 - 10 Mar 2017	Ongoing	Mali	Rift Valley fever	-		2017-02-01			3 (3)	1			No further case awaiting laborat
OEW10-041017		4 - 10 Mar 2017	Ongoing	Congo	Monkeypox	-		2017-02-01			19	7	36,8		Detailed update
OEW10-041017		4 - 10 Mar 2017	Ongoing	Togo	Meningitis	-		2017-02-03			293 (28)	20	6,8		The vaccination coverage
OEW10-041017		4 - 10 Mar 2017	Ongoing	CAR	Monkeypox	-		2017-02-09			5	0	0		No new cases th
OEW10-041017		4 - 10 Mar 2017	Ongoing	Guinea	Measles	-		2017-02-15			2142	6	0,3		Detailed update
OEW10-041017		4 - 10 Mar 2017	Ongoing	Cameroon	Eruptive fever	-		2017-02-20			43	16	37,2		Investigations co
OEW10-041017		4 - 10 Mar 2017	Ongoing	Nigeria	Meningitis	-		2017-02-20			563 (38)	79	14		13 LGAs affecte
OEW10-041017		4 - 10 Mar 2017	Ongoing	Benin	Lassa fever	-		2017-02-21			2 (1)	1			Detailed update
OEW10-041017		4 - 10 Mar 2017	Ongoing	Namibia	Crimean-Congo Haemorrhagic Fever	-		2017-02-23			4 (2)	1	25		Additional positiv
OEW10-041017		4 - 10 Mar 2017	Ongoing	Togo	Lassa fever	-		2017-02-24			5 (2)	0			Detailed update
OEW11-17317		11 - 17 Mar 2017	Ongoing	DRC	Cholera		2	2015-01-01			35923	1045	2,9		742 cases and
OEW11-17317		11 - 17 Mar 2017	Ongoing	Tanzania	Cholera		2	2015-04-04			29415	456	1,6		31% increase in
OEW11-17317		11 - 17 Mar 2017	Ongoing	Sao Tome & Principe	Necrotising cellulitis/ fasciitis		2	2017-01-10			1455	9	0,6		Decrease from
OEW11-17317		11 - 17 Mar 2017	Ongoing	Angola	Cholera	1	2017-01-04			271	11	4,1		No update receiv	
OEW11-17317		11 - 17 Mar 2017	Ongoing	Chad	Hepatitis E	1	2016-09-01			1242	15	1,2		60 cases since la	
OEW11-17317		11 - 17 Mar 2017	Ongoing	Burkina Faso	Dengue fever	-		2016-10-29			2530	20	0,8		No update receiv
OEW11-17317		11 - 17 Mar 2017	Ongoing	Zimbabwe	Typhoid fever	-		2016-11-21			2457 (93)	9	0,4		No update receiv
OEW11-17317		11 - 17 Mar 2017	Ongoing	Nigeria	Lassa fever	-		2016-12-18			267 (91)	56 (40)	20 (44)		Outbreaks in 13
OEW11-17317		11 - 17 Mar 2017	Ongoing	Cabo Verde	Dengue fever	-		2017-01-04			98 (19)	0			No update receiv
OEW11-17317		11 - 17 Mar 2017	Ongoing	Angola	Zika virus	-		2017-01-06			3	0	0,0		No new cases re
OEW11-17317		11 - 17 Mar 2017	Ongoing	Mali	Rift Valley fever	-		2017-02-01			3 (3)	1	33,0		No further case

Sourcing Prevalence Information (Genomics + Seroprevalence)

2. Published Scientific Literature (Screening publications from broad pubmed search)

2023-01-31: African Arboviral genomics Blind ON

Showing 1 to 8 of 2,609 unique entries

Date	Title	Authors
2016-07-01	monikam A Literature Review of Zika Virus.	Plourde AR; Bloch EM
2016-07-01	Zika Virus.	Musso D; Gubler DJ
2010-03-01 35%	West Nile virus.	Rossi SL; Ross TM; Evans JD
2017-04-01	Chikungunya virus: an update on the biology and pathogenesis of this emerging pathogen. Burt FJ; Chen W; Miner JJ; L...	Burt FJ; Chen W; Miner JJ; L...
2018-10-01	Yellow Fever Virus: Diagnostics for a Persistent Arboviral Threat.	Waggoner JJ; Rojas A; Pinsk...
2021-12-02	Chikungunya virus infection: molecular biology, clinical characteristics, and epidemiology ... Khongwichit S; Chansaenroj...	Khongwichit S; Chansaenroj...

Include **Maybe** **Exclude** Reason Label Add Note Highlights ON Upload PDF full-texts

Crimean-Congo hemorrhagic fever: history, epidemiology, pathogenesis, clinical syndrome and genetic diversity.

Crimean-Congo hemorrhagic fever (CCHF) is the most important tick-borne viral disease of humans, causing sporadic cases or outbreaks of severe illness across a huge geographic area, from western China to the Middle East and southeastern Europe and throughout most of Africa. CCHFV is maintained in vertical and horizontal transmission cycles involving ixodid ticks and a variety of wild and domestic vertebrates, which do not show signs of illness. The virus circulates in a number of tick genera, but Hyalomma ticks are the principal source of human infection, probably because both immature and adult forms actively seek hosts for the blood meals required at each stage of maturation. CCHF occurs most frequently among agricultural workers following the bite of an infected tick, and to a lesser extent among slaughterhouse workers exposed to the blood and tissues of infected livestock and medical personnel through contact with the body fluids of infected patients. CCHFV is the most genetically diverse of the arboviruses, with nucleotide sequence differences among isolates ranging from 20% for the viral S segment to 31% for the M

3. Individual engagement with public health offices and scientists

To obtain information not published in scientific literature and potentially not captured in WHO reports

Initial results for 634 papers of systematic review

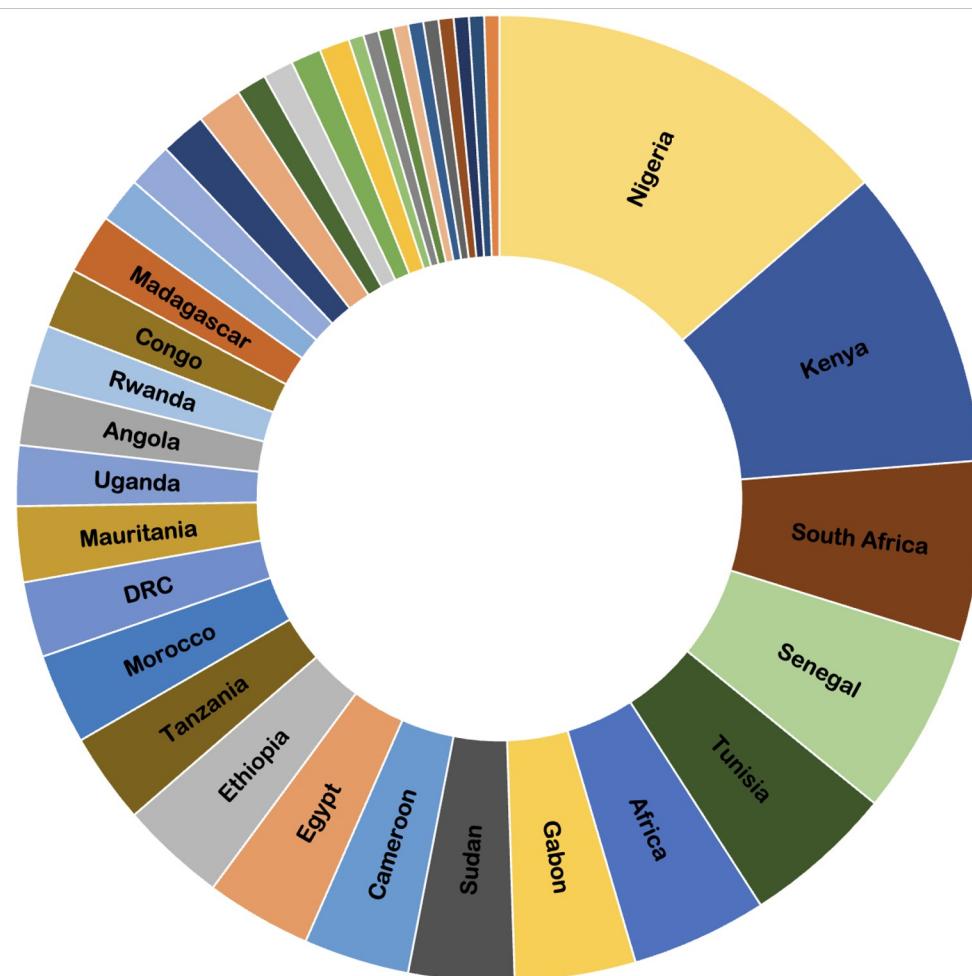


Fig. African countries ranked in order of greatest proportion of arboviral surveillance and outbreak response studies

Initial results for 634 papers included in systematic review

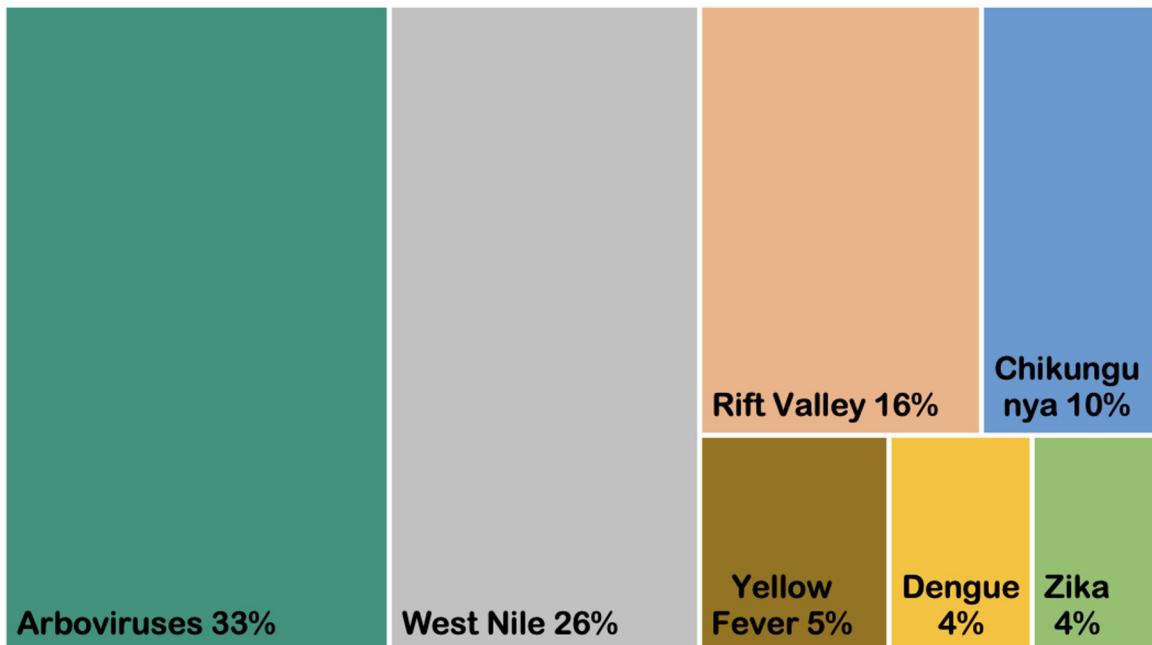


Fig. Tree map displaying the percentage of the six main arboviruses of concern investigated in the screened studies. Studies that encompasses multiple viruses were grouped as 'Arboviruses'.

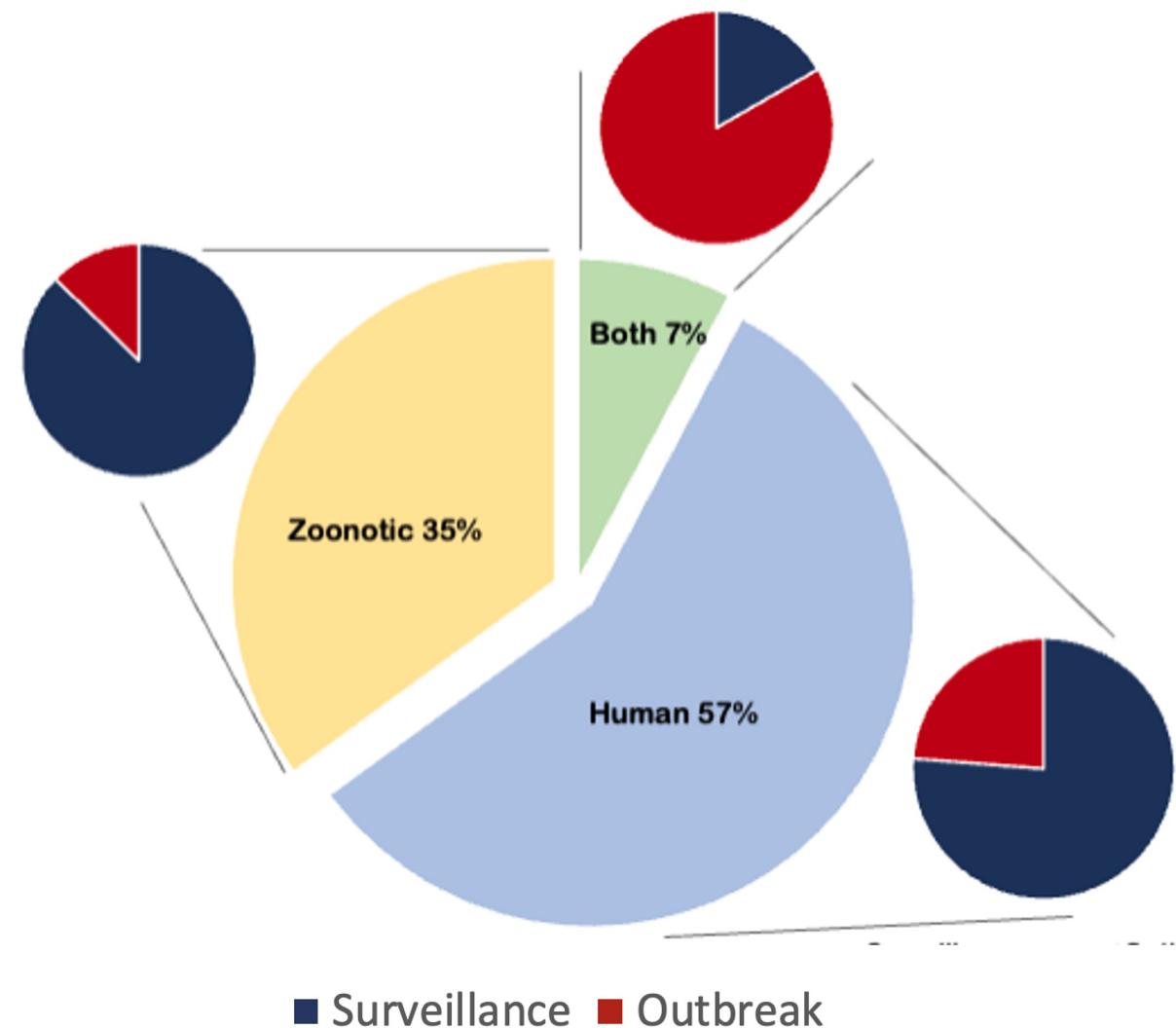
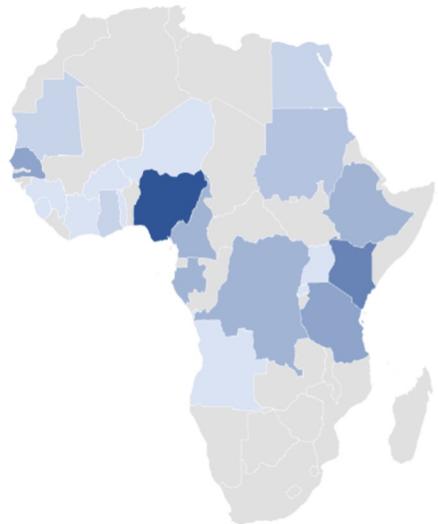


Fig. The considered studies were categorised based on whether subjects were humans, animals or both; and whether the study was in response to an outbreak or routine/surveillance effort.

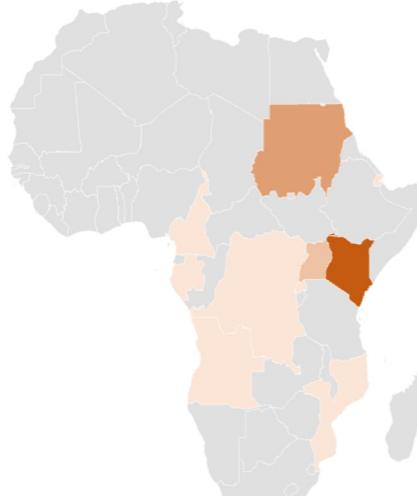
Percent of studies per African country

Arboviruses



Arboviruses
15
2

Chikungunya



Chikungunya
24
5

Dengue



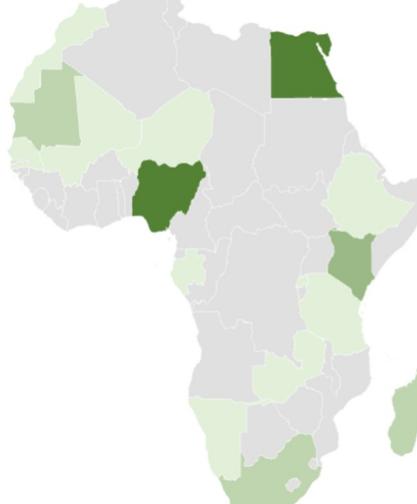
Dengue
25
12,5

Yellow Fever



Yellow Fever
42
8

Rift Valley



Rift Valley
16
3

Zika



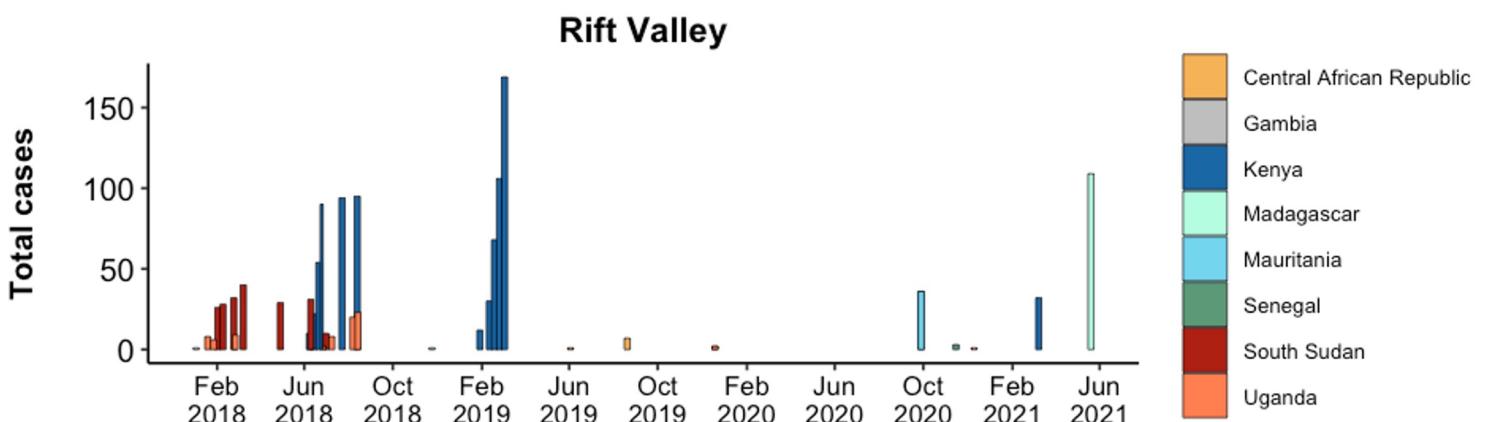
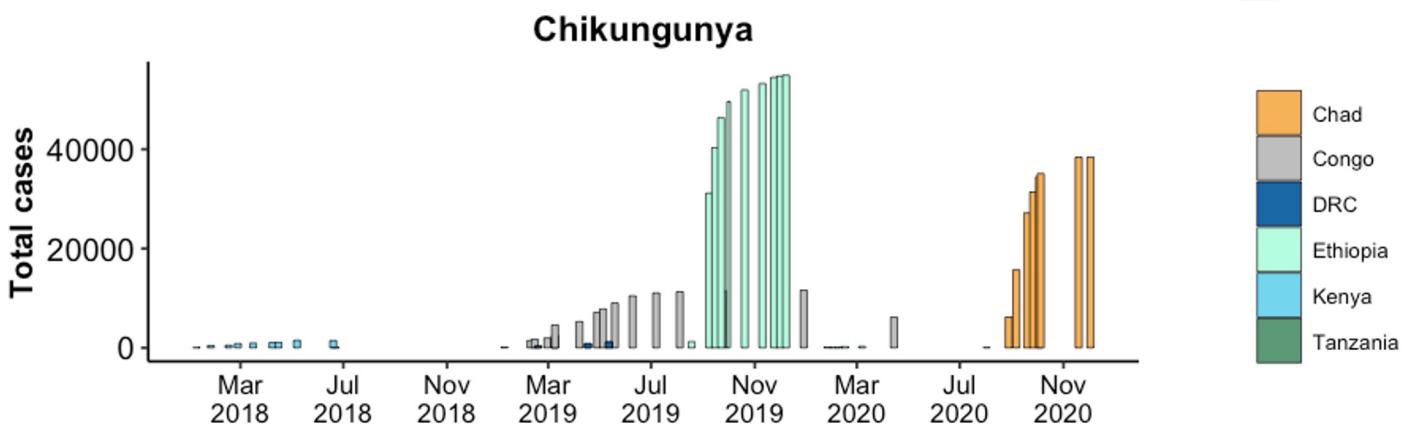
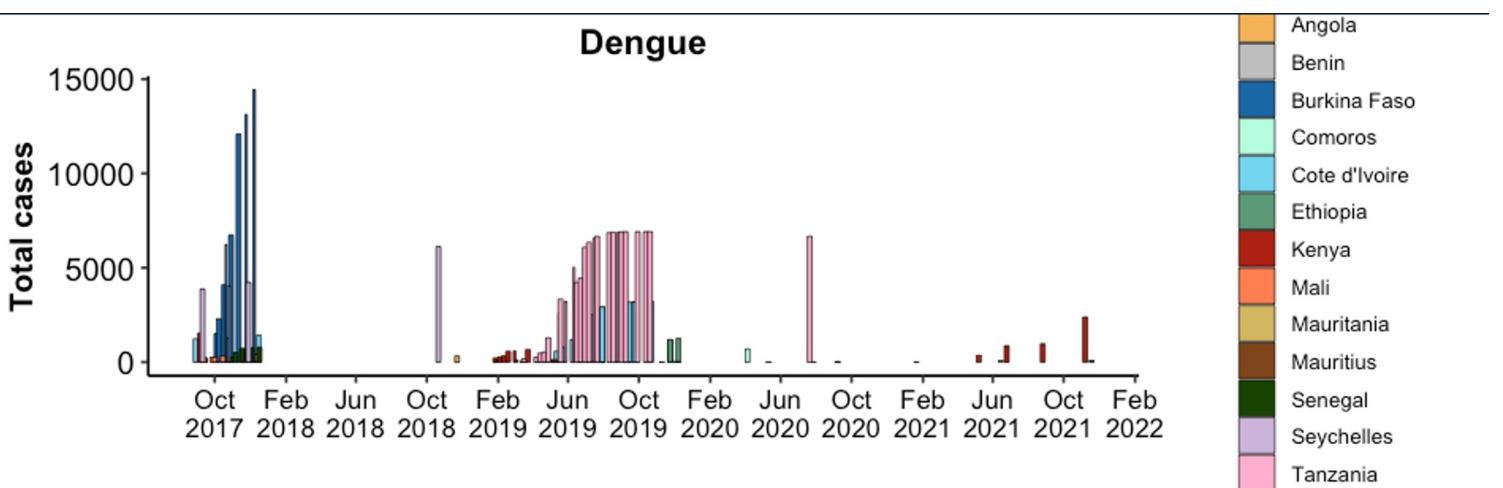
Zika
29
14

West Nile

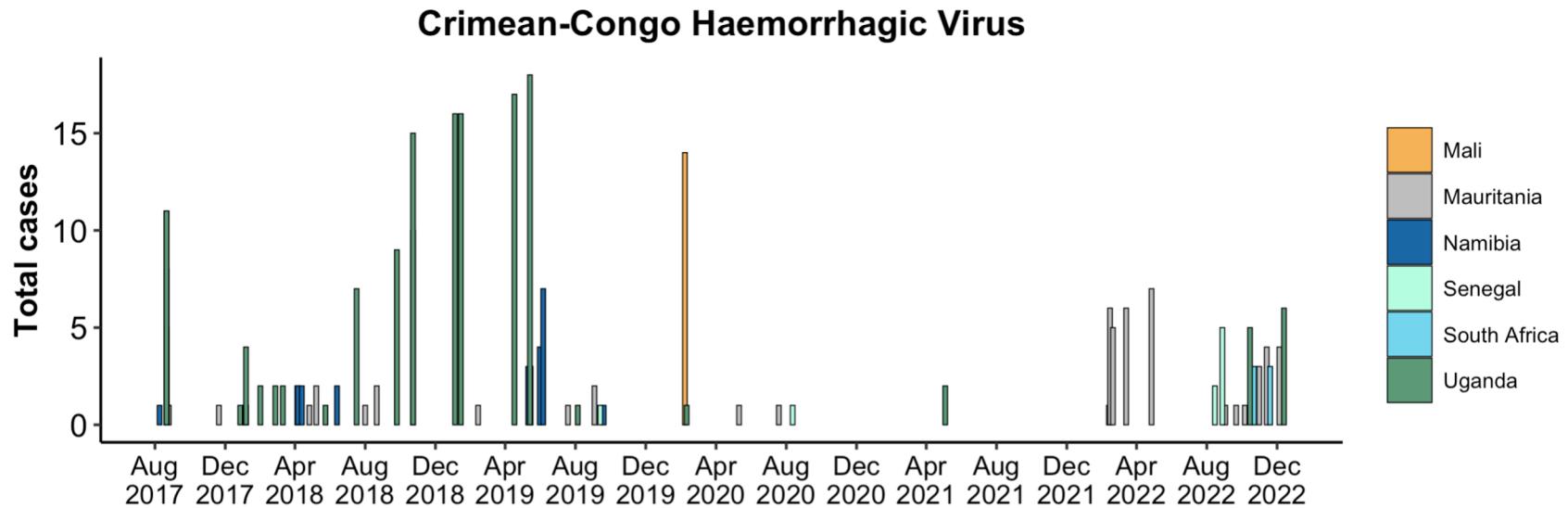


West Nile
19
2

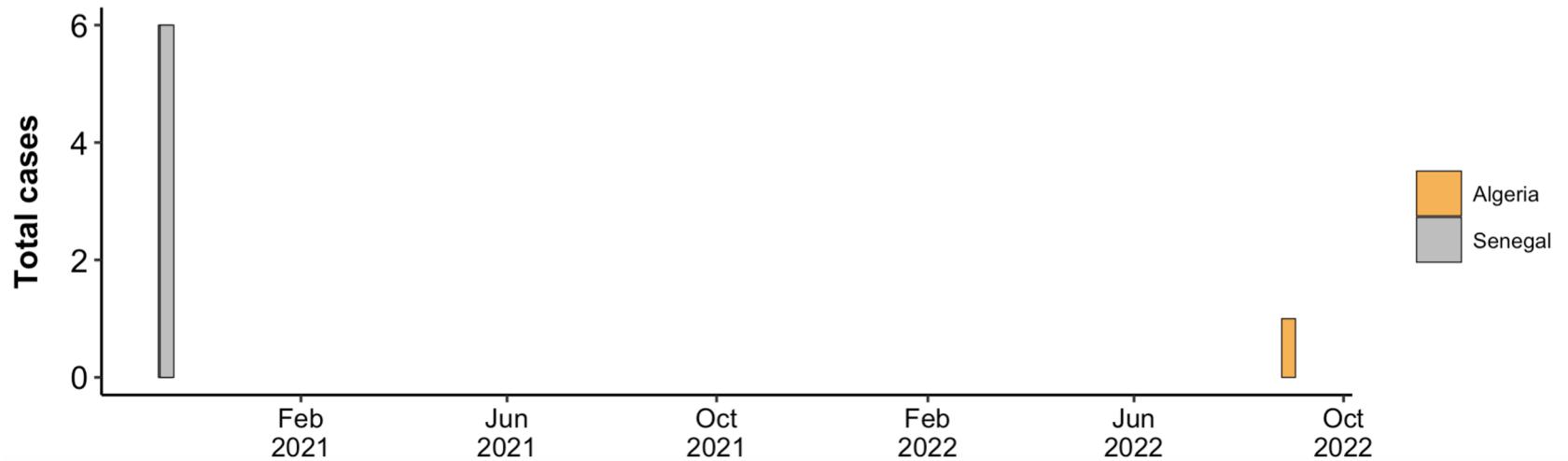
Total cases from WHO Afro outbreak reports



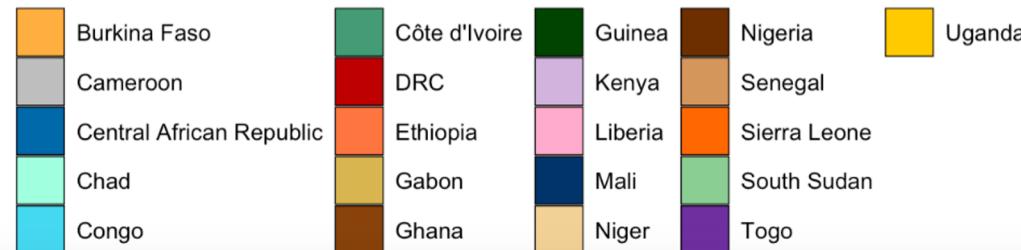
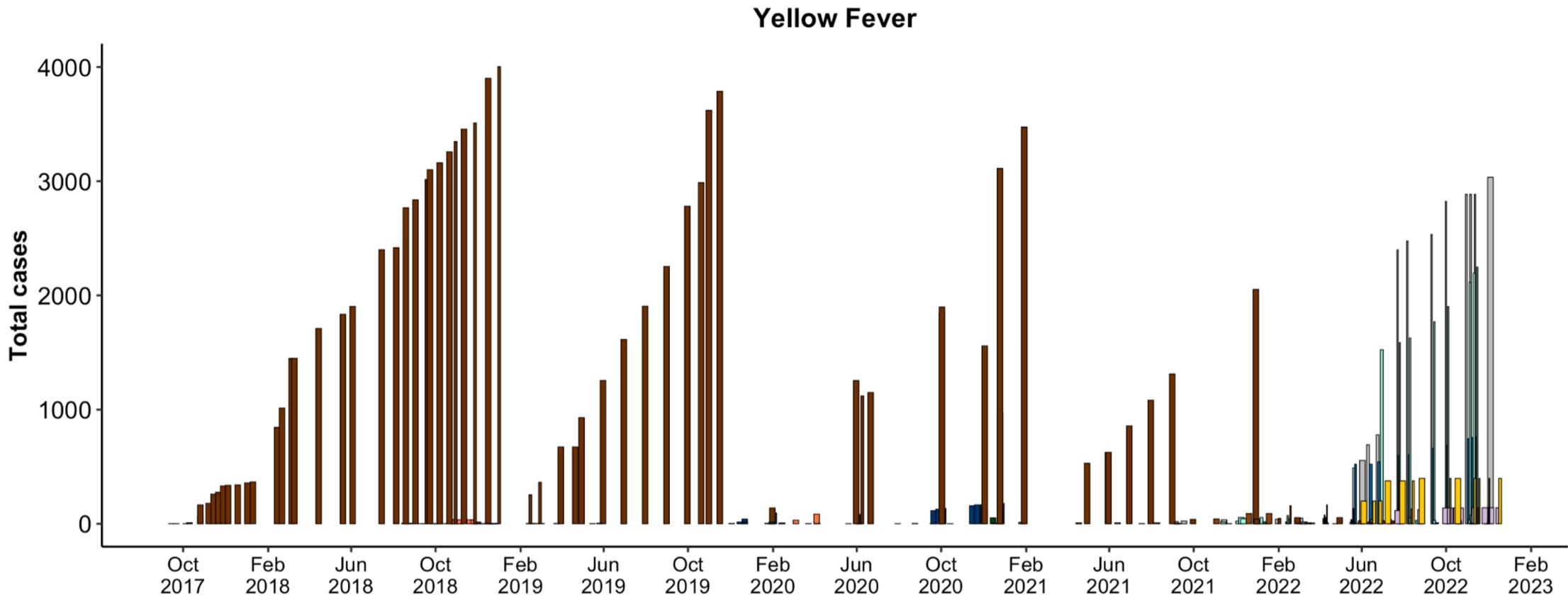
**Total cases from WHO
Afro outbreak reports**



West Nile

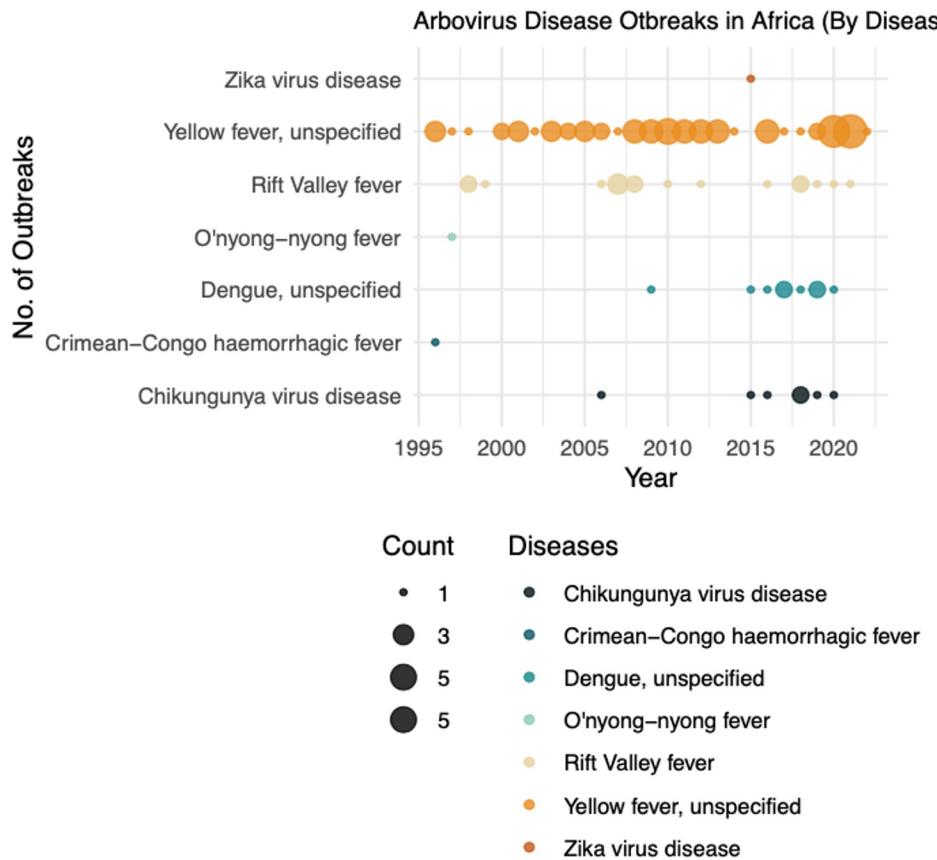


Total cases from WHO Afro outbreak reports

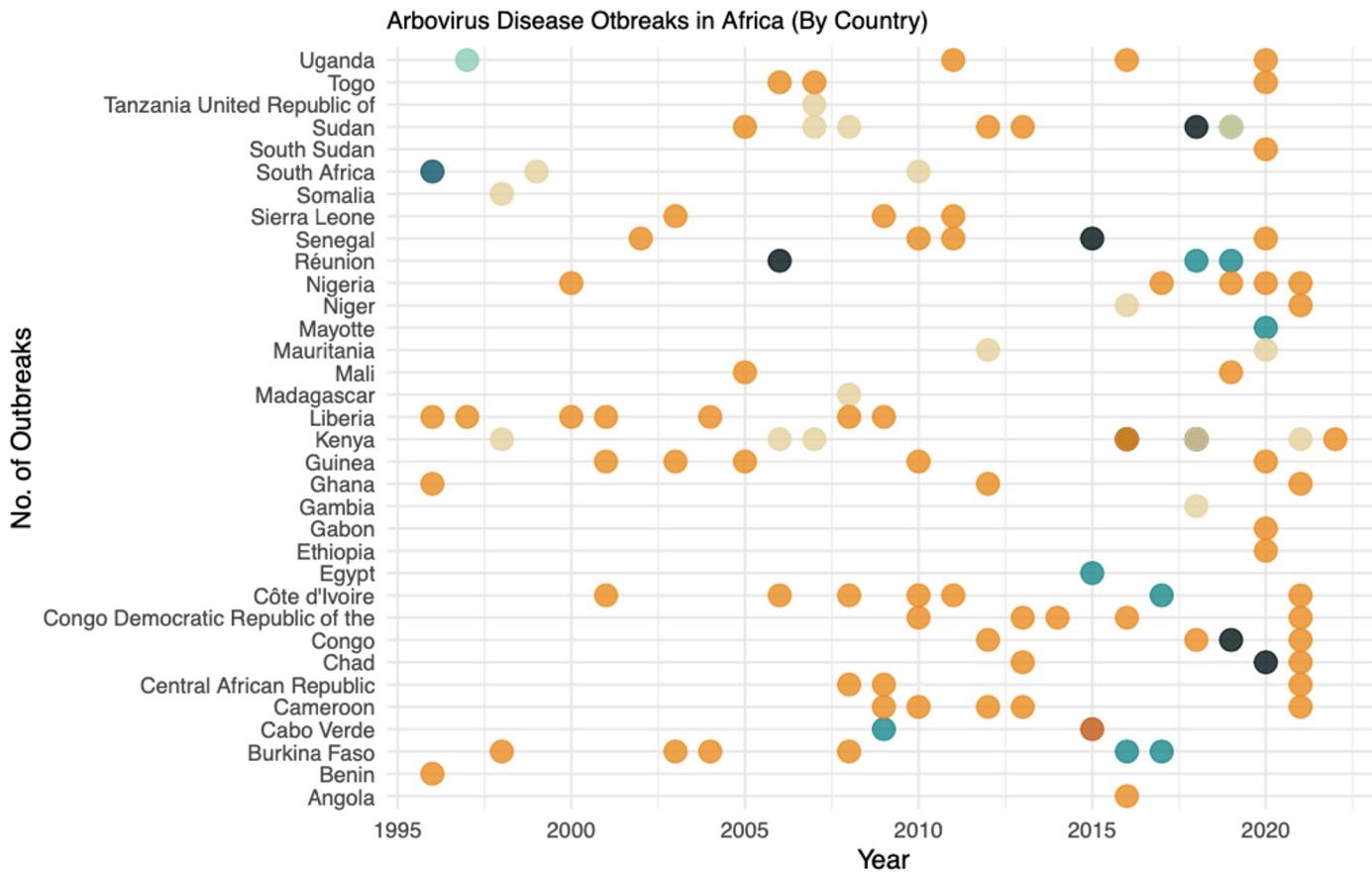


Outbreak notifications

A

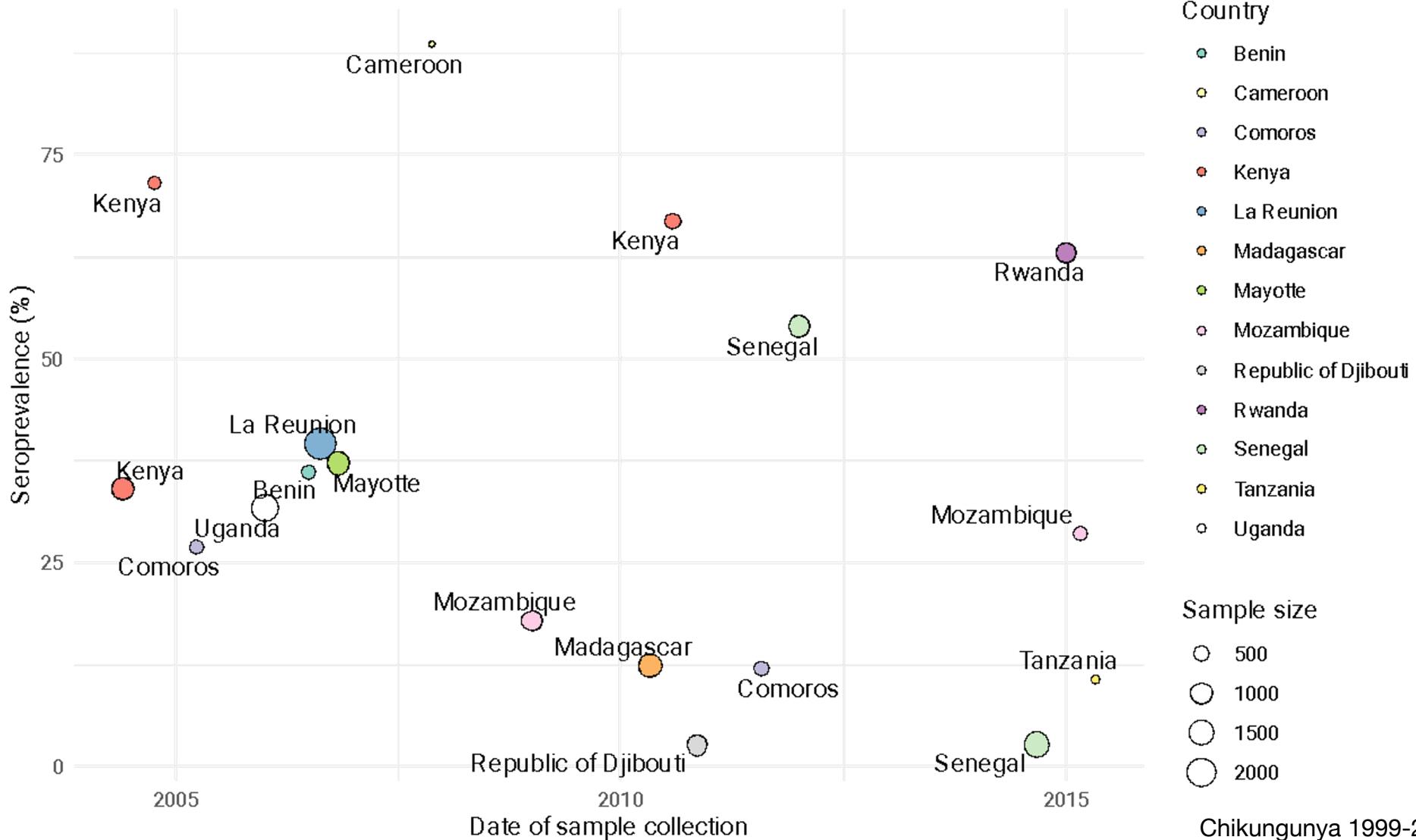


B



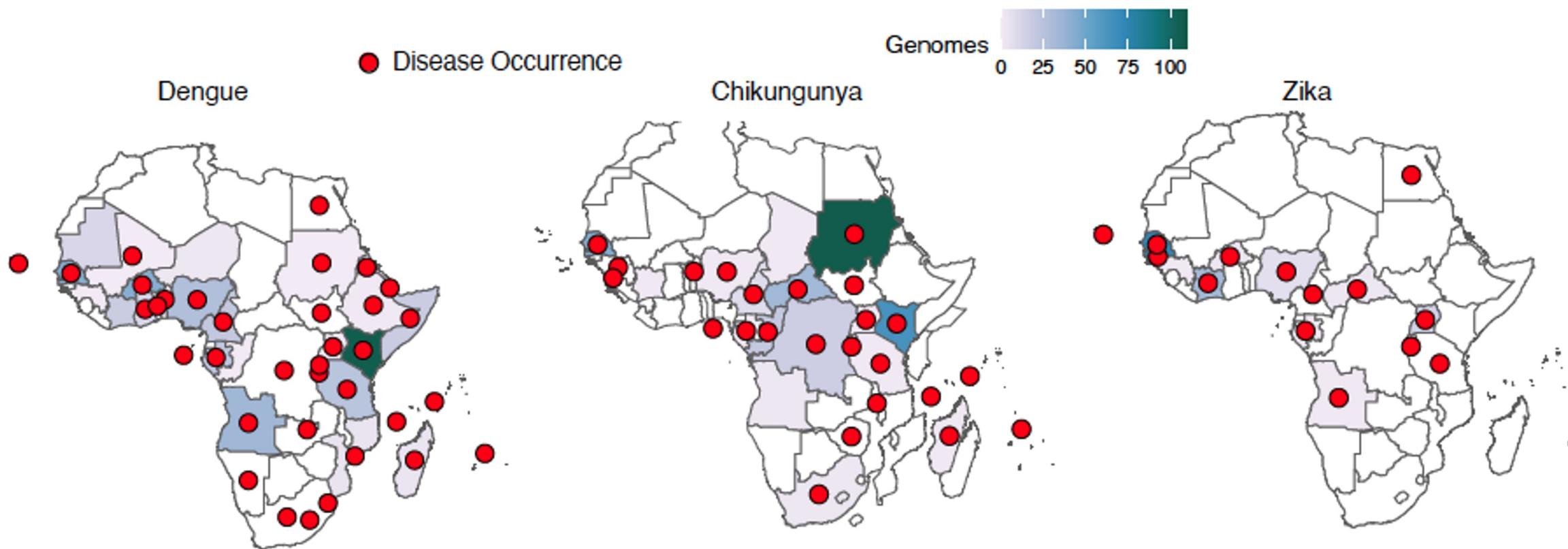
Seroprevalence surveys (e.g. Chikungunya)

Chikungunya Seroprevalence in Africa



The landscape of genomic surveillance of arboviruses in Africa

Genomic vs Disease Surveillance



The landscape of genomic surveillance of arboviruses in Africa

Typing arbovirus genomes



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NO JOBS IN QUEUE

Genome Detective

GENOME DETECTIVE VIRUS TOOL

Version 2.48

AVAILABLE TOOLS

Subtyping tools, identifying subspecies using phylogenetic analysis, are currently available for 19 viruses.

You can submit sequences/contigs in FASTA format or short reads NGS data in FASTQ format. The public service only allows one NGS analysis at a time due to computational demand. For batch analyses of NGS data, please contact us.

- Chikungunya Typing Tool
- Coronavirus Typing Tool
- Dengue Typing Tool
- Enterovirus typing tool
- HCV Recombinant Typing Tool
- HHV82 Virus Typing Tool
- HTLV-1 and 2 Typing Tool
- Hepatitis A Virus Genotyping Tool
- Hepatitis B Virus
- Hepatitis E Virus Genotyping Tool
- Human Immunodeficiency Virus Typing Tool
- Measles Virus Typing Tool
- MonkeyPox Virus
- Norovirus Typing tool
- Panviral Tool
- [Rift Valley Fever Virus](#)
- West Nile Virus
- Yellow Fever Virus Typing Tool
- [Zika Virus Typing Tool](#)

Tool will be extended for Crimean-Congo Hemorrhagic Fever

Genomic surveillance of Rift Valley fever virus: from sequencing to lineage assignment

John Juma, Vagner Fonseca, Samson L. Konongoi, Peter van Heusden, Kristina Roesel, Rosemary Sang, Bernard Bett, Alan Christoffels, Tullio de Oliveira & Samuel O. Oyola [✉](#)

BMC Genomics 23, Article number: 520 (2022) | [Cite this article](#)

1422 Accesses | 3 Citations | 31 Altmetric | [Metrics](#)

10.1186/s12864-022-08764-6

RESEARCH ARTICLE

A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes

Vagner Fonseca^{1,2,3*}, Pieter J. K. Libin^{4,5*}, Kristof Theys^{5*}, Nuno R. Faria⁶, Marcio R. T. Nunes⁷, Maria I. Restovic⁸, Murilo Freire⁸, Marta Giovanetti¹, Lize Cuyvers⁵, Ann Nowe⁴, Ana Abecasis⁹, Koen Deforche¹⁰, Gilberto A. Santiago¹¹, Isadora C. de Siqueira⁸, Emmanuel J. San², Kaliane C. B. Machado⁸, Vasco Azevedo², Ana Maria Bispo-de Filippis¹, Rivaldo Venâncio da Cunha¹², Oliver G. Pybus⁶, Anne-Mieke Vandamme^{5,9}, Luiz C. J. Alcantara^{1,3*}, Tullio de Oliveira^{2*}

[10.1371/journal.pntd.0007231](https://doi.org/10.1371/journal.pntd.0007231)

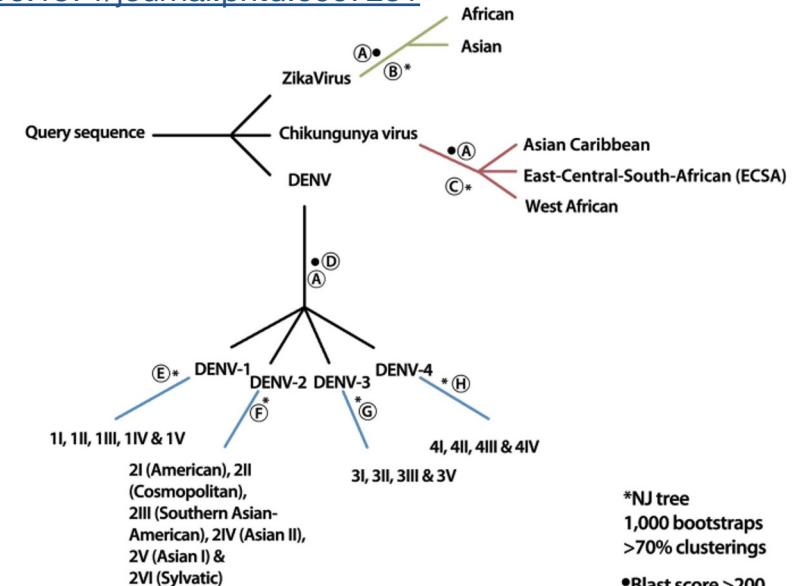


Fig 2. Outline of the classification procedure. Firstly (A), the viral species is determined using BLAST. When the submitted sequence is a *Zika virus*, a Neighbor joining tree is constructed to determine the *Zika* genotype (B). When the submitted sequence is a *Chikungunya virus*, a Neighbor joining tree is constructed to determine the *Chikungunya* genotype (C). When the submitted sequence is a *Dengue virus*, the serotype is determined using another BLAST invocation (D). Based on the inferred serotype, a serotype specific Neighbor joining tree is constructed to determine the *Dengue* genotype (E, F, G, H).

The landscape of genomic surveillance of arboviruses in Africa

Dengue

Africa:

genomes = 457

countries = 30

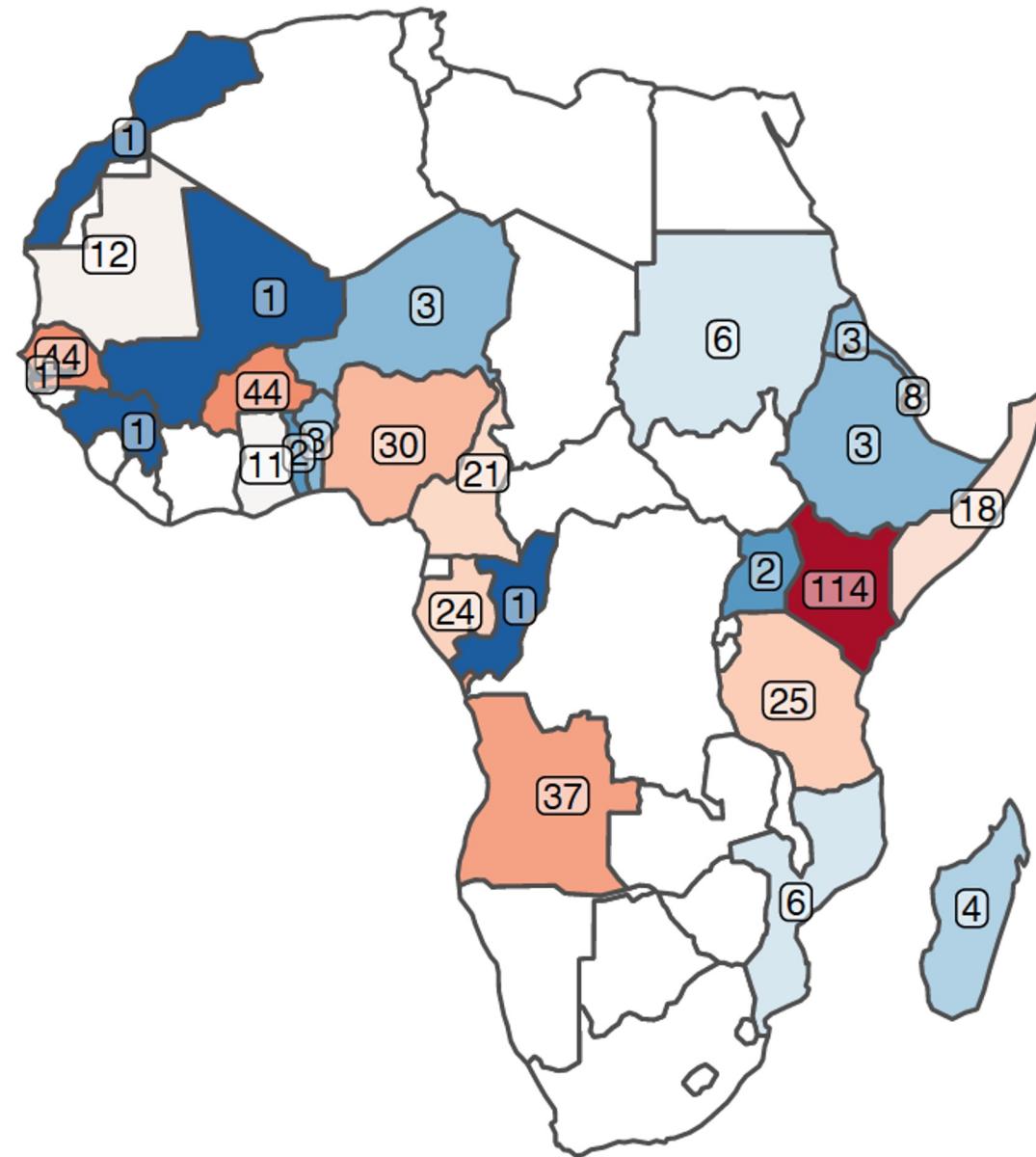
1953-2021

Quality:

Coverage >90% =

215

Genotyped = 208



The landscape of genomic surveillance of arboviruses in Africa

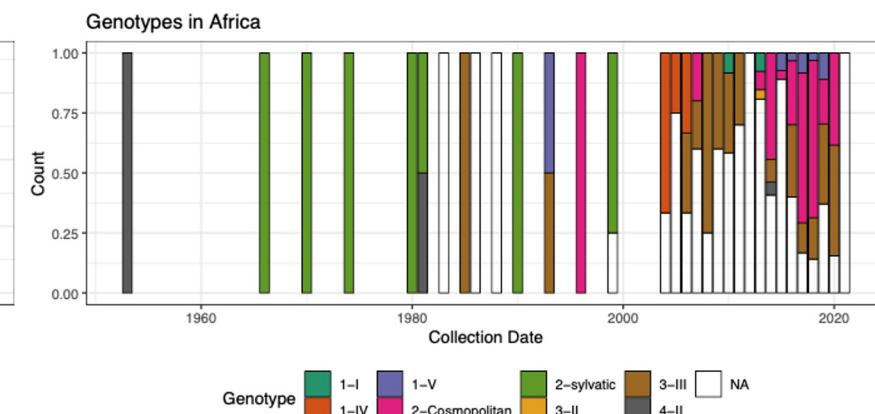
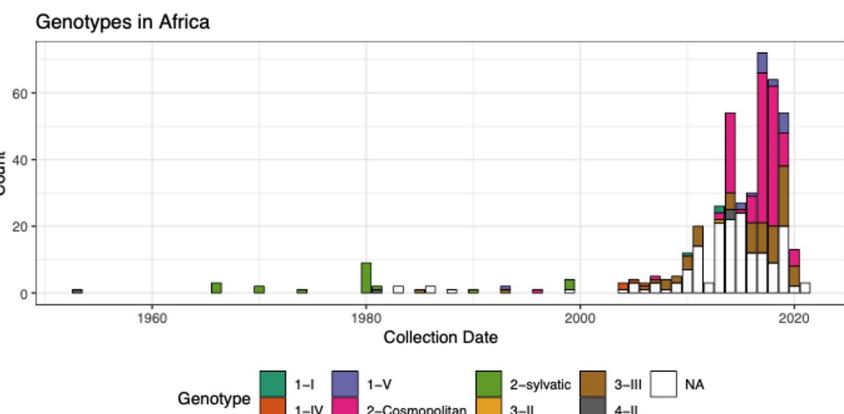
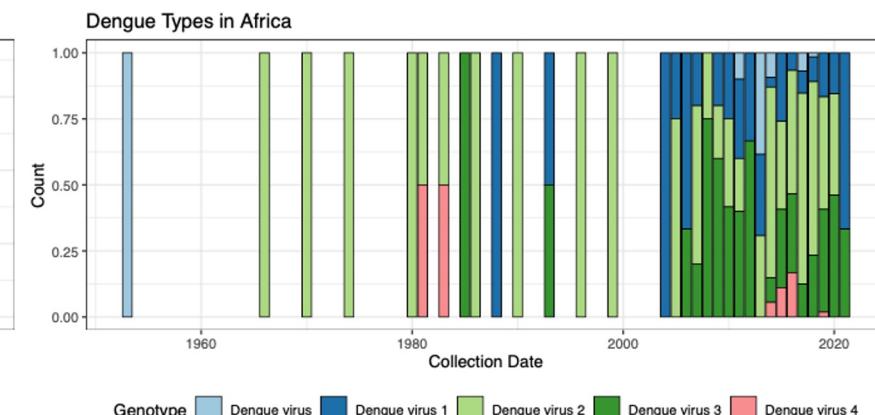
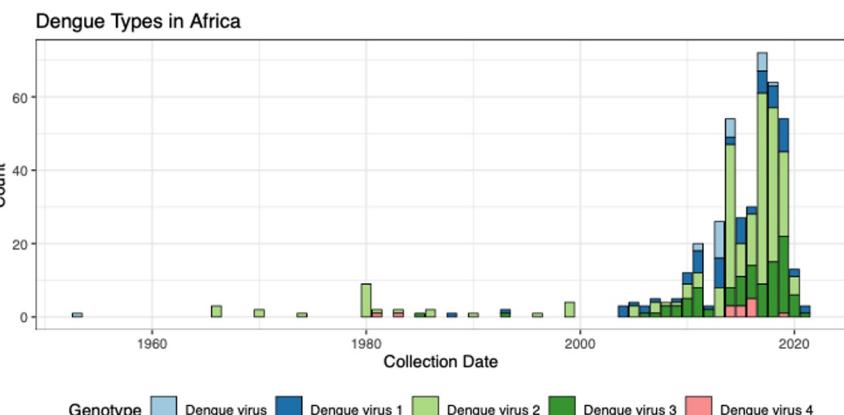
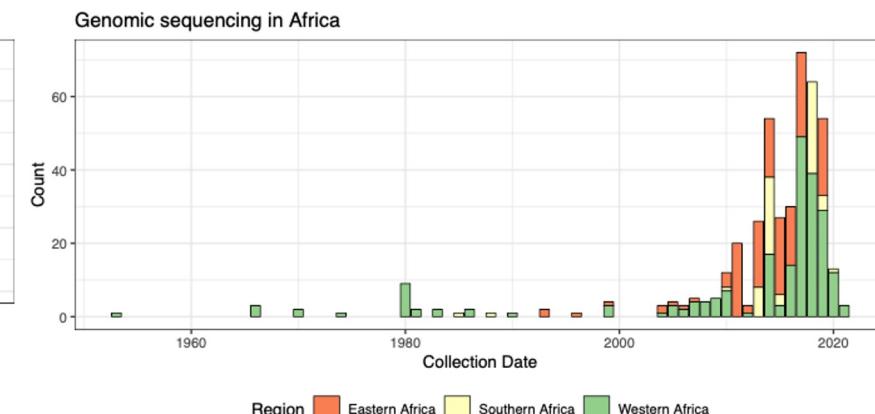
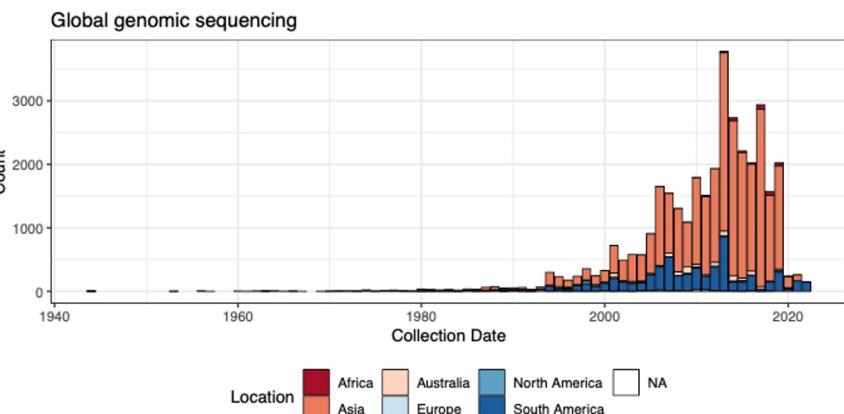
Dengue

Africa:

genomes = 457
countries = 30
1953-2021

Quality:

Coverage >90% =
215
Genotyped = 208



The landscape of genomic surveillance of arboviruses in Africa

Chikungunya

Africa:

genomes = 372

countries = 21

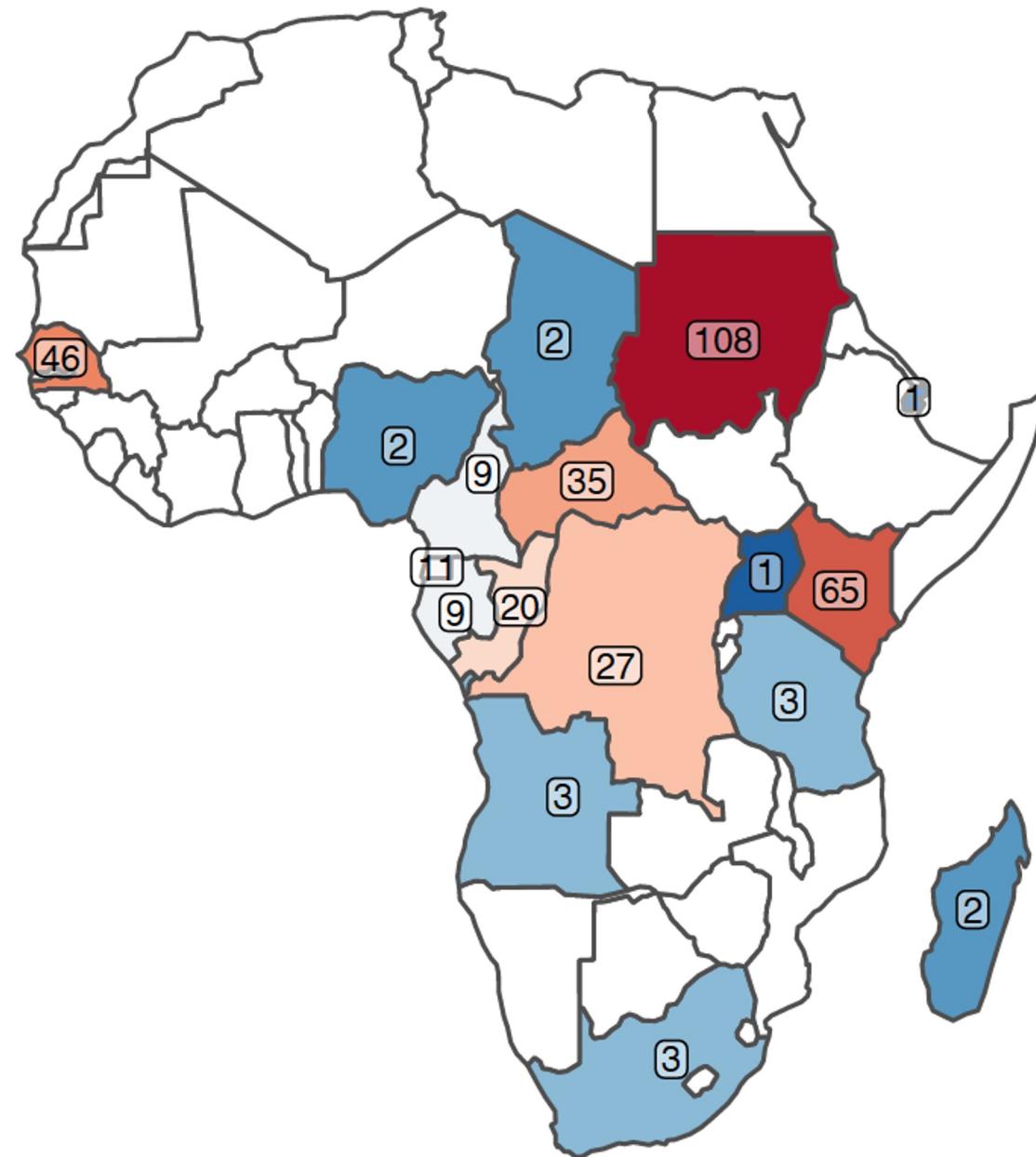
1953-2021

Quality:

Coverage >90% =

316

Genotyped = 724



The landscape of genomic surveillance of arboviruses in Africa

Chikungunya

Africa:

genomes = 372
countries = 21
1953-2021

Quality:

316

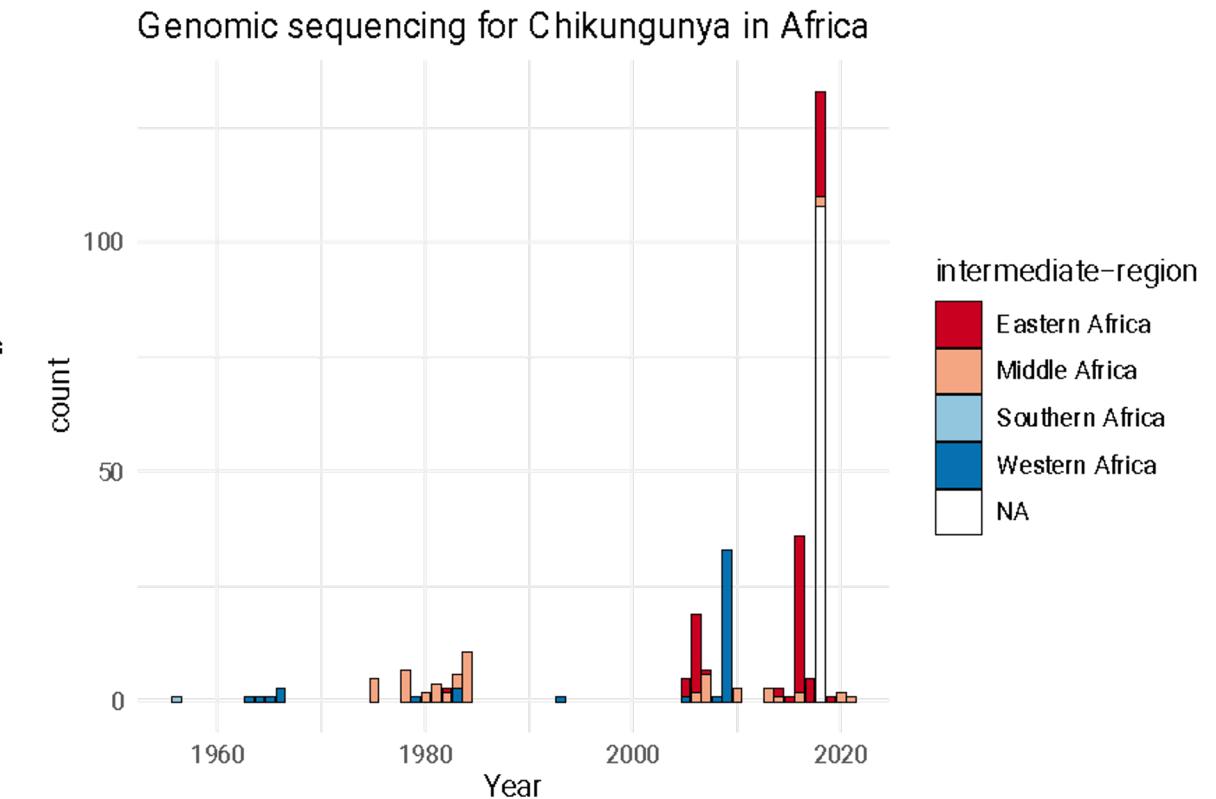
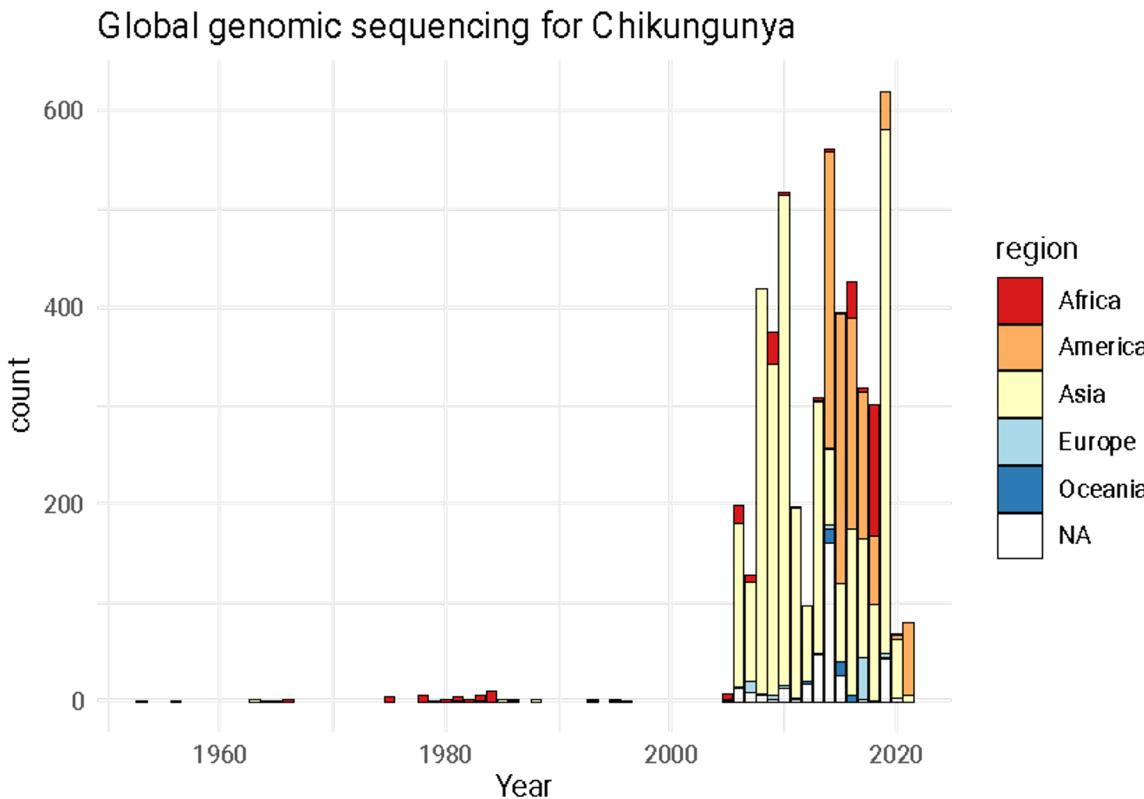
Coverage >90% =

Genotyped = 724

Asian and Caribbean = 0

East-Central-South-African = 626

West African = 98



The landscape of genomic surveillance of arboviruses in Africa

Zika

Africa:

genomes = 167

countries = 10

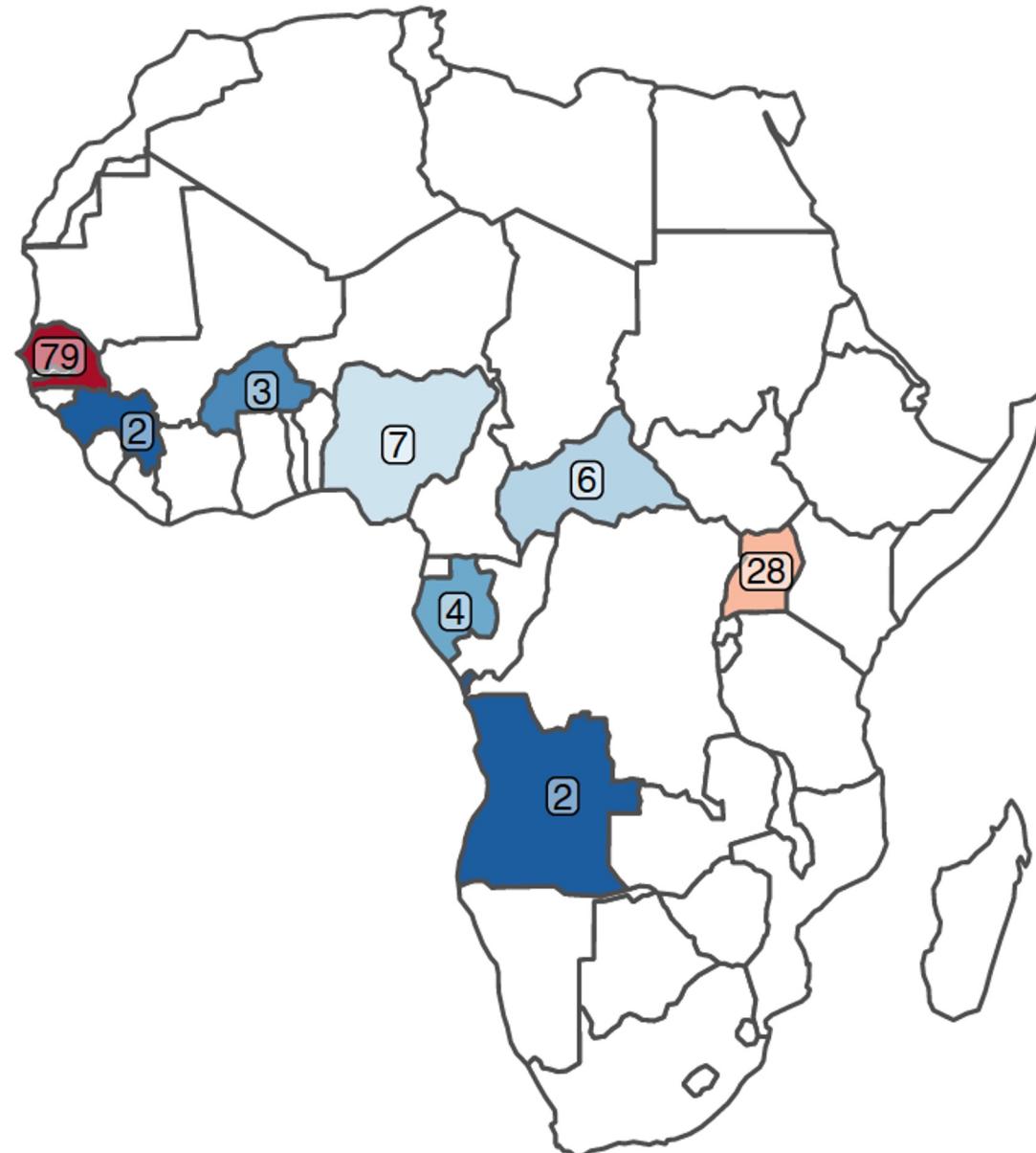
1947-2021

Quality:

Coverage >90% =

47

Genotyped = 150



The landscape of genomic surveillance of arboviruses in Africa

Zika

Africa:

genomes = 167

countries = 10

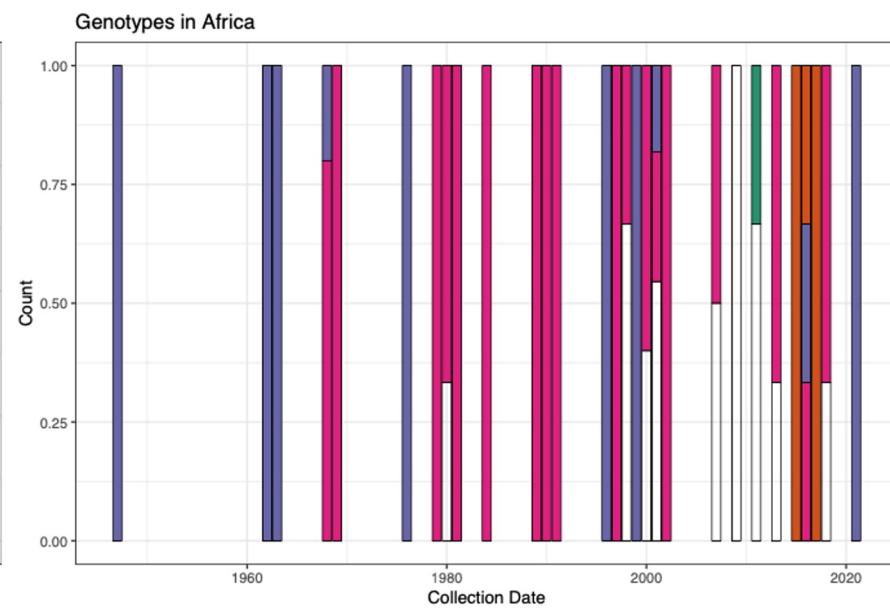
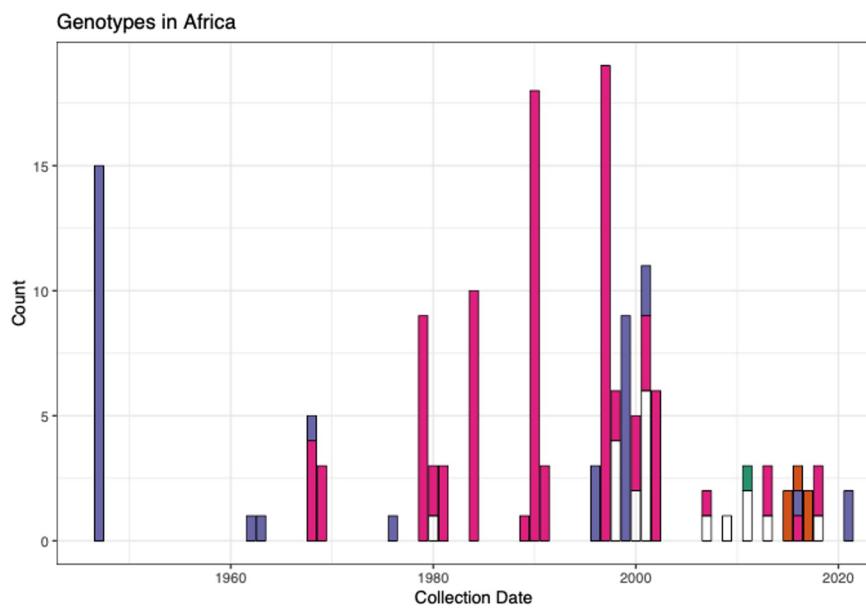
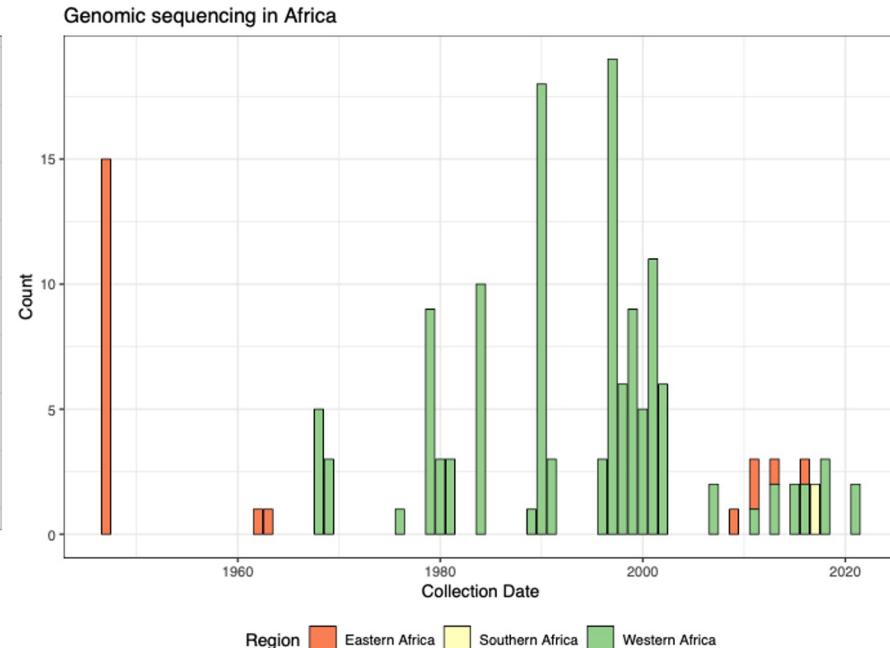
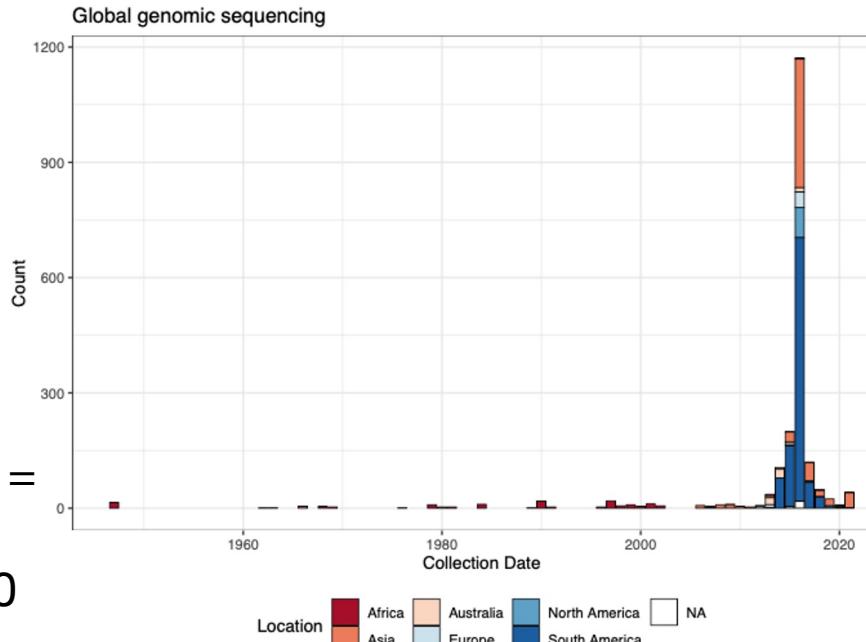
1947-2021

Quality:

Coverage >90% =

47

Genotyped = 150



Genotype African/East_African Asian East_African West_African NA

Genotype African/East_African Asian East_African West_African NA

The landscape of genomic surveillance of arboviruses in Africa

Rift Valley Fever

Africa:

genomes = 1006

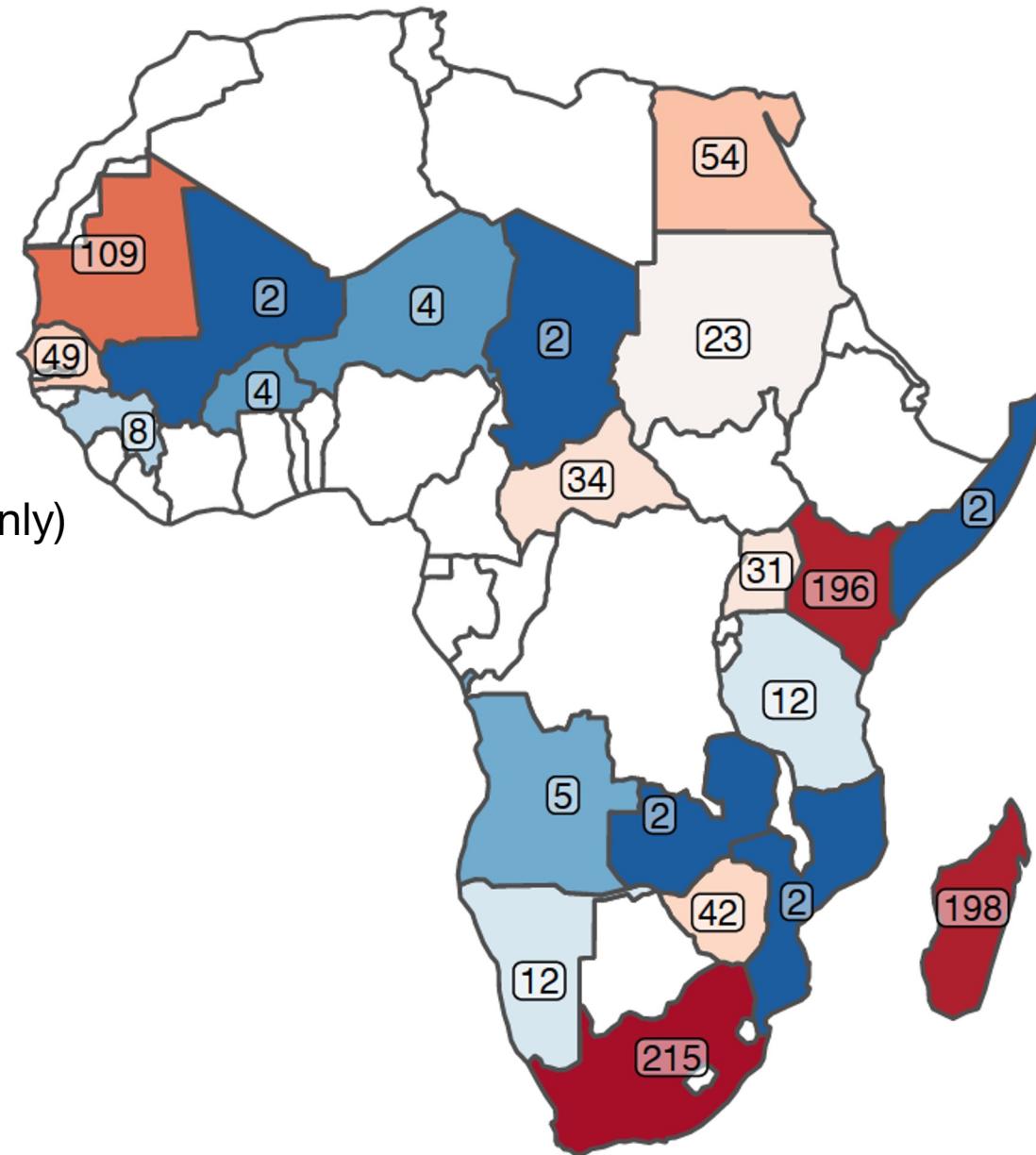
countries = 20

1944-2021

Quality:

Coverage >90% = 175 (3 segments
different lengths)

Genotyped = 317 (Segment M only)



The landscape of genomic surveillance of arboviruses in Africa

Rift Valley Fever

Africa:

genomes = 1006

countries = 20

1944-2021

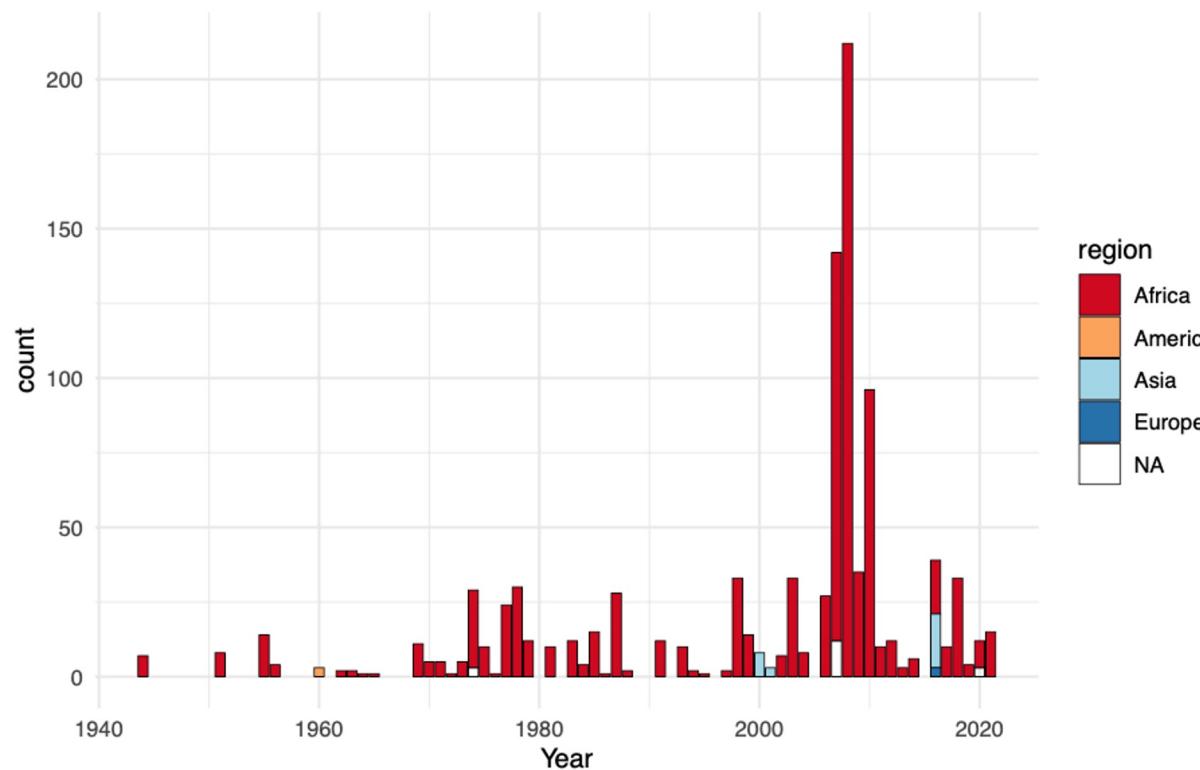
Quality:

Coverage >90% = 175 (3 segments

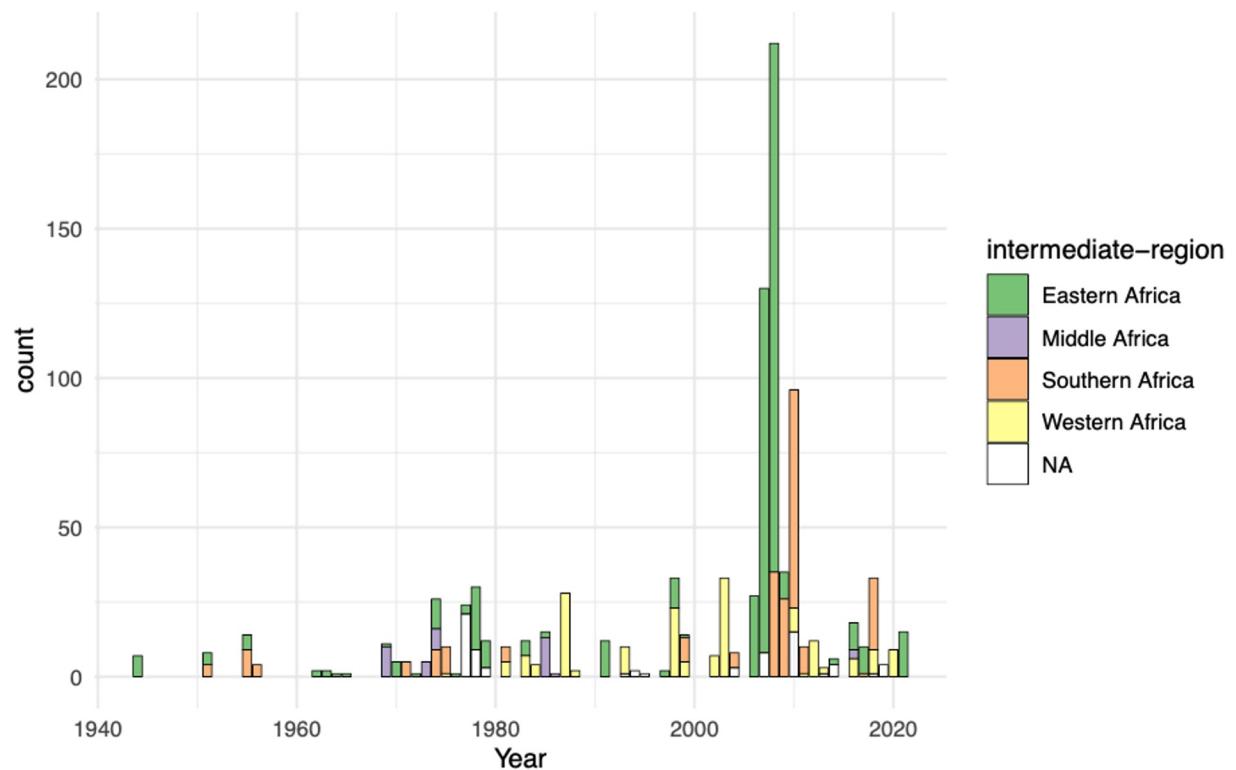
different lengths)

Genotyped = 317 (Segment M only)

Global genomic sequencing for Rift Valley Fever



Genomic sequencing for Rift Valley Fever in Africa



The landscape of genomic surveillance of arboviruses in Africa

Yellow Fever

Africa:

genomes = 185

countries = 17

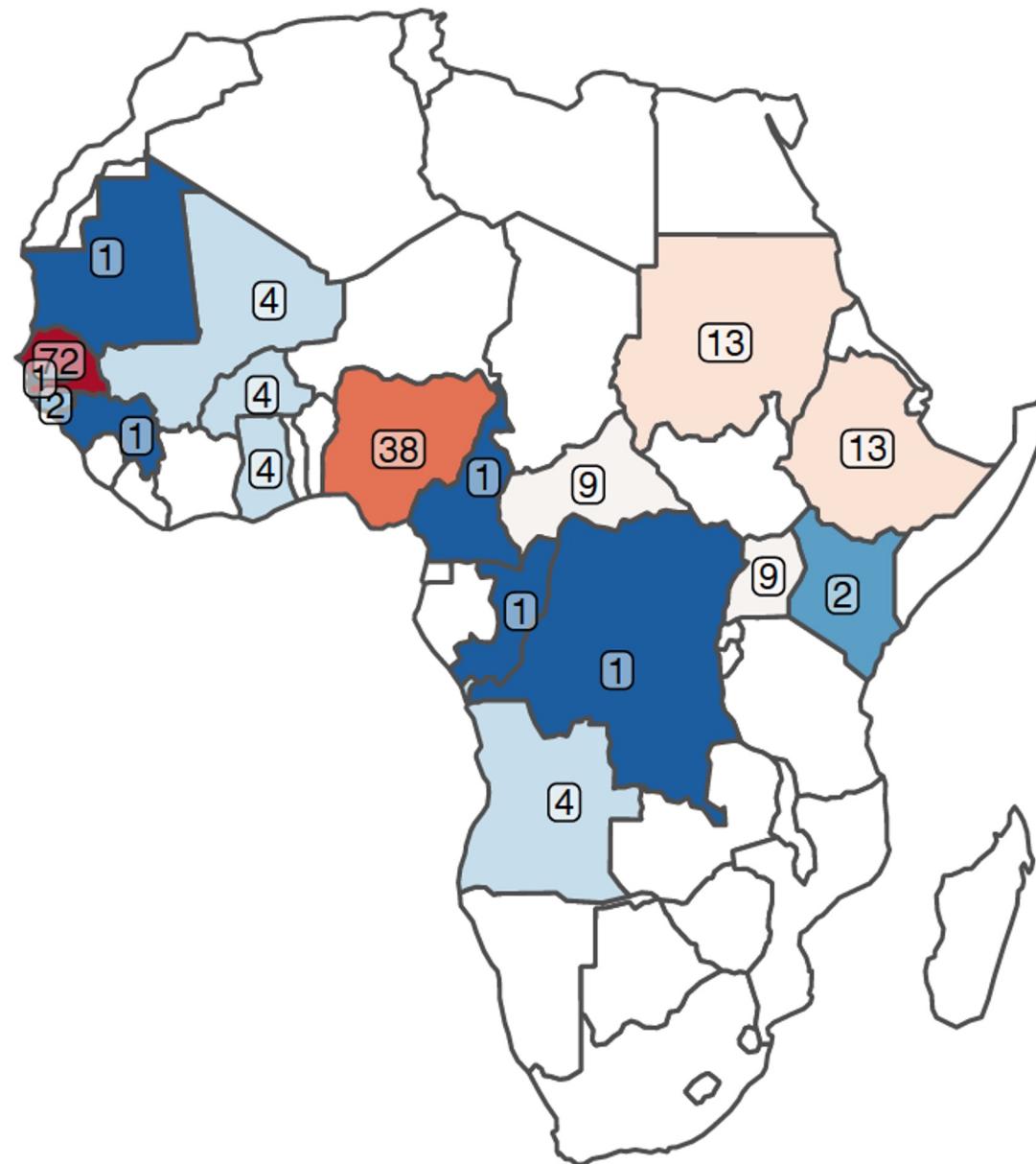
1927-2021

Quality:

Coverage >90% =

64

Genotyped = 177



The landscape of genomic surveillance of arboviruses in Africa

Yellow Fever

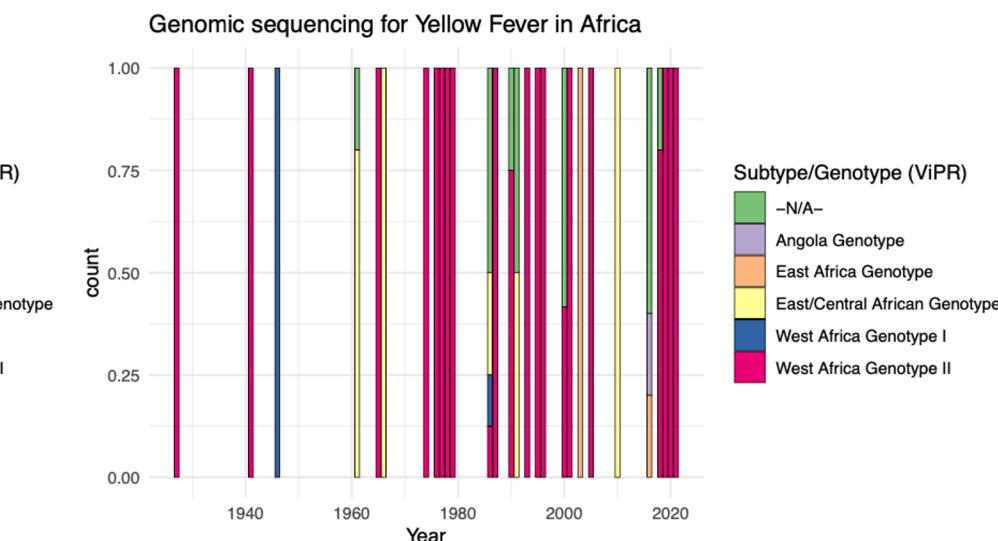
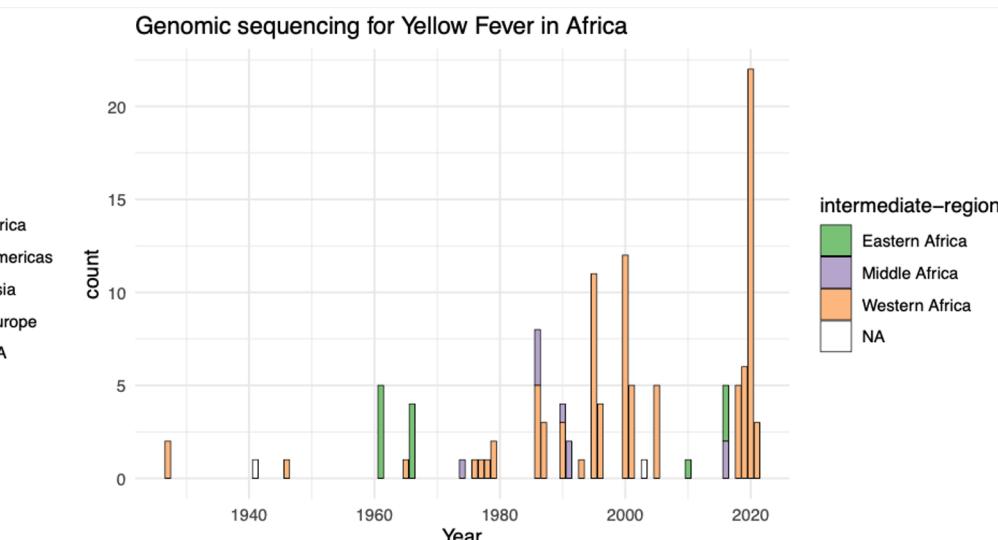
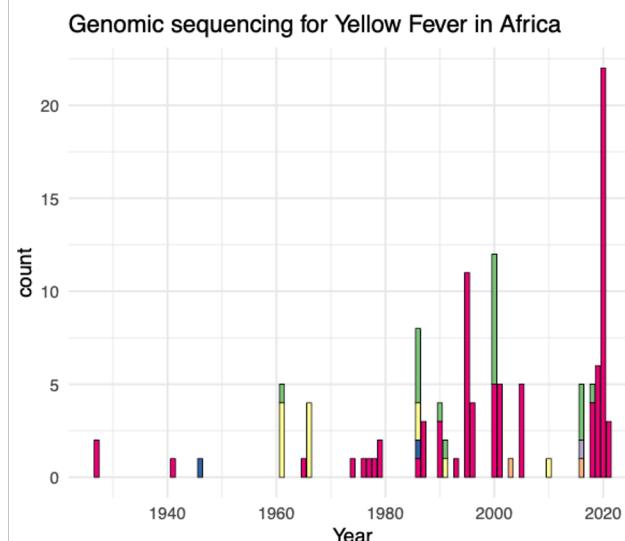
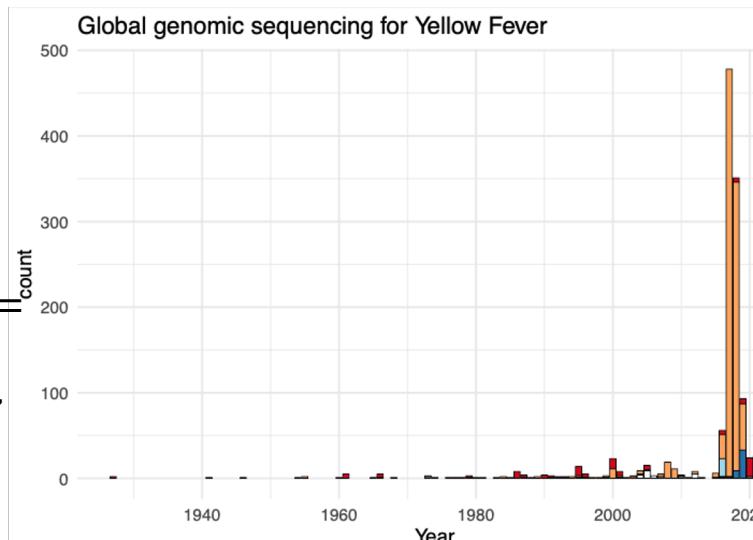
Africa:

genomes = 185
countries = 17
1927-2021

Quality:

64

Coverage >90% =
Genotyped = 177



The landscape of genomic surveillance of arboviruses in Africa

West Nile Fever

Africa:

genomes = 181

countries = 15

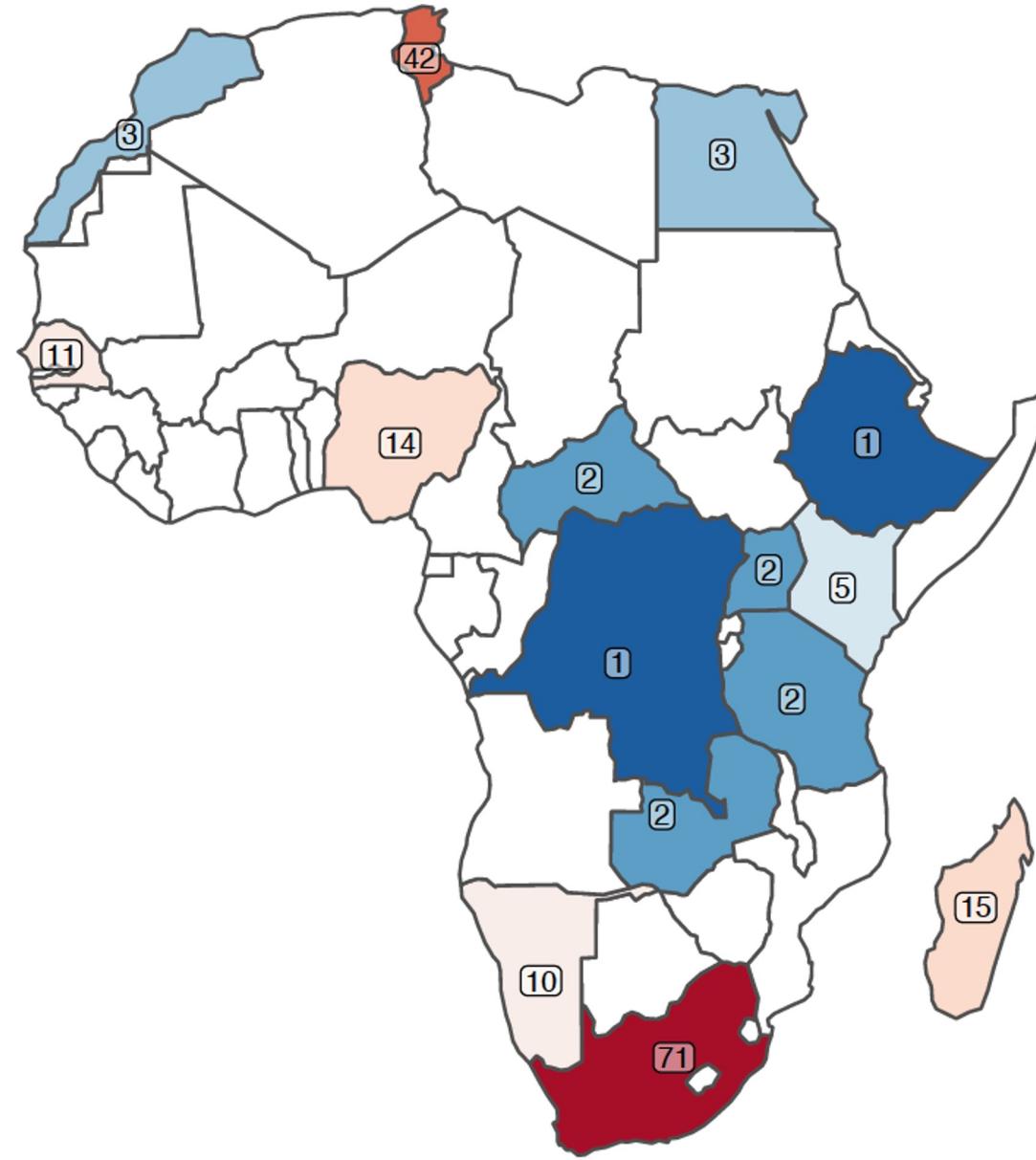
1958-2020

Quality:

Coverage >90% =

29

Genotyped = 167



The landscape of genomic surveillance of arboviruses in Africa

West Nile Fever

Africa:

genomes = 191

countries = 15

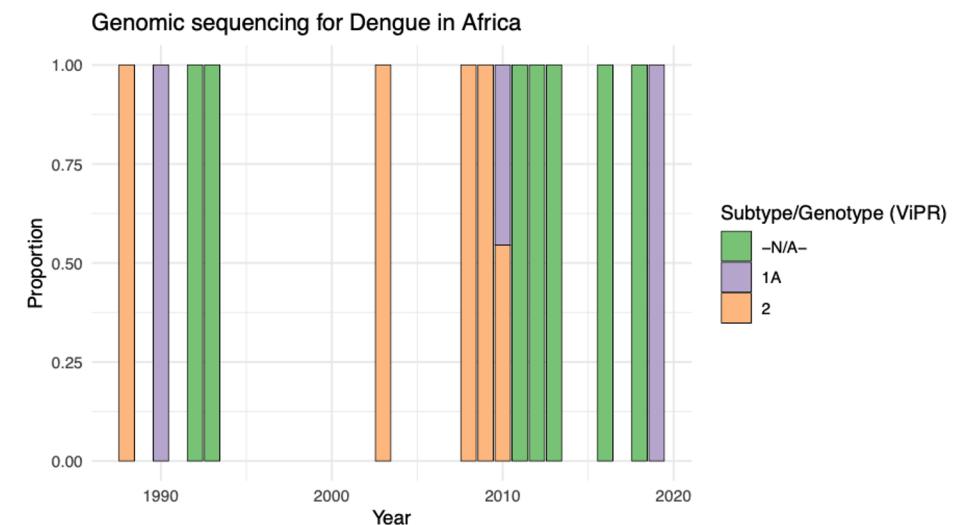
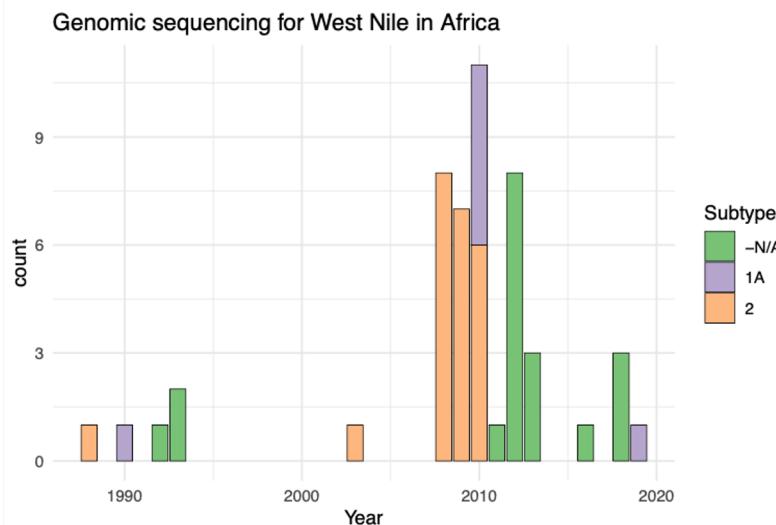
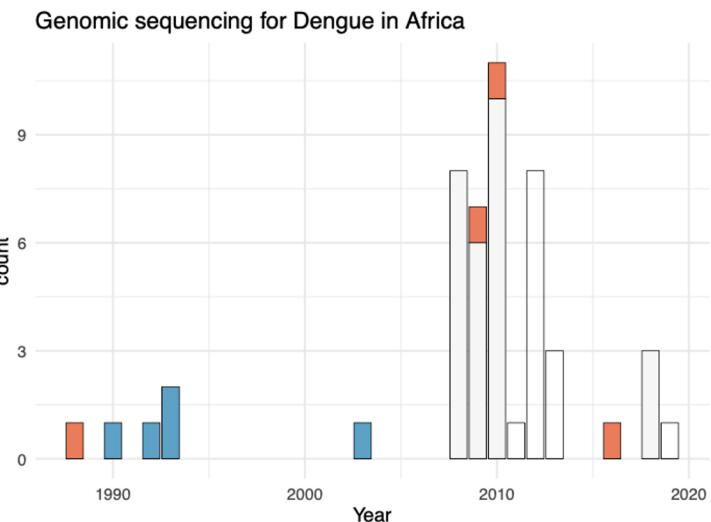
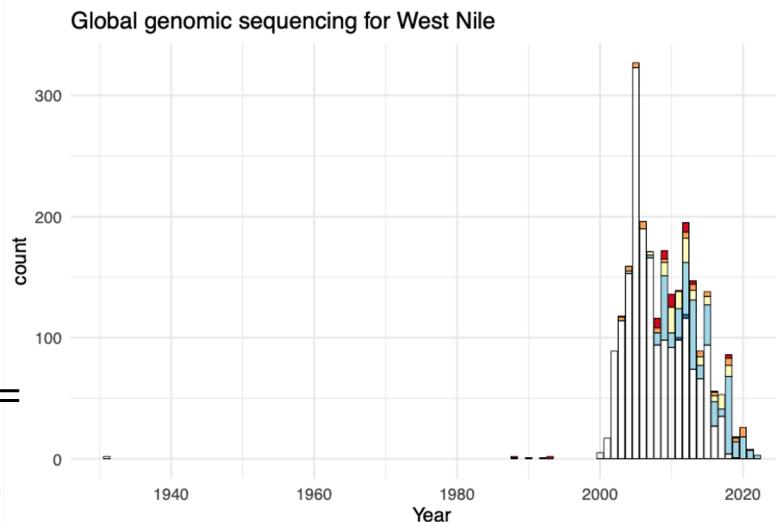
1958-2020

Quality:

Coverage >90% =

29

Genotyped = 167



The landscape of genomic surveillance of arboviruses in Africa

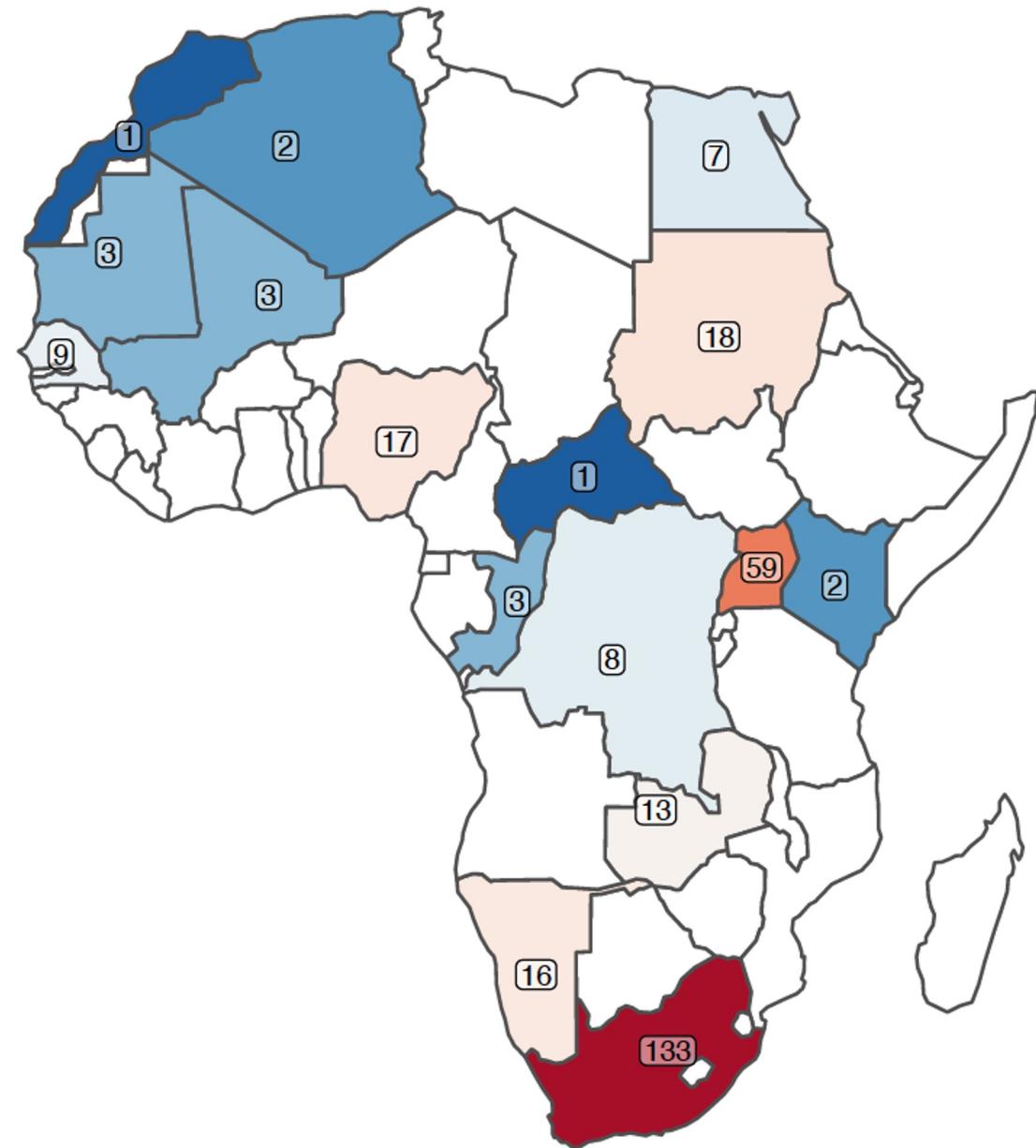
Crimean Congo Hemorrhagic Fever

Africa:

genomes = 303

countries = 16

1956-2019



The landscape of genomic surveillance of arboviruses in Africa

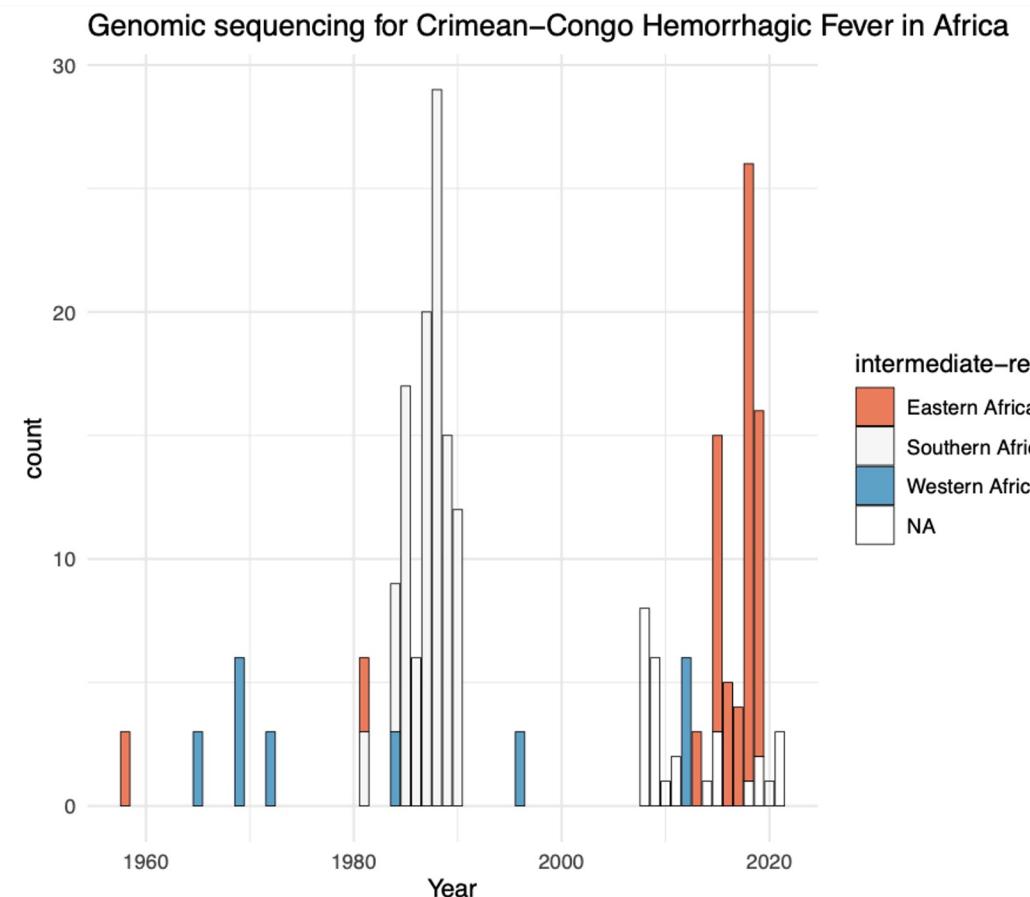
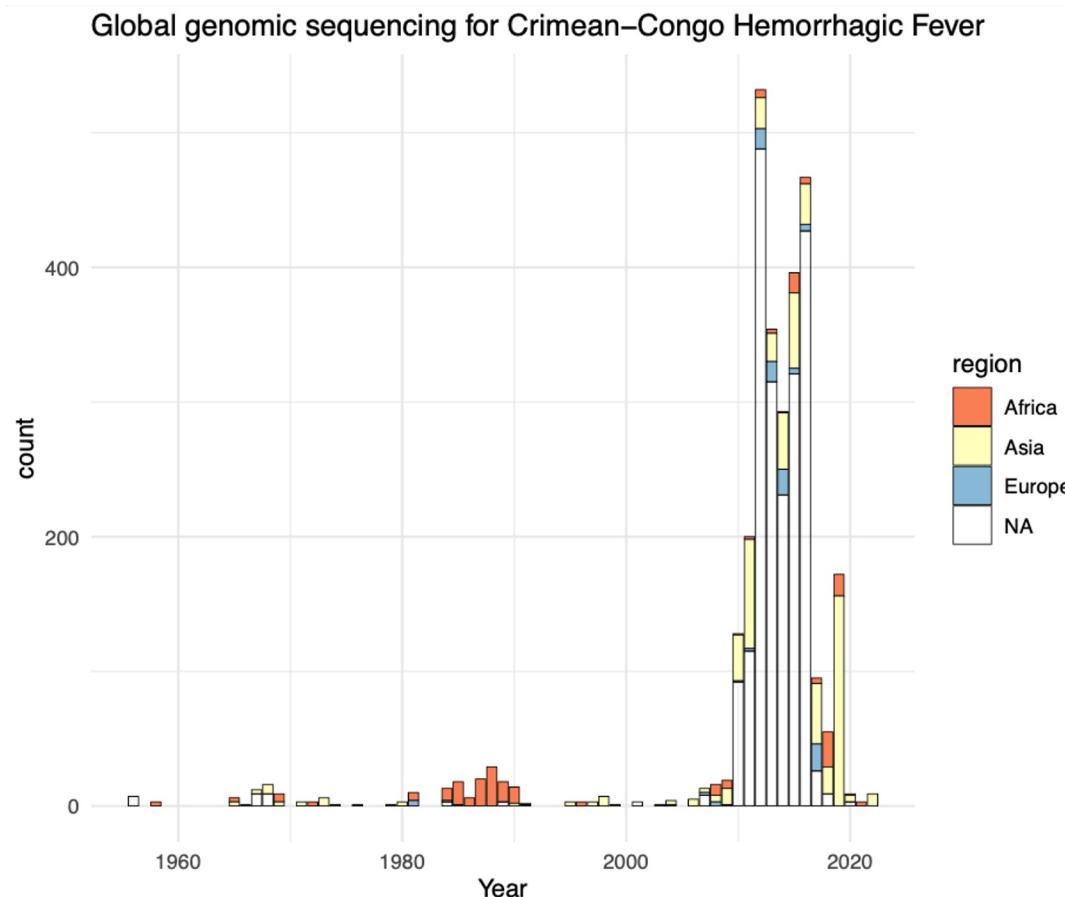
Crimean Congo Hemorrhagic Fever

Africa:

genomes = 303

countries = 16

1956-2019



Transmission Dynamics of Arboviruses in Africa

Questions to Answer

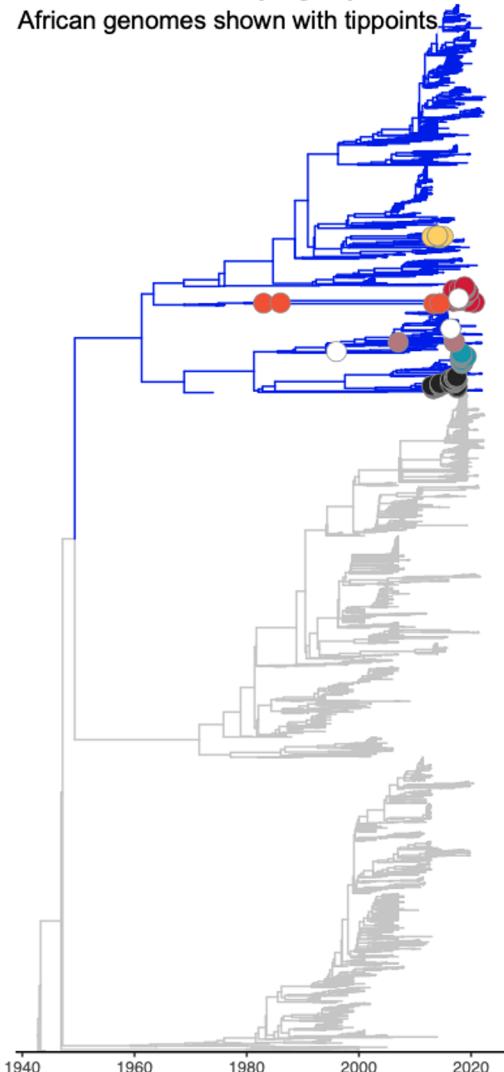
- What are the levels of importations vs endemicity in Africa?
- Are the effective population sizes of the relevant pathogens increasing in Africa? (indicates endemic circulation)
- What are the risks of importations of Arboviruses from Asia and Americas?
- What are the risks of local transmission/outbreaks/epidemics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

Dengue Phylogenetics & Transmission Dynamics in Africa

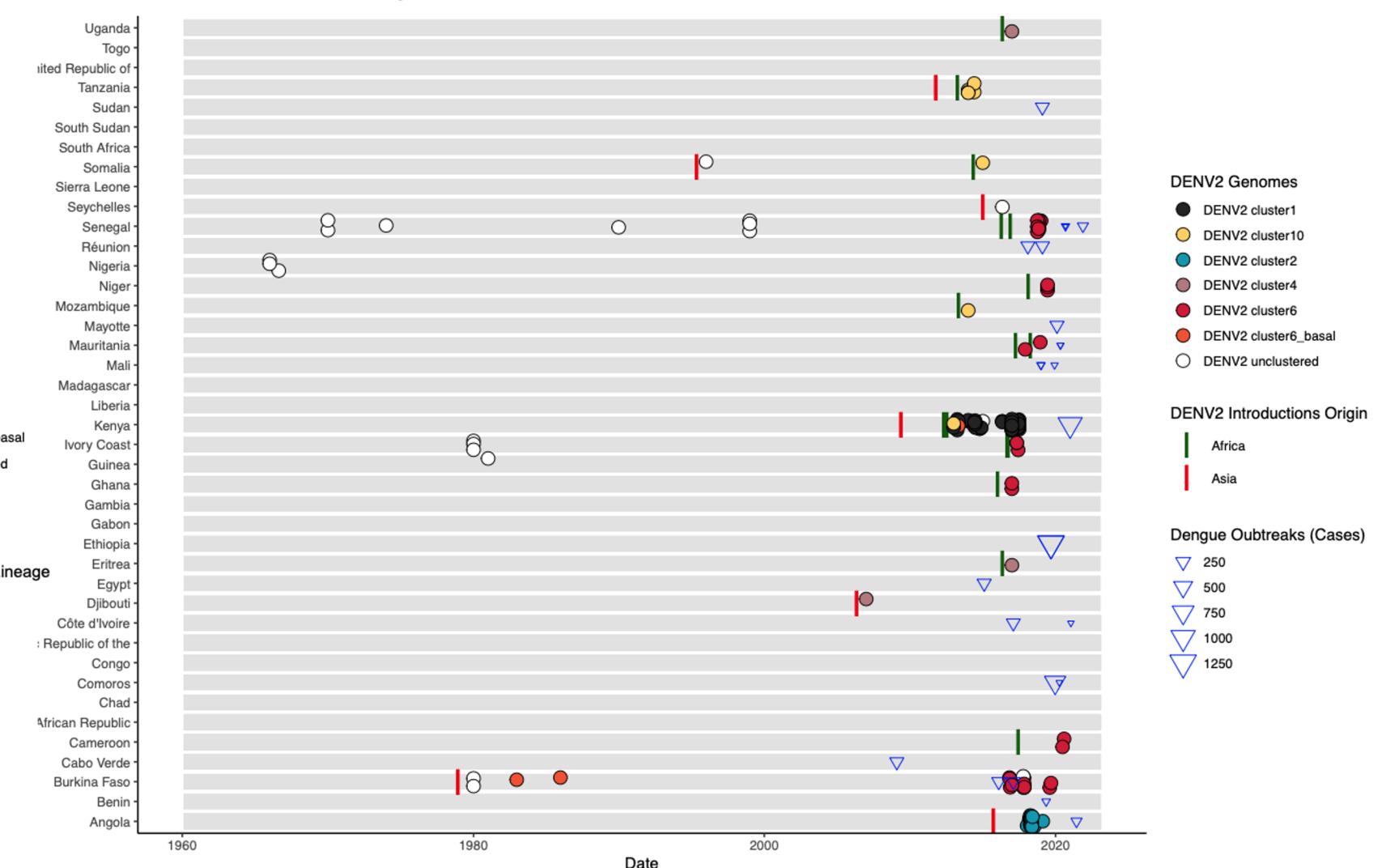
DENV2 - Multiple introductions into Africa - Multiple continental transmission clusters - Evidence of endemic circulation

DENV2 Global Phylogeny

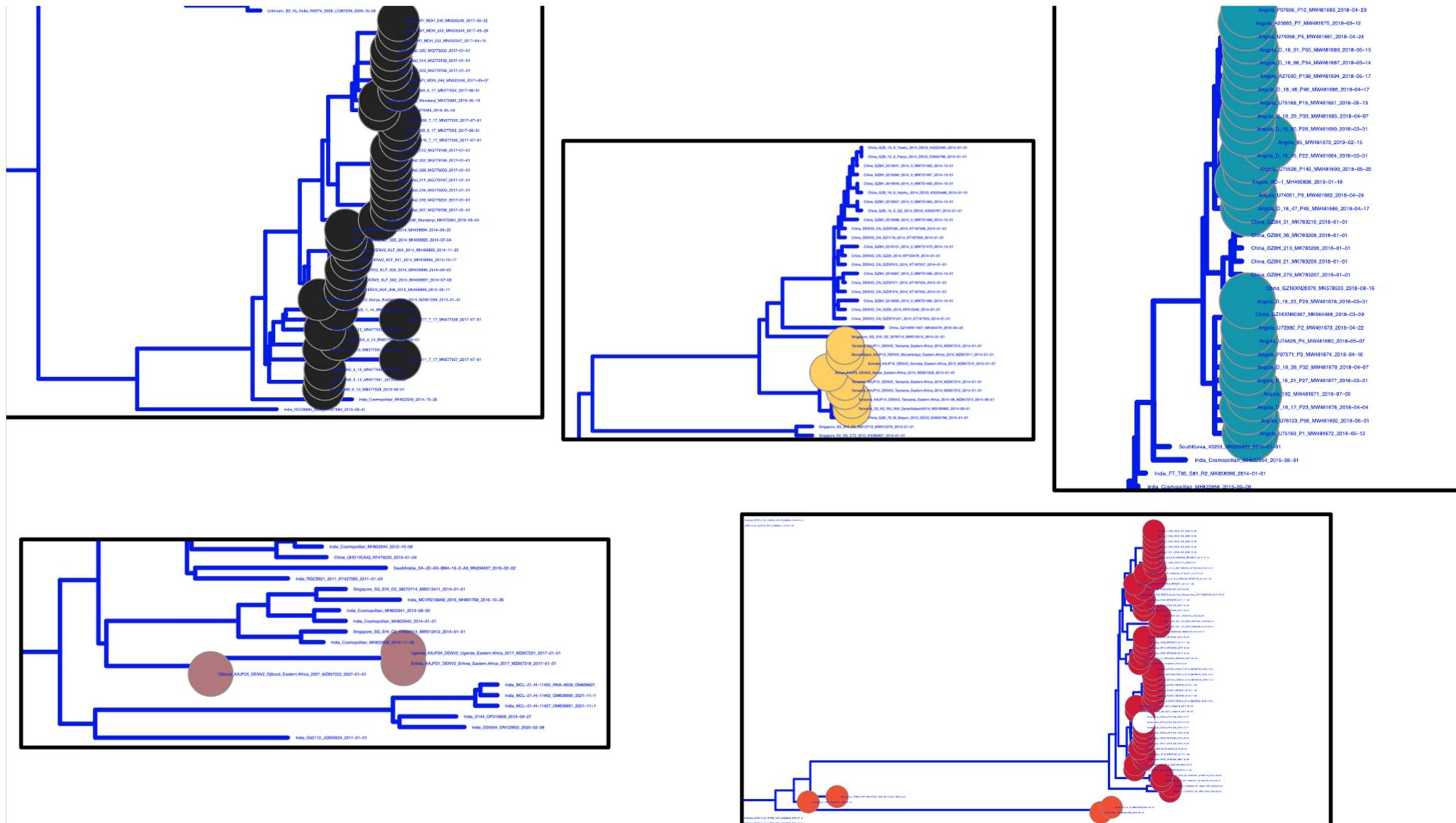
African genomes shown with tippoints



DENV2 Transmission Dynamics in Africa



DENV2 - Multiple introductions into Africa - Multiple continental transmission clusters



Next steps

- Continue with literature review
- Gather datasets from literature review
- 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!**