

Genomic classification tool for Rift Valley fever virus

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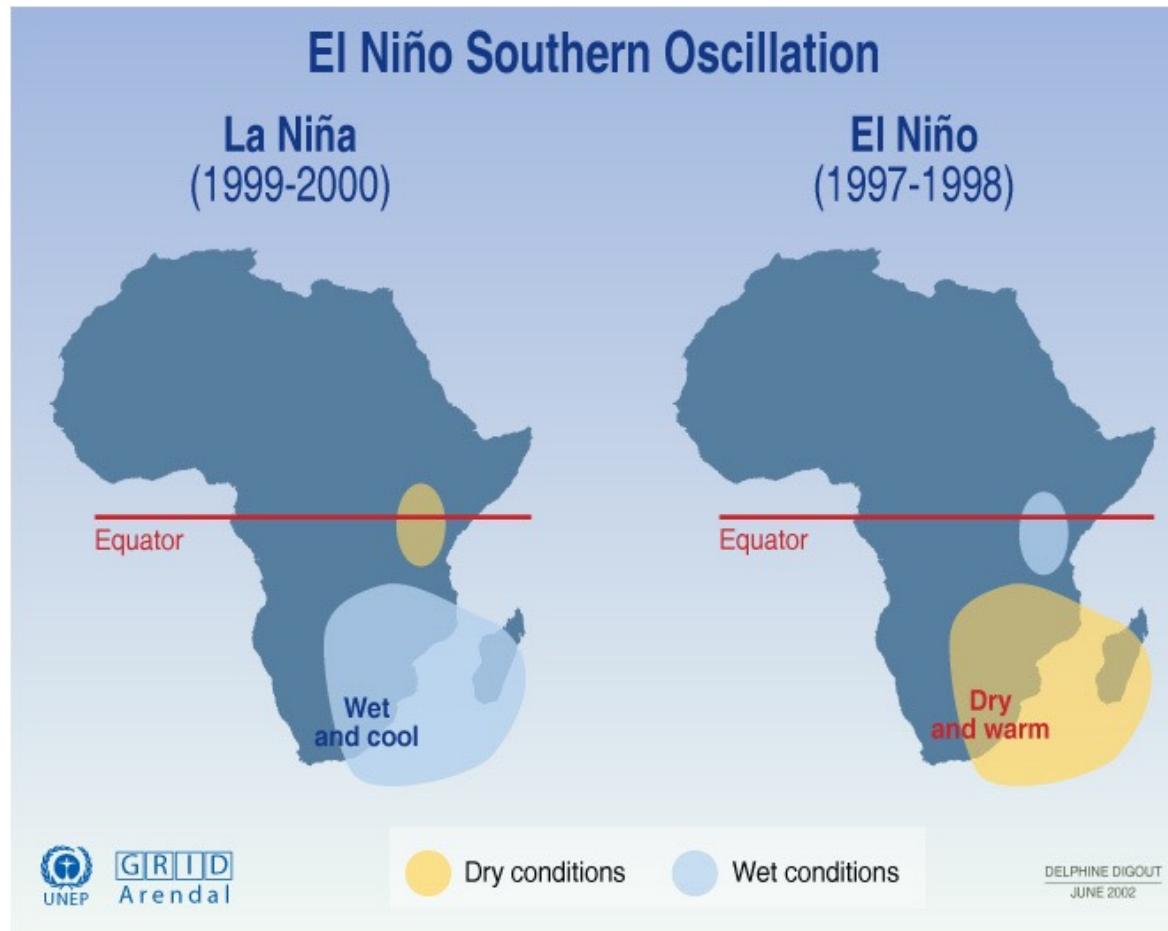
Prof. Alan Christoffels

CLIMADE Africa Working Group
Nairobi, 04-04-2023



Germ theory vs Terrain theory

“The microbe is nothing, the terrain is everything” – Louis Pasteur



Oct 1997 – Jan. 1998: Rainfall increased **60-100 times** than seasonal average.

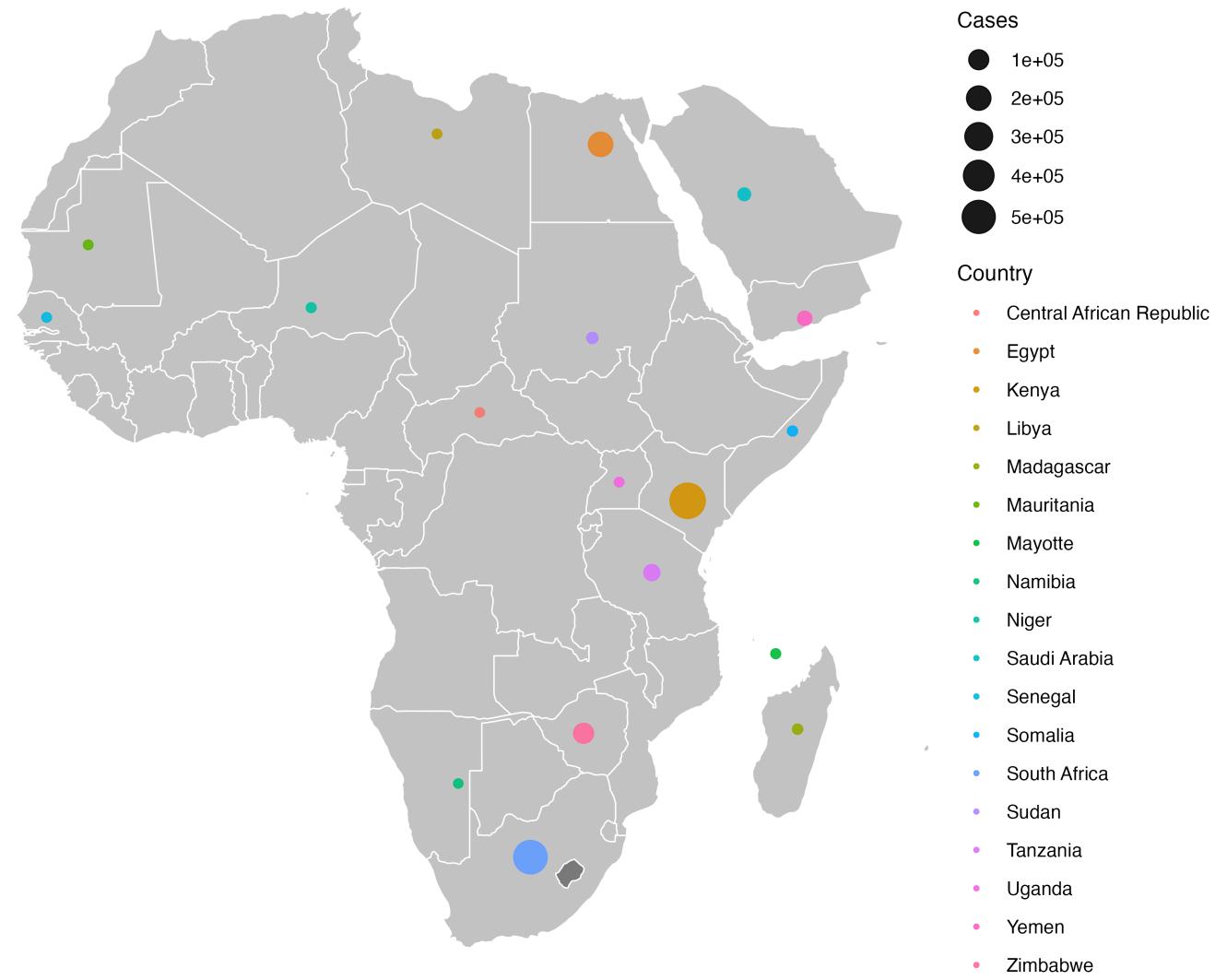
Deaths in animals: 70% sheep and goats, 20-30% cattle and camels.

89,000 human cases in Kenya and Somalia, **250 deaths**.

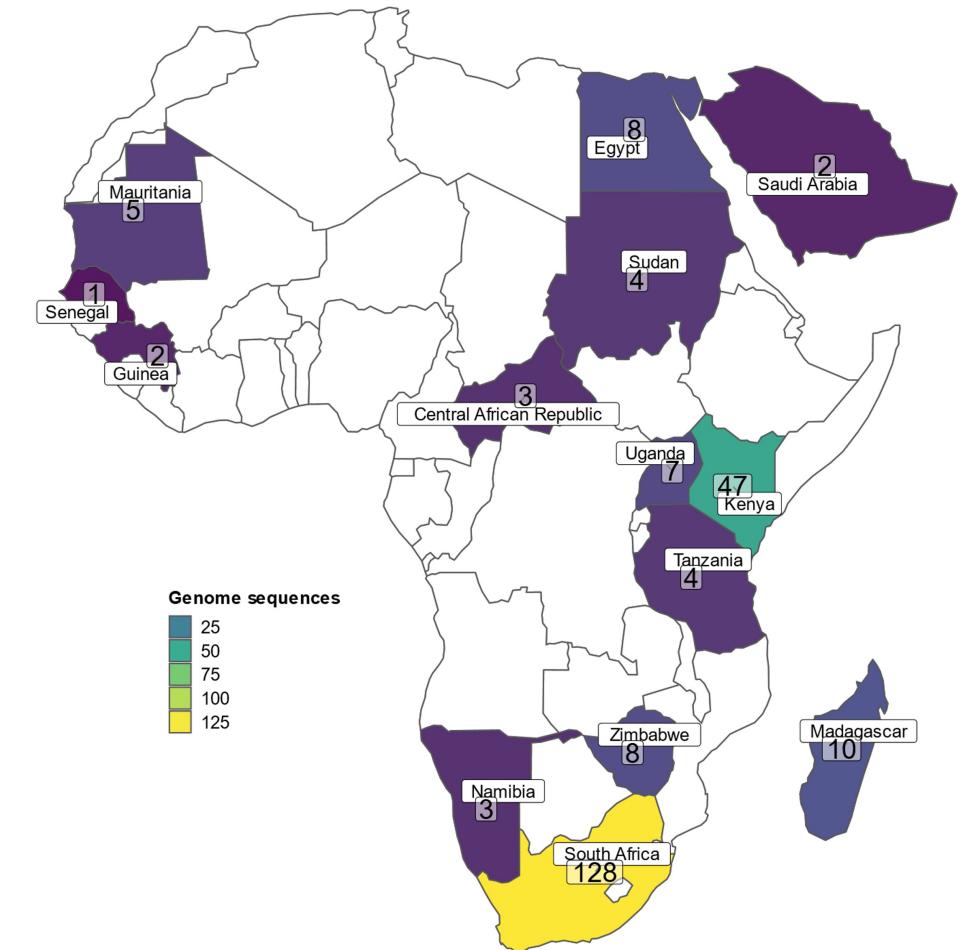
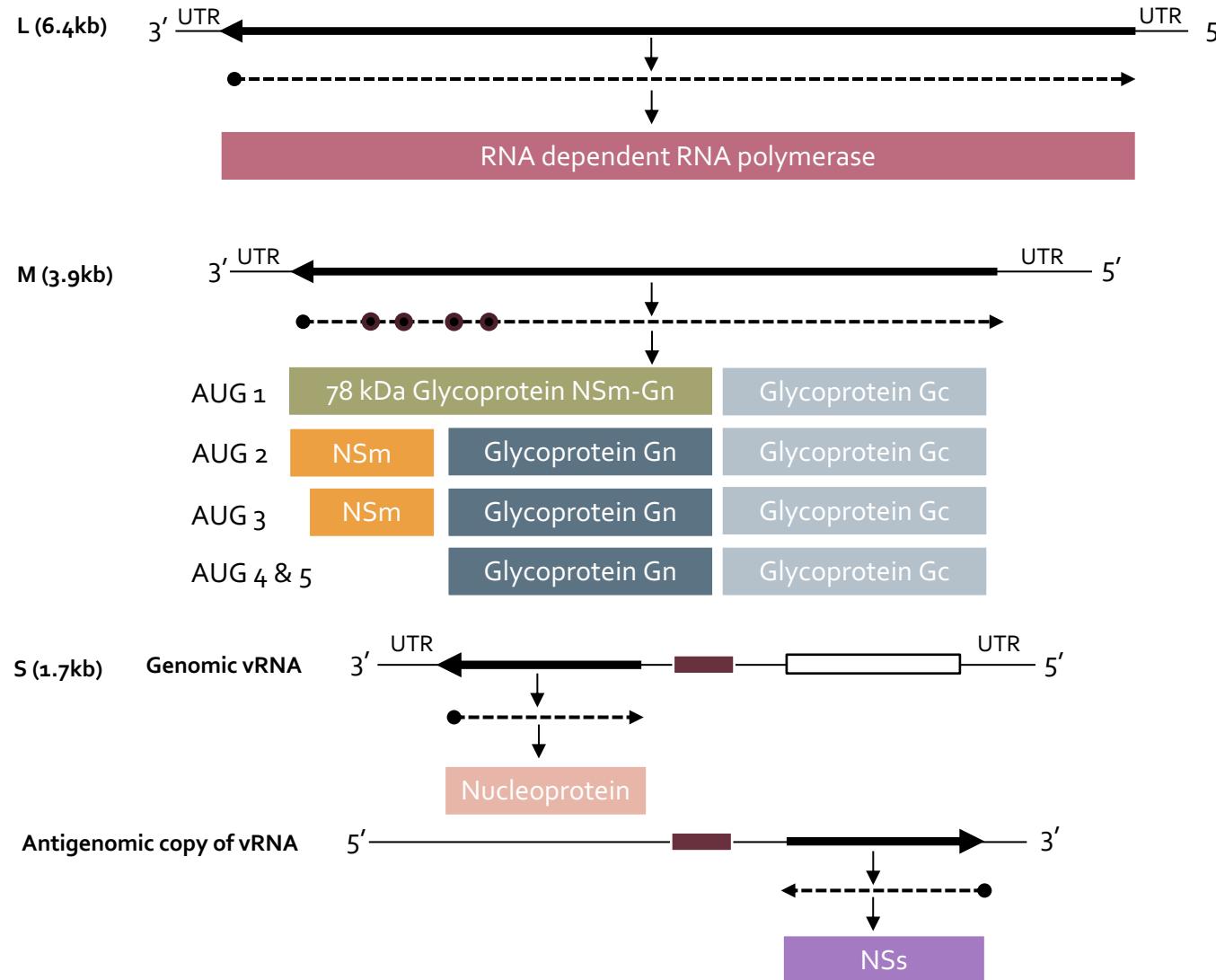
'Viral soup' – other infections e.g., bluetongue - WHO

What is Rift valley fever (RVF)?

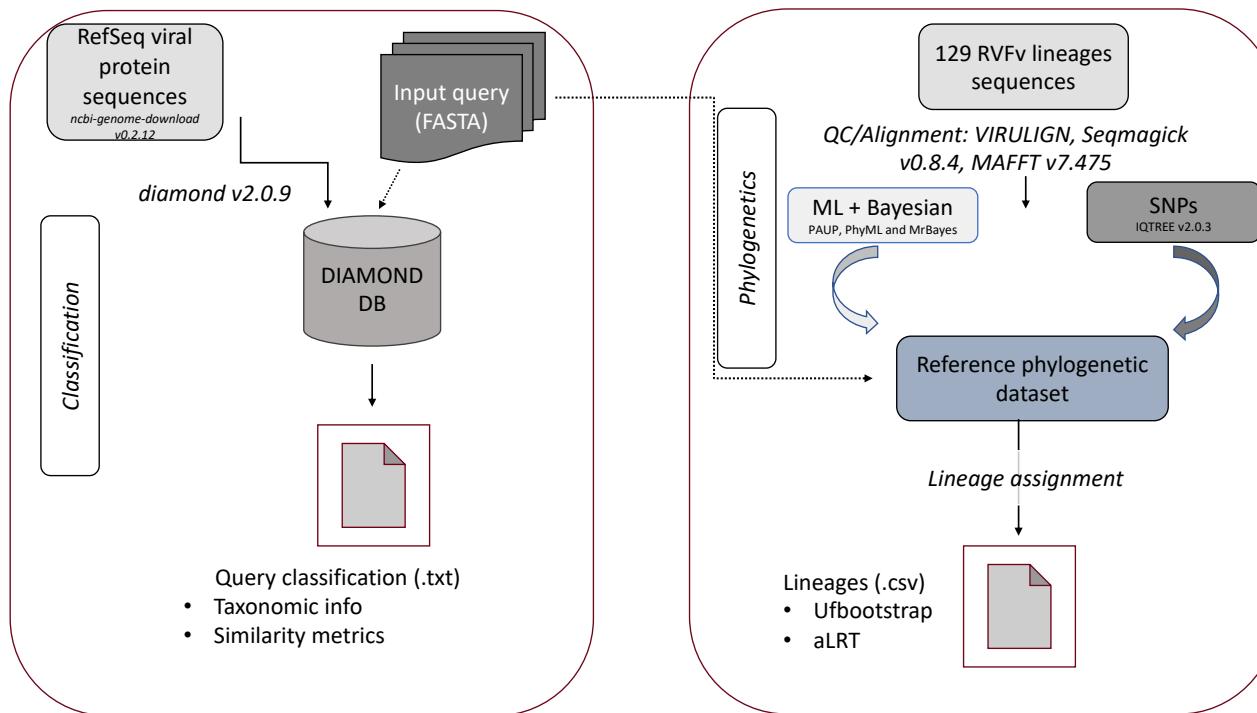
- **Endemic** in sub-Saharan Africa. The CFR is 10-30% in animals and 1-50% in humans (hemorrhagic form)
- Ability to ravage **non-endemic** territories.
- Huge **economic losses**
~\$60M in Kenya (2006-2007 outbreak, ~\$17.8M in 2010 outbreak in South Africa).



Lineage assignment of RVFV genomic sequences

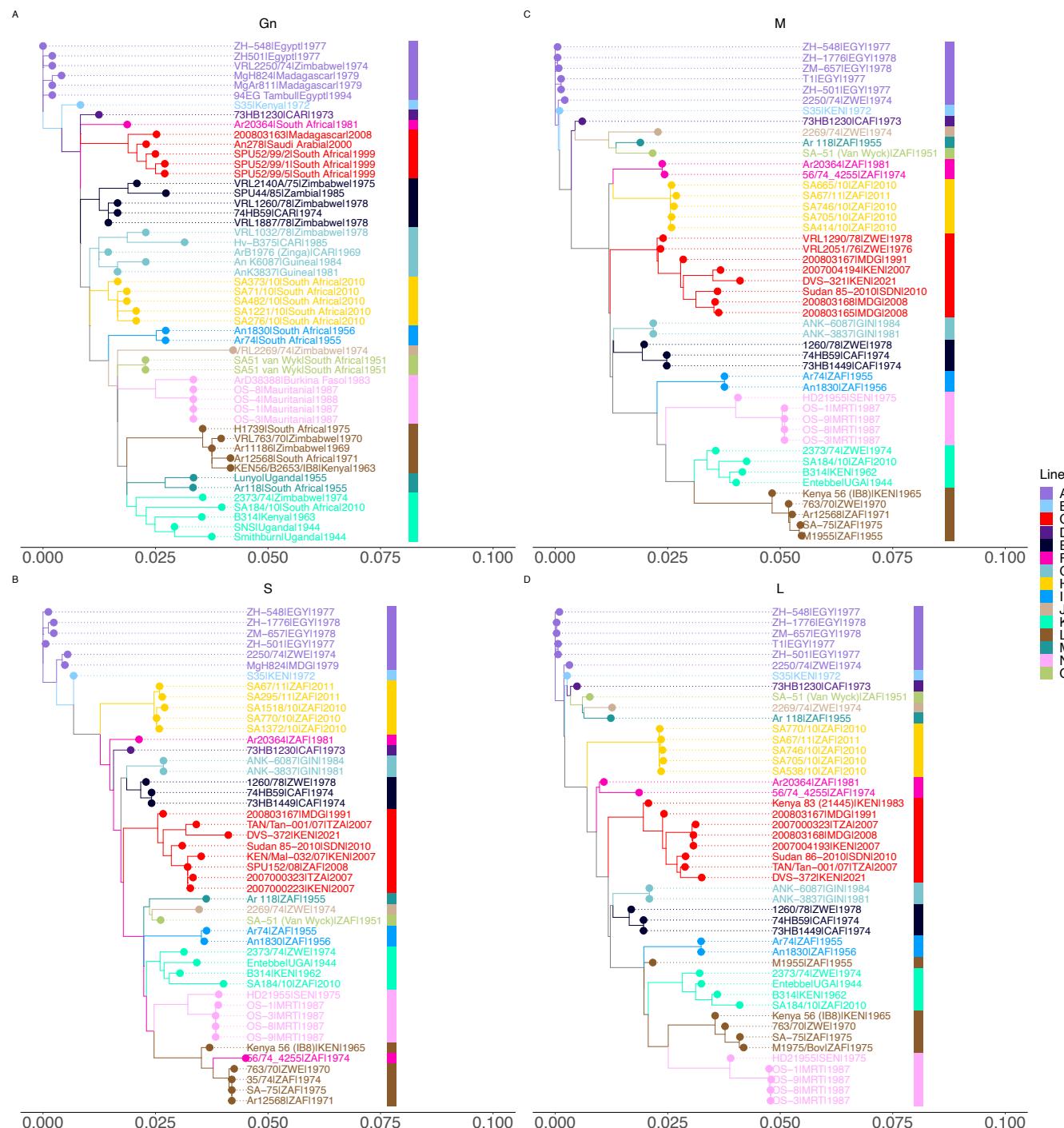


Lineage assignment ...



- Applied the nomenclature (A-O) proposed by Grobbelaar et al. 2011
- For complete genome sequences (L, M and S), retrieved sequences (**n=234**) from NCBI.
- Identified representative taxa to build lineage defining SNPs.

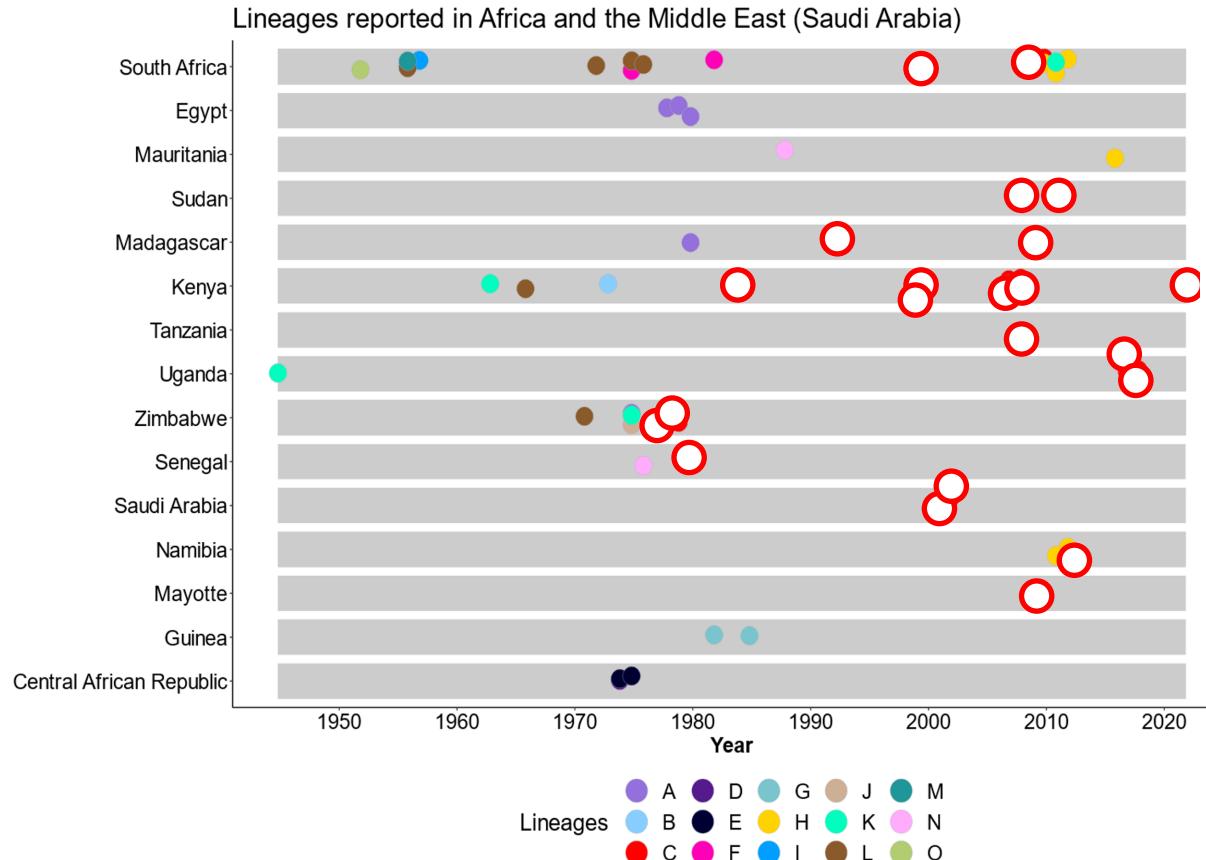
Representative taxa – lineage defining SNPs



Classifier	Representative taxa
Glycoprotein Gn	51
Complete L genome sequences	47
Complete M genome sequences	47
Complete S genome sequences	47

Congruency in representative taxa tree topology.

RVFV lineages circulating in Africa



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

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

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Performance evaluation and testing

Lineage	Known	TP	TN	FP	FN	TPR	FPR	ACC
A	10	10	224	0	0	100.0	0.0	100.0
B	1	1	233	0	0	100.0	0.0	100.0
C	88	88	146	0	0	100.0	0.0	100.0
D	1	1	233	0	0	100.0	0.0	100.0
E	3	3	231	0	0	100.0	0.0	100.0
F	2	2	232	0	0	100.0	0.0	100.0
G	2	2	232	0	0	100.0	0.0	100.0
H	105	105	129	0	0	100.0	0.0	100.0
I	2	2	232	0	0	100.0	0.0	100.0
J	1	1	233	0	0	100.0	0.0	100.0
K	4	4	230	0	0	100.0	0.0	100.0
L	8	8	226	0	0	100.0	0.0	100.0
M	1	1	233	0	0	100.0	0.0	100.0
N	5	5	229	0	0	100.0	0.0	100.0
O	1	1	233	0	0	100.0	0.0	100.0

TP = True Positives

FP = False Positives

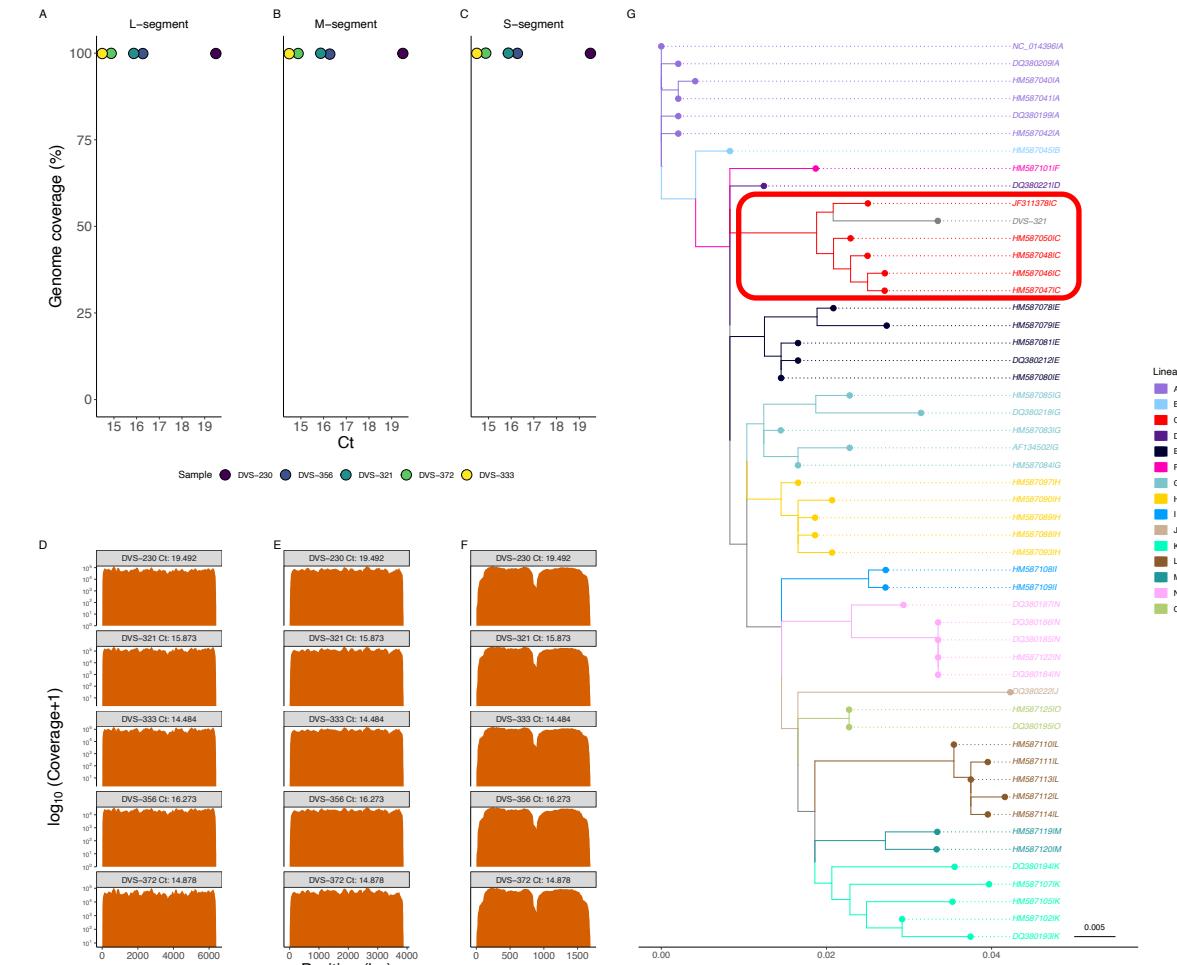
TN = True Negatives

FN = False Negatives

TPR = True Positive Rate / Sensitivity

FPR = False Positive Rate / Specificity

ACC = Accuracy



Availability

```
nextflow run main.nf \
--input 'data/test/*.fa' \
--segment Gn \
--outdir output-dir \
-work-dir work-dir \
```

<https://github.com/ajodeh-juma/rfvtyping>

<https://www.genomedetective.com/app/typingtool/rfv/>

Conclusions

- A user-friendly lineage assignment tool for characterizing and tracking circulating RVFV lineages in the region.
- The tool is useful in tracing outbreaks and supporting genomic-based surveillance efforts.
- The tool offers option to assign lineages using partial glycoprotein sequences in instances where complete genomic segment sequences cannot be readily obtained.

- Samuel Oyola, Bernard Bett, Kristina Roesel (ILRI)
- Rosemary Sang & Samson Konongoi (KEMRI)
- Alan Christoffels & Peter Van Heusden (University of Western Cape, SANBI)
- Tulio de Oliveira (Stellenbosch University, CERI, UKZN)
- Vagner Fonseca (PAHO-WHO)
- Isidore Nsengimana (Sokoine University, RAB)
- Amos Abuta (CVL)



Thanks!



Next steps

