Classification and Phylogenetic Typing of Rift Valley fever virus

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- We have developed a user-friendly open-source tool for classifying and assigning lineages of Rift Valley fever virus consensus genomes/sequences with high specificity, sensitivity and accuracy.

- This tool will be useful in tracing the origin of outbreaks and supporting surveillance and vaccination efforts.

Background

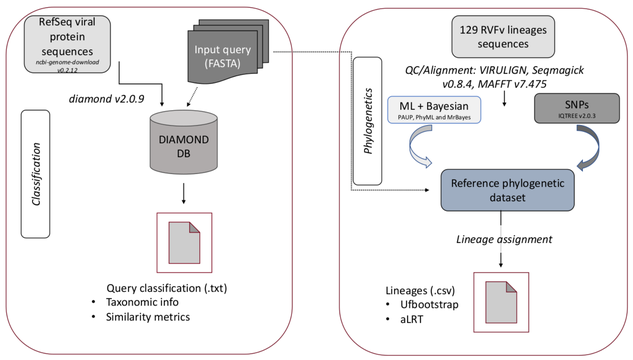
- Rift Valley fever virus (RVFV) has a complex evolutionary history that is greatly influenced by the dramatic changes to environment throughout Africa in the past 150 years [1].

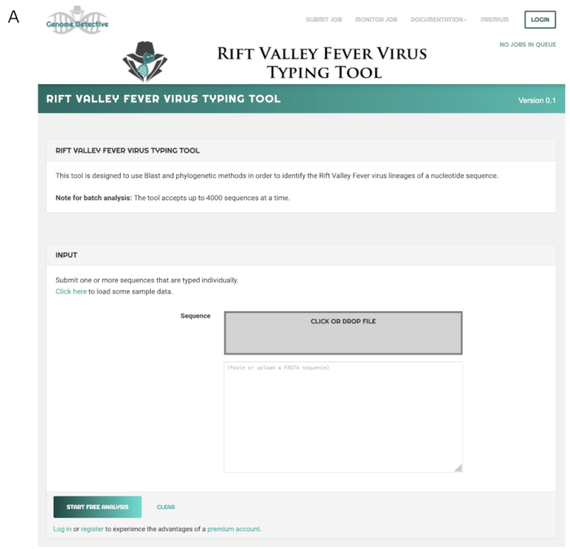
- RVFV has a stable genome but no well-defined variable sites have been identified that can be used to differentiate different strains. This can only be achieved through genome sequencing[2].

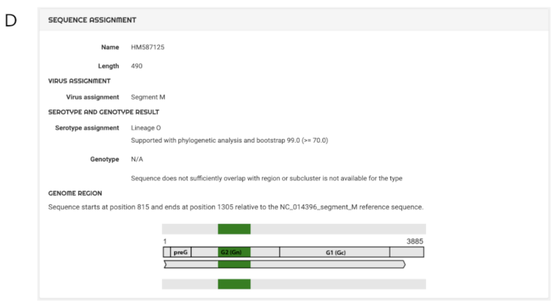
- There is the need for methods that can reliably classify arbovirus sequences.

- Genomic surveillance to elucidate genetic diversity of viruses is crucial for understanding transmission dynamics, virus evolution and disease outcome.

Methods







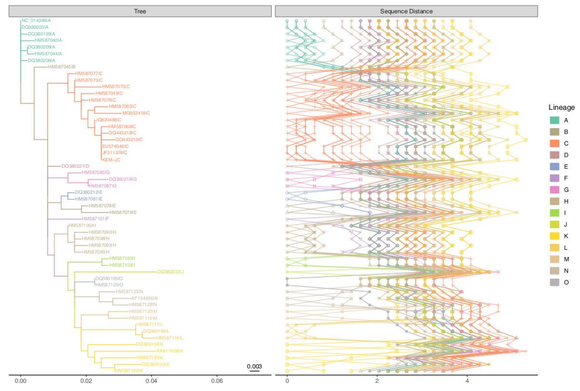
Accession	lineage	aLRT	UFbootstrap	Length	Percent_Ns	Aligned_Length	SubjectID	Segment	Product	PercentIdentity
KEM-JC	C	100	100	3885	1.21	3582	YP_003848705.1	M	glycoprotein	99.4
KEM_ND	C	100	100	3885	0.77	3591	YP_003848705.1	M	glycoprotein	98.8
KEM-BR	C	100	100	3885	0.62	3591	YP_003848705.1	M	glycoprotein	99.0

Availability

http://krisp.ukzn.ac.za/app/typingtool/rvfv/

https://github.com/ajodeh-juma/rvfvtyping

Output



References

1. Pepin, M., Bouloy, M., Bird, B. H., Kemp, A. & Paweska, J. Rift Valley fever virus (Bunyaviridae: Phlebovirus): An update on pathogenesis, molecular epidemiology, vectors, diagnostics and prevention. *Vet. Res.* **41**, (2010).

2. Gaudreault, N. N., Indran, S. V., Balaraman, V., Wilson, W. C., & Richt, J. A. (2019). Molecular aspects of Rift Valley fever virus and the emergence of reassortants. *Virus Genes*, *55*(1), 1–11. https://doi.org/10.1007/s11262-018-1611-y

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