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 welldefined 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



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.

А	Genome Detective			SUBI	TIT JOB MONITOR JOB	DOCUMENTATION - PREMIUM LOGIN	B P	HYLOGENETIC	ANALYSIS DETAILS					
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	TYPING TOOL								 Bootstrap support: 99.0 Download the alignment (NEXUS format, FASTA format) 					
	RIFT VALLEY FEVER VIRUS TYPING TOOL								 Phylogenetic Tree (export as PDF, NEXUS Format) 					
		TIEVER		TOOL		Version 0.1					1647110			
								Layout						
	RIFT VALLEY FE	EVER VIRUS TYPI	NG TOOL					Rectiline	ar ~		HM587123_N	DQ360189_L HM587116_L		
	This tool is design	ned to use Blast ar	nd phylogenetic methods	s in order to identify the	Rift Valley Fever virus lineag	es of a nucleotide sequence.		Transform	1			HM587111_L HM587120_M HM587119_M DQ380193_K		
	Note for batch an	alysis: The tool ac	ccepts up to 4000 sequer	nces at a time.				None	~		HM587102_K HM587105_K	KX611606_H DQ380194_K		
								Show la	abels		HM587109_1 HM587108_1	EU574046_C GQ443219_C		
								✓ Color branches						
	INPUT							Lineage A HM587049_C MG953418_C						
	Submit one or more sequences that are typed individually.							Lineage B Lineage C	_		HM587073_C HM587077_C	HM587075_C		
	Click here to load some sample data.							Lineage D	_	DQ3e02	HM587085_G	87_G		
	Sequence CLICK OR DROP FILE							Lineage E Lineage F	=		HM587101_F HM587090_H HM587093_H HM587098_H			
								Lineage G	<u> </u>	H	HM587095_H 587100_H DQ380212_E HM587081_E			
	(Paste or upload a FASTA sequence)							Lineage I	_		HM587045_B DO380199_A	8_E HM587079_E		
								Lineage J Lineage K	_		HM587040_A NC_014396_A DQ380203_A DQ380209_A			
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	Log in or register to experience the advantages of a premium account.													
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	You may bookmark this page to revisit results of this job (59c6e5b6-4e13-4439-9a4a-34f01ed62149) later.								Length 490					
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									SEROTYPE AND GENOTYP	PE RESULT				
	Vie								Serotype assignment	Lineage O				
									A	Supported with phylogenetic analysis and boo	otstrap 99.0 (>= 70.0)			
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	Assignment Sequences count Percentage Legend									1		3885		
	Lineage C 1 100%									preG G2 (Gn)	G1 (Gc)			
	Total 1 100%													
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							•							
			Download results: XM	ML File Table (Excel for	mat) Table (CSV format) S	Sequences (Fasta format)								
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Accession	lineage	aLRT	UFbootstrap	Length	Percent_Ns	Aligned_Length	SubjectID	Segment	Product	PercentIdentity
KEM-JC	С	100	100	3885	1.21	3582	YP_003848705.1	Μ	glycoprotein	99.4
KEM_ND	С	100	100	3885	0.77	3591	YP_003848705.1	Μ	glycoprotein	98.8
KEM-BR	С	100	100	3885	0.62	3591	YP_003848705.1	Μ	glycoprotein	99.0





Availability

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

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

Output



References

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).

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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