Genomic characterization of Rift Valley Fever Virus and co-circulating zoonotic pathogens from human samples from selected sites in Kenya

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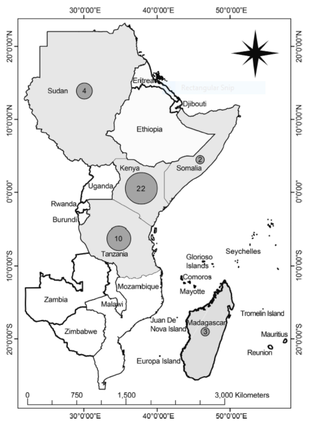
Background

Human Rift Valley Fever (RVF) infections in Kenya and in the East African region at large are being detected more frequently over wide geographical areas.

Areas of concern:

- Occurrence in new areas and at times not necessarily associated with heavy rains.
- Human infections on the increase in the last decade.
- What virus lineage/lineages are responsible?



No. of RVF Outbreaks 1912-2010, M Baba et al., 2016

Virus monitoring is critical

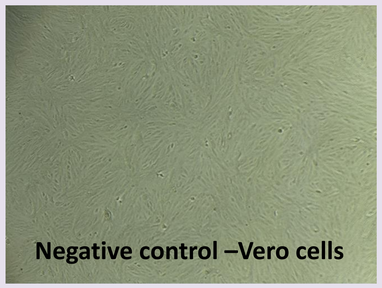
- Limited Genetic diversity data - epidemic and inter epidemic.
- Most studies/scientific outputs associated with outbreak periods.
- RVF activity shown to occur during IEP in endemic countries (Sumaye et al., 2013).
- Concern that virus activity and evolution can occur below the threshold of detection methods by public health or animal health authorities during inter epidemic periods (Bird et al., 2008).
- Virus may go undetected due to minimum surveillance in hosts and vectors.

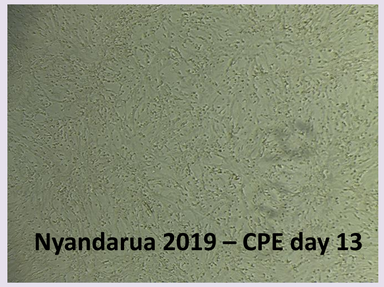
Approach

Year	No. of Archived Human samples	Central	Rift Valley	Coast	Eastern
1997/98	800	0	414	0	386
2006/07	856	83	122	525	126
2014	2	1	0	1	0
2019	112	112	0	0	0
2020	10	0	0	0	10
2121	7	0	0	0	7
Total	**1,787**	**196**	**536**	**526**	**529**

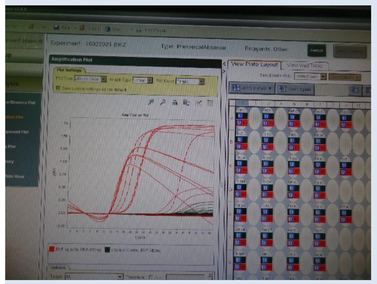
- 1,787 human serum samples identified in repository 1997-2021 with accompanying clinical information
- 200 inoculations performed in KEMRI BSL3

Preliminary Findings





Diverse CPE types observed



Real Time PCR

- 70 CPE positive potential isolates harvested
- RNA extracted (Qiagen)
- RVF real time PCR performed using the altona RVF kits
- 25 RVF positive isolates detected.

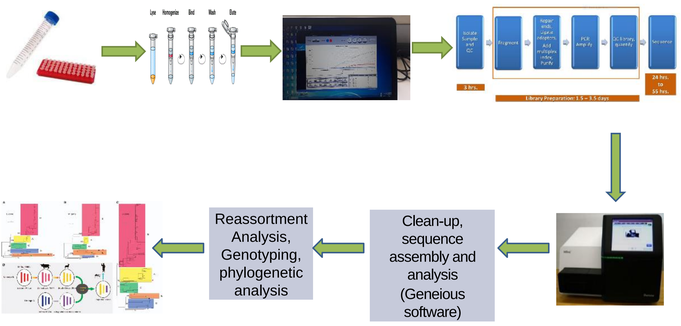
Sequencing

sample_name	before_trim	after_trim	mapped	pct_mapped	pct_N_bases	pct_covered_bases	longest_no_N_run	qc_pass
KEM-BR	1495184	474814	20357	4.29	0.37	99.63	6381	TRUE
KEM-ND	598576	177778	13521	7.61	0.37	99.63	6381	TRUE
250618	618832	192024	26340	13.72	0.30	99.70	6386	TRUE
500618	2179348	559776	9870	1.76	0.31	99.69	6385	TRUE
HA-HAR	13341438	3839408	1429	0.04	8.53	91.47	1060	TRUE
KEM-JC	495888	150560	7043	4.68	0.50	99.50	6373	TRUE
K2	4284186	1295680	90222	6.96	0.28	99.72	6387	TRUE
sample_name	before_trim	after_trim	mapped	pct_mapped	pct_N_bases	pct_covered_bases	longest_no_N_run	qc_pass
KEM-JC	495888	150560	1730	1.15	1.21	98.79	3839	TRUE
500618	2179348	559776	7174	1.28	0.57	99.43	3864	TRUE
KEM-BR	1495184	474812	6790	1.43	0.62	99.38	3862	TRUE
250618	618832	192024	26674	13.89	0.26	99.74	3875	TRUE
K2	4284186	1295680	62675	4.84	0.28	99.72	3874	TRUE
KEM-ND	598576	177778	7457	4.19	0.77	99.23	3856	TRUE
sample_name	before_trim	after_trim	mapped	pct_mapped	pct_N_bases	pct_covered_bases	longest_no_N_run	qc_pass
KEM-BR	1495184	474812	9507	2.0	4.32	95.68	838	TRUE
250618	618832	192024	12545	6.53	2.37	97.63	847	TRUE
KEM-JC	495888	150560	3628	2.41	4.97	95.03	832	TRUE
500618	2179348	559780	10055	1.8	4.32	95.68	836	TRUE
KEM-ND	598576	177778	4601	2.59	3.31	96.69	829	TRUE
HA-HAR	13341438	3839402	1094	0.03	8.93	91.07	819	TRUE
K2	4284186	1295678	124590	9.62	3.08	96.92	848	TRUE

>95% genome recovery from 7 human isolates

Sample ID	Year of collection	Location/Region	Lineage	Length	Aligned length	Segment	Product	Percent ID
500618	2018	Marsabit/N.Eastern	C	3885	3591	M	Glycoprotein	99.0
250618	2018	Wajir/N.Eastern	C	3885	3591	M	Glycoprotein	99.4
KEM JC	2007	Baringo/R. Valley	C	3885	3582	M	Glycoprotein	99.4
KEM ND	2007	Baringo/R. Valley	C	3885	3591	M	Glycoprotein	98.8
KEM BR	2007	Kilifi/Coast	C	3885	3591	M	Glycoprotein	99.0
K2	2007	Kilifi/Coast	C	3885	3591	M	Glycoprotein	99.4
Lineages identified								

Methods



Future activities

- Generate libraries and full genome sequences of all the PCR RVF positive isolates.
- Attempt to characterize the non RVF positive isolates using a metagenomics approach.
- Continue with pathogen isolation attempts in cell culture.

Anticipated results and conclusion

Outputs from this study will be pivotal in understanding RVF epidemiology, evolution, and pathogen co-circulation in the country and region. Identification of co-circulating pathogens is a step towards better understanding and response and update any existing baselines of zoonotic pathogen activity in a region.

References

- R. D. Sumaye,E.Geubbels, E.Mbeyela, andD.Berkvens, "Interepidemic transmission of rift valley fever in livestock in the Kilombero river valley,Tanzania: a cross-sectional survey," *PLoS Neglected Tropical Diseases*, vol. 7, no. 8,Article ID e2356, 2013.
- Bird BH, Githinji JW, Macharia JM, Kasiiti JL, Muriithi RM, Gacheru SG, et al. Multiple virus lineages sharing common recent ancestry were associated with a large Rift Valley fever outbreak among livestock in Kenya during 2006–2007. J Virol. 2008; 82:11152–66. doi:10.1128/JVI.01519-08

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