

Genomic Characterization of Rift Valley Fever Virus, South Africa, 2018

Appendix

Appendix Table 1. Primers used for amplification and sequencing of the Rift Valley Fever virus genomes, South Africa, 2018.

| Name | Segment, amplicon (binding site) | Sequence (5'–3') |
|--|----------------------------------|------------------------|
| Primers used during amplification and sequencing | | |
| RVF-LA-F | Large, amplicon A (1–17) | acacaaggcgccaatc |
| RVF-LA-R | Large, amplicon A (2182–2163) | GGCTCACCTGCTATTCTCTG |
| RVF-LB-F | Large, amplicon B (2040–2059) | ATCATGGAGGGCTTTGTCTC |
| RVF-LB-R | Large, amplicon B (3404–3384) | CTACTATCATCTGATCCTTGC |
| RVF-LC-F* | Large, amplicon C (4216–4233) | ggtgtgtgtcatcattg |
| RVF-LC-R | Large, amplicon C (6372–6352) | acacaaagaccgccaatattg |
| RVF-LH-F | Large, amplicon H (3018–3037) | GCTATGTGAGTTCACCTCTC |
| RVF-LH-R* | Large, amplicon H (4590–4570) | gtgtgagctagagttgcttc |
| RVF-MD-F | Medium, amplicon D (1–15) | acacaaagaccggtgc |
| RVF-MD-R* | Medium, amplicon D (1342–1326) | cctgaccattagcatg |
| RVF-ME-F* | Medium, amplicon E (771–790) | ccaaatgactaccagtcagc |
| RVF-ME-R | Medium, amplicon E (2284–2264) | GATAGCTCACTTGAGACAGTT |
| RVF-MF-F | Medium, amplicon F (1714–1732) | ATGGCTGCATAGTGTGTGC |
| RVF-MF-R | Medium, amplicon F (3885–3870) | cacaaagaccggtgc |
| RVF-SG-F* | Small, amplicon G (1–22) | acacaaagctccctagagatac |
| RVF-SG-R* | Small, amplicon G (1693–1677) | acacaaagaccctagtg |
| Primers used only for sequencing | | |
| RVF-LA-SF | Large, amplicon A (664–682) | AGACTGAGAGAGAGTTGCT |
| RVF-LA-SR | Large, amplicon A (874–855) | TCATTCCCTTCAGCAAAGAA |
| RVF-LC-SF | Large, amplicon C (5587–5606) | GCATCAGACAATGATCTCAG |
| RVF-LC-SR | Large, amplicon C (5744–5725) | tcacatatctcaaggatggc |
| RVF-MD-S | Medium, amplicon D (690–672) | ctttgcaatgatggtgc |
| RVF-MF-SF1 | Medium, amplicon F (2412–2431) | GCAGAGTTTTTCATTTGTTGG |
| RVF-MF-SF2 | Medium, amplicon F (3021–3040) | GCTTTCTCTAAGGGCTCTGT |
| RVF-SG-SF | Small, amplicon G (762–781) | CTCCAATCCCAGATGTTGAG |
| RVF-SG-SR | Small, amplicon G (1025–1007) | agccatgagaagaggagag |

*Published primers (1).

Appendix Table 2. Sequence differences between viruses RV2613–1/RSA/2018, RV2613–2/RSA/2018 and RV2613–3/RSA/2018, and other Rift Valley fever viruses with complete genome sequences available in GenBank.*

| Closest related isolates | | | | | |
|--------------------------|---------------|-------------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Isolate | Year isolated | Species; location | No. differences, segment L (%) | No. differences, segment M (%) | No. differences, segment S (%) |
| RV2613/RSA/2018 | 2018 | Ovine; Jacobsdal, FS, RSA | 0 | 2–5 nt (0.05–0.13) | 1 nt(0.06) |
| BIM-01/2016 | 2016 | Human; Beijing, China | 30 nt (0.47) | 22–26 nt (0.57–0.67) | 7–8 nt(0.41–0.47) |
| RVFBJ01/2016 | 2016 | Cell culture isolate of BIM-01_2016 | 29 nt (0.45) | 24–28 nt (0.62–0.73) | 7–8 nt(0.41–0.47) |
| Kakamas-09 | 2009 | Ovine; Kakamas, NC, RSA | 103 nt (1.61) | 78–82 nt (2.01–2.11) | 29–30 nt (1.72–1.78) |
| Entebbe-44 | 1944 | Mosquito; Entebbe, Uganda | 167 nt (2.62) | 116–120 nt (2.05–2.12) | 44–45 nt (2.60–2.66) |
| Ken Rintoul-57 | 1951 | Ovine; Kenya | 210 nt (3.29) | 129–130 nt (3.33–3.43) | 40–41 nt (2.36–2.42) |

*FS, Free State Province; NC, Northern Cape Province; nt: nucleotide; RSA, Republic of South Africa.

Reference

1. Grobbelaar AA, Weyer J, Leman PA, Kemp A, Paweska JT, Swanepoel R. Molecular epidemiology of Rift Valley fever virus. *Emerg Infect Dis.* 2011;17:2270–6.
<https://doi.org/10.3201/eid1712.111035>