Zika virus 1308258v

NCPV were not initially given any origin or strain information for this Zika virus, but partial sequencing of the Envelope gene[1] gave 98% identity to strain MR766 (DQ859059).

Further investigation with the depositor's records revealed that it is most likely to be **Strain MP1751**, isolated from Aedes africanus mosquitoes captured in Zika Forest, Uganda, in November 1962[2].

Metagenomic sequence analysis of NCPV batches #1420, #1421, #1315 indicated these are all most similar to the DQ859059 sequence of MR766. Phylogenetic analysis indicated that sequence DQ859059 is an outlier compared to the other sequences of MR766 available on Genbank.

The passage history prior to deposit with NCPV included up to four passages between 1962-1972, by an unknown method. This was followed by one passage in Vero cells in 2011.

See batch-specific Certificate of Analysis for number of passages in NCPV.

References

1. **Faye O, Faye O, Dupressoir A, Weidmann M, Ndiaye M and Sall AA (2008). One-step RT-PCR for detection of Zika virus. *J Clin Virol* 43:96-101.**
2. **Haddow, AJ, (1964). Twelve isolations of Zika Virus from *Aedes (Stegomyia) africanus* (Theobald) taken in and above a Uganda Forest. *Bull. Wld Hlth Org*. 31:57-69.**