Complete Genome Sequences of Five Zika Virus Isolates

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Zika virus is an emerging human pathogen of great concern due to putative links to microcephaly and Guillain-Barre syndrome. Here, we report the complete genomes, including the 5’ and 3’ untranslated regions, of five Zika virus isolates, one from the Asian lineage and four from the African lineage.

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| Isolate  | Source       | Location | Date        | Passage history | Genome/ORF size (nucleotides) | Accession no. |
|----------|--------------|----------|-------------|----------------|------------------------------|---------------|
| FSS13025 | Homo sapiens | Cambodia | 8/8/2010    | Vero × 4        | 10,807/10,272               | KU955593      |
| DAK AR D41671 | Aedes taylori | Senegal | 12/14/1984 | AP61 × 1, C6/36 × 1, Vero × 3 | 10,806/10,272 | KU955595      |
| DAK AR D41662 | Aedes taylori | Senegal | 12/6/1984  | AP61 × 1, C6/36 × 1, Vero × 3 | 10,806/10,272 | KU955592      |
| DAK AR D41525 | Aedes africanus | Senegal | 11/20/1984 | AP61 × 1, C6/36 × 1, Vero × 3 | 10,806/10,272 | KU955591      |
| MR-766   | Macaca mulatta | Uganda  | 4/1947     | SM × 150, Vero × 2  | 10,795/10,260               | KU955594      |

a AP61, Aedes pseudoscutellaris cells; C6/36, Aedes albopictus cells; SM, suckling mouse; Vero, African green monkey kidney cells.

b ORF, open reading frame.

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addition of ambiguous characters (N’s) onto the 5′ and 3′ ends of the reference.

The assembled, complete genomes (7) ranged in size from 10,795 to 10,807 nucleotides; the 5′ UTRs were 106 to 107 nucleotides and the 3′ UTRs were 428 to 429 nucleotides, respectively. The MR-766 stock we sequenced contained a 12-nucleotide in-frame deletion in the polyprotein, which it shared with AY632535, but is not present in LC002520. However, our sequence does not share the five additional single nucleotide insertions/deletions present in AY632535. All sequenced isolates contained the conserved, dinucleotide complimentary terminal sequences that are characteristic of the Flavivirus genus (5′ – AG . . . CU – 3′ [6]).

Nucleotide sequence accession numbers. Genome accession numbers to public databases are listed in Table 1.

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