

1 **Complete Coding Genome Sequence for a Novel Multicomponent Kindia Tick Virus**  
2 **Detected from Ticks Collected in Guinea**

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4 Running title: Genome Sequence for Kindia Tick Virus from Guinea

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## 25 ABSTRACT

26 Kindia tick virus (KITV) is a novel multicomponent virus first detected by direct sequencing of  
27 *Rhipicephalus geigy* ticks in Guinea in 2017. Here, we present a complete coding genome  
28 sequence for all four segments of KITV/2017/1. This virus appears to be evolutionarily related to  
29 unclassified flaviviruses, such as Alongshan virus.

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## 31 ANNOUNCEMENT

32 The multicomponent (segmented) tick flaviviruses evolutionarily related to the unsegmented  
33 viruses of the genus *Flavivirus* have been recognized since only 2014 (1-4). This group of  
34 unclassified segmented tick-borne flaviviruses now includes Alongshan virus, Jingmen tick virus  
35 (JMTV) and Mogiana tick virus (MGTV), which have been detected in Asia, Europe and South  
36 America, respectively. These diverse and globally distributed viruses are capable of infecting a  
37 wide range of hosts, such as ticks, animals and humans (1–8). However, only a few complete  
38 genome sequences have been reported for JMTV (Kosovo and China), Alongshan virus (China)  
39 and MGTV (Brasilia).

40 Here, we report the complete coding genome sequences for the first African isolate, named  
41 Kindia tick virus (KITV), from *Rhipicephalus geigy* collected from domestic cattle (*Bos taurus*)  
42 in Kindia, Guinea, West Africa. Twenty-six pools of 5 ticks each were frozen in liquid nitrogen,  
43 crushed by plastic pestles, homogenized in phosphate-buffered saline and used for RNA isolation  
44 with TRIzol reagent (Invitrogen Co., USA). Total RNA was quantified with a Qubit RNA Assay  
45 Kit (Invitrogen Co., USA) following the manufacturer's instructions. RNA-seq libraries were  
46 constructed with an NEBNext Ultra RNA Library Prep Kit for Illumina (New England Biolabs).  
47 Sequencing was performed using a MiSeq Reagent Kit v3 for 600 cycles. Cutadapt (version  
48 1.18) and SAMtools (version 0.1.18) were used to remove the Illumina adaptors and duplicate  
49 reads. After removing adapters, the read length was 108-118 bases, with the numbers of reads

per pool ranging from 151,282 to 540,929. The contigs were assembled *de novo* using the MIRA assembler with default parameters (version 4.9.6). In five pools, we found Mogiana-like fragments using BLASTN. These fragments were aligned to the reference genome segments of Mogiana tick virus isolate MGTV/V4/11 (4). The average coverage of the four segments was 35, 18, 52, and 30, respectively. The complete sequences for KITV/2017/1 were verified by Sanger sequencing of Seg 2 (2 short fragments), Seg 3 (1 sf) and Seg 4 (2 sf), with gaps or low coverage, as previously described (9). Total RNA from tick pools positive for KITV/2017/1 was used for first-strand DNA synthesis using a Reverta-L Kit (Interlabservice, Russia). The KITV/2017/1 genetic material was amplified by PCR with specific primers designed based on draft NGS sequences (available on request), with subsequent PCR fragment isolation and sequencing. The sequences for two detected KITVs (KITV/2017/1 and KITV/2017/2) were also deposited in GenBank. The nucleotide identity between KITV/2017/1 and KITV/2017/2 was 99.7% (Seg 1), 99.4% (Seg 2), 98.1% (Seg 3), and 99.3% (Seg 4). KITV contains putative open reading frames (ORFs) congruent with JMTV and MGTV, namely, nonstructural protein 1 (Seg 1), VP1 (Seg 2), NSP2 (Seg 3), VP2 and VP3 (Seg 4). The sizes of the sequenced segments (ORFs) are 2968 (2743), 2805 (2262), 2667 (2427) and 2725 (2351) bases, with CG contents of 52.3%, 54.9%, 54.4% and 54.2% for each segment, respectively. The lengths of the 5' UTR and 3' UTR were different for each segment and were 97-156 and 121-387 bases, respectively. The 5' UTR conservative motif GCAAGTGCA typical for JMTV was found in four segments, and the 3' UTR conservative motifs GGCAAGTGC and CAAGTG were also found in Seg 2 and Seg 4 of KITV. The divergence between KITV and MGTV/JMTV based on nucleotide sequence was 7–28% (Seg 1), 7.7–20.6% (Seg 2), 2.3–29.3% (Seg 3), and 0.4–22% (Seg 4), and based on amino acid sequences, it was 3.1–21.8% (Seg 1), 3.4–20.3% (Seg 2), 1.3–20.8% (Seg 3), and 0.2–15% (Seg 4), as evaluated by BLAST. Given these similarities, we suggest that KITV is a new member of the multicomponent (segmented) tick-borne flavivirus group and possibly represents a new species together with MGTV.

76 **Data availability.** GenBank accession numbers for the viral sequences: [MH678723](#) and  
 77 [MH678727](#) (Seg 1), [MH678724](#) and [MH678728](#) (Seg 2), [MH678725](#) and [MH678729](#) (Seg 3),  
 78 and [MH678726](#) and [MH678730](#) (Seg 4); complete sequences [MK673133](#) (Seg 1), [MK673134](#)  
 79 (Seg 2), [MK673135](#) (Seg 3), and [MK673136](#) (Seg 4); and Sequence Read Archive accessions  
 80 [SRX5930668](#) to [SRX5930671](#) under project [PRJNA545394](#). The annotations have also been  
 81 deposited into GenBank for these sequences.

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