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Inhangapi Virus: Genome Sequencing of a Brazilian Ungrouped Rhabdovirus Isolated in the Amazon Region

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We report here nearly complete genome sequence of Inhangapi virus (INHV) strain BEAR177325, which was isolated from a pool of sandflies (*Lutzomyia flaviscutellata*) in the Utinga neighborhood, Belém (01°28′S 48°27′W), State of Pará, Brazil, in 1969. The genome of this virus showed similarity with members belonging to the family *Rhabdoviridae*.

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The family *Rhabdoviridae* belongs to the order *Mononegavirales* and currently is composed of 67 members distributed in 11 genera and an unassigned genus (1). Rhabdoviruses are enveloped, have a helical nucleocapsid bullet shape, and are approximately 100 to 430 nm long and 45 to 100 nm in diameter. Rhabdoviruses have single-stranded, negative-sense, and nonsegmented RNA. The rhabdoviruses present five structural genes (N, P, L, M, and G) (2), accessory genes, and intergenic regions (3, 4). Viruses belonging to this family infect a variety of animals (vertebrates and invertebrates) and plants (5, 6), and transmission often requires arthropod vectors (mosquitoes, sandflies, and ticks) (1). Sigma virus (type species *Drosophila melanogaster* sigma virus [DmelSV]) is an exception, because it is transmitted vertically among parent flies (i.e., through both eggs and sperm) (5).

The Inhangapi virus (INHV) (BEAR177325) was isolated from a pool of sandflies (*Lutzomyia flaviscutellata*) in the Utinga neighborhood, Belém (01°28′S and 48°27′W) (7), State of Pará, Brazil, in 1969. The nearly complete genome of INHV is around 12,020 bp and contains the five typical rhabdovirus genes N, P, M, G, and L.

Classic tests, such as complement fixation and neutralization tests, and transmission electron microscopy suggest that INHV is a member of the family *Rhabdoviridae* (7).

INHV particles were precipitated using polyethylene glycol 8000 (PEG 8000) centrifugation, as previously described (4), and the supernatant was treated with DNase and RNase (Ambion) for host contaminant removing. RNA extraction was followed by full-length genome sequencing using two different next-generation sequencing platforms: GS FLX 454 (Roche Life Science) and Ion Torrent (Life Technologies). Regardless of the sequencing platform used, the method for obtaining the genome basically involved the following steps: RNA fragmentation, library preparation (cDNA), emulsion PCR, and sequencing, as previously described (8, 9). The sequencing steps were carried out at the genomic core of the Center for Technological Innovation, Evandro Chagas Institute, Brazilian Ministry of Health, Ananindeua, Brazil.

The genome was obtained employing a *de novo* hybrid assembly strategy using both Ion Torrent and GS FLX 454 reads with the software Mira 4.0. Visual inspection was performed with the software Geneious version 6.1.4. The total genome recovered was 12,020 nucleotides (nt) in length, with a mean coverage of 383-fold. The five main genes 3′-N−P-M-G-L-5′ were recognized, as well as the putative accessory gene (pAG1) between the G and L genes. This is the report of the nearly complete genome sequence for the original passage to INHV, an ungrouped Brazilian rhabdovirus.

Nucleotide sequence accession number. The nearly complete genome sequence has been deposited in GenBank under the accession number KR604694.

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