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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Novel Hantavirus Variant of Rio Mamoré Virus, Maripa Virus, from French Guiana

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We report the first complete genome sequence of Maripa virus identified in 2009 from a patient with hantavirus pulmonary syndrome in French Guiana. *Maripa virus* corresponds to a new variant of the *Rio Mamoré virus* species in the *Bunyaviridae* family, genus *Hantavirus*.

Hantaviruses are zoonotic negative-stranded RNA viruses belonging to the *Bunyaviridae* family, genus *Hantavirus*. These viruses are distributed throughout the world (3). While certain types are nonpathogenic in humans, others are responsible for hemorrhagic fever with renal syndrome in the Old World and hantavirus pulmonary syndrome (HPS) in the New World.

The presence of hantavirus in French Guiana, on the northeast coast of South America, was first suggested following a serological survey (5). A systematic serological screening was then implemented allowing the identification of a first native case of HPS in 2008 (4). This was followed by two more fatal cases, in 2009 and 2010. Molecular investigations demonstrated that they corresponded to the same strain, named Maripa virus (1, 4).

We report here the full genome sequence of Maripa virus, which was identified from a patient presenting with HPS in French Guiana in 2009. His serum was positive by IgM capture as described elsewhere (4). Total RNA was extracted from the lung using a NucliSens easyMAG bio-robot (bioMérieux). cDNA was prepared with SuperScript III reverse transcriptase (RT; Invitrogen). Sequence of the small (S), medium (M), and large (L) segments was generated by RT-PCR, using different combinations of primers. Overlapping amplicons were generated for each segment, cloned, and then sequenced by Beckman Coulter Genomics (Takeley, United Kingdom). One contig sequence of each segment was assembled using MEGA5 software (9).

The complete sequence of the S segment is 1,946 bp long, with a 5′ noncoding region (5′NC) of 40 bp, followed by a coding sequence of 1,287 bp and a 3′NC of 619 bp. The complete sequence of the M segment is 3,684 bp long, with a 5′NC of 48 bp, a coding sequence of 3,417 bp, and a 3′NC of 219 bp, while the complete sequence of the L segment is 6,562 bp long, with a coding sequence of 6,462 bp flanked by a 5′NC of 34 bp and a 3′NC of 66 bp. A full-genome BLAST search returned the Bolivian Rio Mamoré virus as the closest match for the three segments. Pairwise alignment of the predicted gene products among Maripa virus and the other New World hantaviruses showed the highest amino acid identities with Rio Mamoré virus, with the N, Gn/Gc precursor, and L proteins having 97.7%, 96.4%, and 95.8% identities, respectively.

Phylogenetic analyses, based on the coding region of the three segments, were conducted using the Bayesian approach (8) with previously published Hantavirus sequences. They showed, for each segment, that Maripa virus is closely related to Rio Mamoré virus, whose different strains have formerly been reported in Western Paraguay, Bolivia, Peru, and the Amazonian region of Maranhão, Brazil (1, 2, 6).

These data present the first complete genome sequence of Maripa virus and demonstrate that it corresponds, according to the International Committee on Taxonomy of Viruses (ICTV) criteria (7), to a new strain of the Rio Mamoré virus species that widely circulates in South America.

Nucleotide sequence accession numbers. GenBank accession numbers of the S, M, and L segments of Maripa virus are JQ611712, JQ611713, and JQ611714, respectively.

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