

Characterization of the Bujaru, frijoles and Tapara antigenic complexes into the sandfly fever group and two unclassified phleboviruses from Brazil

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Abstract

The genus *Phlebovirus* includes the sandfly fever viruses and tick-transmitted uukuviruses. Sandfly fever group viruses have been isolated from various vertebrate species and from phlebotomines and occasionally alternative arthropods, e.g. mosquitoes, or ceratopogonids of the genus *Culicoides*. Uukuniemi serogroup viruses have been isolated from various vertebrate species and from ticks. Despite the public health importance of some viruses of the genus, the genomic diversity of phleboviruses that could be incriminated as causative of human or veterinary diseases remains underestimated. Here we describe the nearly complete sequences and genomic characterization of two phleboviruses belonging to the Bujaru antigenic complex: the prototype species and the Munguba virus. Furthermore, six previously unclassified phleboviruses isolated in Brazil were also sequenced and characterized: Ambe, Anhangá, Joa, Uriurana, Urucuri and Tapara viruses. The results of the phylogenetic analysis indicated that these viruses group with viruses of three antigenic complexes (Bujaru, Tapara and frijoles clades), with two unclassified phleboviruses. We also performed genomic reassortment analysis and confirmed that there were no events for the viruses described in this study, but we found a new potential reassortment in Medjerda Valley virus, which contains S and L segments of Arbia virus, and probably a unique M segment, both viruses circulate in the same geographic region, indicating these two isolates represent two distinct viruses. This study provides insights into the genetic diversity, classification and evolution of phleboviruses.

INTRODUCTION

At present, more than 350 named bunyaviruses are subdivided into order Bunyavirales based on serological, morphological and genomic features [1]. Of these, the genus *Phlebovirus* is composed of approximately 70 named viruses, which, based on serological methods, are classified into two antigenic groups: the phlebotomus fever (or sandfly fever) group and the Uukuniemi group [2].

Phleboviruses possess a genome organization typical of other members of the order Bunyavirales, with a tripartite negative-sense RNA genome with components named as

large segment (LRNA), which encodes the viral RNA-dependent RNA polymerase (RdRp); medium segment (MRNA), which encodes two envelope glycoproteins (Gn and Gc) and a non-structural protein (NSm); and small segment (SRNA), with an ambisense coding strategy, which encodes the viral nucleocapsid (N) protein in the negative-sense orientation and a non-structural protein (NSs) that is encoded in the positive sense [2, 3].

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Received 11 October 2016; Accepted 26 January 2017

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Keywords: phleboviruses; genetic characterization; sandfly fever group; ungrouped phlebovirus; Brazilian Amazon.

Abbreviations: CF, complement fixation; ML, maximum likelihood; RdRp, RNA-dependent RNA polymerase.

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Three supplementary figures and three supplementary tables are available with the online Supplementary Material.