

Genetic Characterization of Small (s)-Segment Genome Puumala Virus Strain Kazan

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Abstract

© 2016, Springer Science+Business Media New York. The Republic of Tatarstan is one of the most active endemic regions for nephropathia epidemica (NE) in the Russian Federation. Annually, over 1000 cases of NE are registered, with an average mortality rate of 0.43 %. NE is a zoonosis where human become infected by inhaling a hantavirus-contaminated aerosol. Puumala virus is commonly detected in NE cases. Although NE cases have been registered in the region since 1958, little is known about the genetic variability of Puumala virus circulating in Tatarstan. We conducted phylogenetic analysis of the full length (1828 nt) small (S) segment genome sequence of Puumala virus RNA isolated from four bank voles (*Myodes glareolus*) captured during the 2014 outbreak. These virus sequences were compared to known sequences of Puumala viruses from nearby regions such as Samara and the Republic of Bashkortostan, as well as to European isolates. We found that there was over 89 % nucleotide identity between Puumala virus sequences isolated from the bank voles captured in Tatarstan. Sequence identity between Puumala viruses from the Tatarstan bank voles and the sequences from Republic of Bashkortostan and the Samara region were 90–95 %. Less similarity was found between Tatarstan sequences and Puumala strains circulating in Europe (79.7–87.7 %). Taken together, these data suggest that Puumala viruses circulating within the bank vole population in the Republic of Tatarstan are phylogenetically closer to the viruses circulating in neighboring regions of Russia.

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Keywords

Bunyaviridae, Hantaviruses, Hemorrhagic fever with renal syndrome (HFRS), Nephropathia Epidemica (NE), Puumala virus, S-segment

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