Секция «Вирусология»

Puumala orthohantavirus genetic variation in the Volga Federal District

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The Volga Federal District (VFD) of Russia is endemic for hemorrhagic fever with renal syndrome (HFRS), with *Puumala* orthohantavirus (PUUV) been identified as the main cause of the disease [1]. PUUV is carried by bank vole and its genome contains three segments: small (S), medium (M), and large (L) [2]. Well-characterized 8 genetic lineages of PUUV have been identified in Eurasia [3]. However, the genetic variation of PUUV strains in the VFD is not well understood.

Rodents were captured in Ulyanovsk oblast (UO) and the Udmurtia Republic (UR). Total RNA was extracted from lung tissues of bank voles and used for RT-PCR analysis. Twelve PCR amplicons containing the full S segment coding sequences (CDS) (1302 bp) were obtained and used for DNA sequencing. For comparisons, we used Mega 6 program and sequences from the Genbank database.

Out of the 117 samples, 14 were PUUV RNA positive. Comparison analysis revealed high similarities among the sequences obtained from PUUV strains captured within the same site. The lower identity was observed when comparing sequences from different trapping sites and previously identified PUUV sequences in Russia.

All identified UR and UO PUUV sequences belong to the RUS genetic lineage. Phylogenetic analysis revealed that UO and UR PUUV S segment CDS formed three (3) subclades according to their trapping sites (Figure 1). Samples from UR formed subclade 1, while subclade 2 and 3 contained strains from UO. Interestingly, UO samples were captured in the left and right bank of the Volga River areas, respectively. Subclade 2 samples fell in the branch with samples from the Republic of Tatarstan (RT), whilst samples in Subclade 3 did not belong to any previously identified PUUV strain sublineages of RUS lineage. These discrepancies of UO sequences could be a result of the Volga River, which acts as a natural barrier to the movement of bank voles.

One genetically distinct of PUUV group was identified in UO. These results could suggest the existence of another PUUV genetic sublineage in the central areas of UO. This data could aid in the understanding of PUUV variations in these areas.

This work is part of Kazan Federal University Strategic Academic Leadership Program. Part of this work was conducted with the support of RFBR perspective grant 19-34-60012 given to Emmanuel Kabwe.

References

1) Davidyuk, Y.N., Kabwe, E., Shakirova, V.G., Martynova, E.V., Ismagilova, R.K., Khaertynova, I.M., Khaiboullina, S.F., Rizvanov, A.A. and Morzunov, S.P. Characterization of the Puumala orthohantavirus strains in the northwestern region of the Republic of Tatarstan in relation to the clinical manifestations in hemorrhagic fever with renal syndrome patients // Frontiers in pharmacology. 2019, №10, p.970.

2) Plyusnin, A., Vapalahti, O. and Vaheri, A. Hantaviruses: genome structure, expression and evolution // Journal of General Virology. 1996, №77(11), pp.2677-2687.

3) Castel, G. et al. Complete Genome and Phylogeny of Puumala Hantavirus Isolates Circulating in France // Viruses. 2015, №7(10), pp.5476–5488.

Illustrations

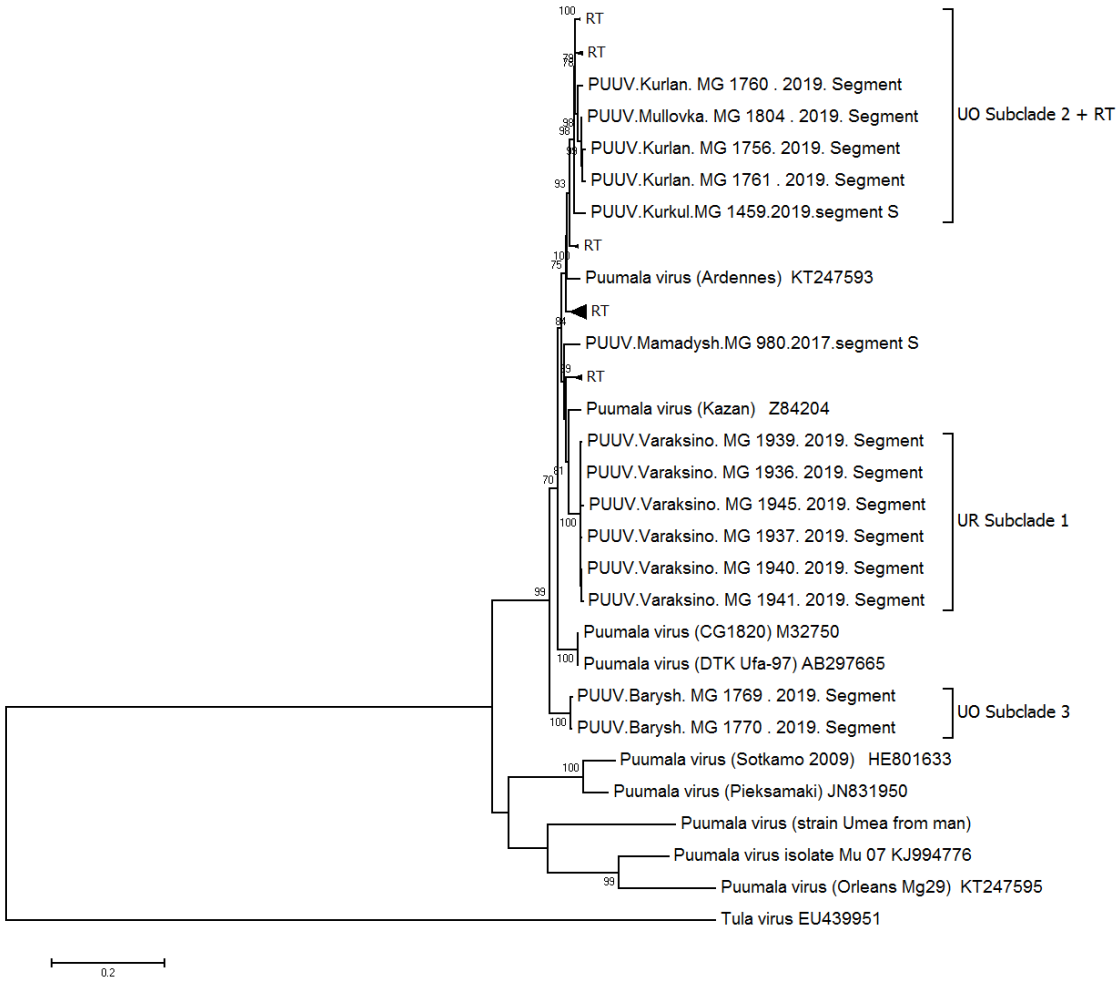

Рис. 1. Figure 1 Phylogenetic tree calculated based on the full coding region (CDS) of PUUV S segment sequences obtained from bank voles trapped in Ulyanovsk oblast and Udmurtia Republic.