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GENOTYPIC DIFFERENTIATION AND EVOLUTIONARY DYNAMICS OF *PUUMALA ORTHOHANTAVIRUS* (PUUV)

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Abstract

PUUV is a causative agent of haemorrhagic fever with renal syndrome [1]. Its current classification is not standardized and relies on geographic lineages, but inconsistencies arise between the names of the lineages and their actual distribution, and in some cases, intralineage genetic diversity is higher than interlineage diversity. In this study, we propose a standardized classification based on genetic distances to resolve taxonomic ambiguities.

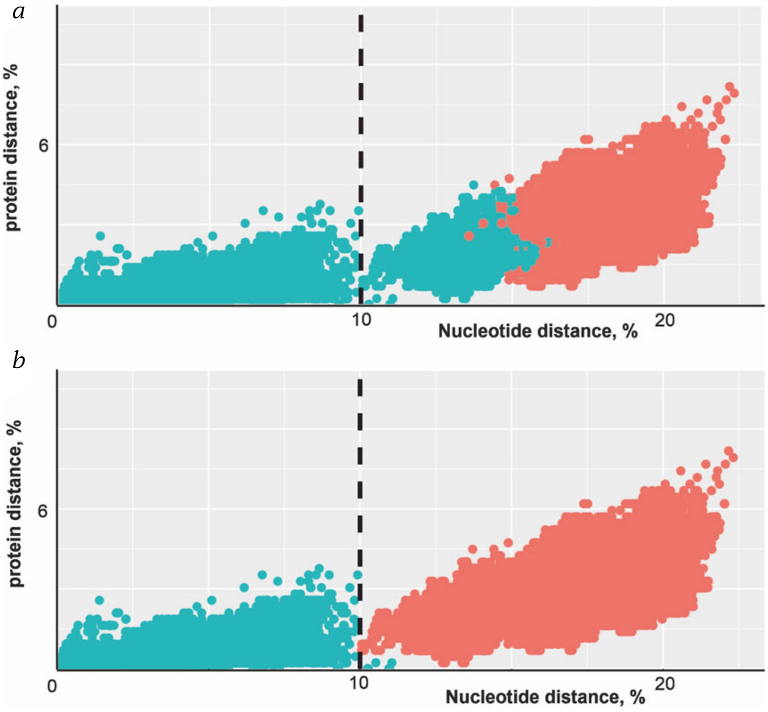
Materials and methods

We analyzed 505 complete S segment sequences from GenBank, focusing on the gene encoding nucleocapsid protein. Recombination and reassortment events were assessed using RDP4 [2], GIRaF [3], and phylogenetic incongruence analysis. Pairwise nucleotide and amino acid sequences were calculated for all possible pairs of sequences. Each pair of sequences in the dataset was represented by a dot on the plot with coordinates reflecting the nucleotide and amino acid sequence distance between them. Each dot was coloured according to whether the virus pair consisted of inter- or intragroup viruses (see figure).

Results

A “10 % nucleotide difference” threshold was applied to delineate genotypes.

PUUV was subdivided into 21 distinct genotypes, with lineages like CE, RUS, FIN, and N-SCA further divided into geographically coherent subgroups. Reassortment events were rare but detected, confirming segment exchange in PUUV evolution. The S segment, due to its stability and low recombination frequency, proved optimal for phylogenetic analysis.



Scatter plot of amino acid and nucleotide distances for pairs of PUUVs S segments: *a* — intralineage virus pairs were indicated by cyan dots, interlineage virus pairs by red dots. Lineage assignments were made according to [4, 5]. The threshold of 10 % nucleotide difference is shown as a vertical dashed line; *b* — implementation of tentative quantitative criteria for the PUUV taxonomic assignment at the subspecies level. Intracluster virus pairs (difference less than 10 % nucleotide distance) are indicated by cyan dots, intercluster (difference more than 10 % nucleotide distance) virus pairs by red dots. The threshold of 10 % nucleotide difference is indicated as a vertical dashed line

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Conclusion

The proposed 10 % nucleotide difference criterion provides a robust, quantitative framework for PUUV genotyping, enhancing taxonomic clarity and reflecting evolutionary relationships. This study highlights limitations of geographic-based classification.

Significance

This work suggests a more transparent hantavirus taxonomy, offering a reproducible method for genotype classification that can be extended to other segmented RNA viruses. It underlines the applicability of genetic distance metrics to viral phylogeny.

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