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Heterogeneity of the distribution of genetic variants of the rabies virus in the territory of the Russian Federation

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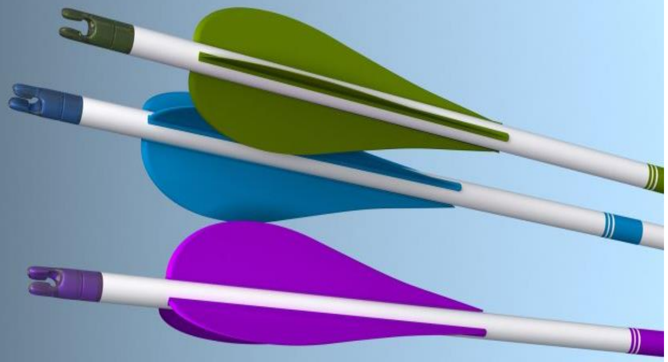
Rabies

- Rabies is a disease that poses a huge threat, both in medical and veterinary aspects.
- To control the relevance of traditional vaccine strains, it is necessary, among other things, to monitor changes in the genome of various "wild" strains.

Rabies

Selection of sequences



The selection of sequences for the study

was carried out according to the description in the GenBank database.

- Phylogenetic analysis of nucleotide sequences was carried out using the MEGA X program with an open license.
- The construction method was the maximum likelihood method incorporated in the program algorithms.

The selection of sequences for the study

- Before phylogenetic analysis, automatic alignment of sequences was carried out, which was incorporated in the MEGA X program using the Alignment Clustal W algorithm.
- Two phylogenetic trees were built: according to the N (nucleoprotein) gene sequences and according to the G (glycoprotein) gene sequences.

Research results

- Analysis of phylogenetic trees showed the presence of clusters of closely related sequences from a number of regions (Lipetsk region, Tyva, Altai) with the simultaneous presence of heterogeneous clusters into which sequences from different regions were combined.
- From the point of view of molecular evolution, this fact suggests that *in a number of regions of the country there are conditions for the isolated circulation of genetic variants*.

- Carriers of the rabies virus are migrating from region to region.
- After adding to the analysis additionally those nucleotide sequences that were obtained in other countries, it is possible to see the distribution of rabies virus gene sequences obtained in Russia over various groups of sequences.
- Therefore, we see the absence of a single phyletic group with the sequences of any other countries.

Research perspectives

- The results are confirmed by constructing trees for both genes.

- It can be assumed that in the future the heterogeneity of strains will continue to increase, and in the future, updating of vaccine strains of the rabies virus will be required.