GENETIC VARIABILITY OF VESICULAR STOMATITIS PHOSPHOLIPID GENE ISOLATED FROM VARIOUS HOSTS

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Abstract
The study analyzed the genetic heterogeneity of the vesicular stomatitis virus (VSV) phospholipid gene among isolates obtained from various host and different geographical regions. 40 nucleotide sequences were analyzed with MEGA 10. Results showed the high level of nucleotide polymorphism of VSV phospholipid gene and differentiation of strains due to their serotype.
Keywords: *vesicular stomatitis virus, the phosphoprotein gene, phylogenetic analysis*

Introduction. The vesicular stomatitis virus (VSV) is an RNA-containing virus that belongs to the *Rhabdoviridae* family. VSV is classified into two main serotypes: New Jersey and Indiana, and is known to cause outbreaks among cattle, pigs, and horses [1]. Infections induced by VSV generally do not lead to high mortality rates; however, they have significant economic consequences due to potential losses in livestock production [2]. The VSV genome consists of 11161 nucleotides in length and encodes five structural proteins: phospholipid, nucleoprotein, glycoprotein, matrix protein, and RNA-dependent RNA polymerase.

The purpose of the presented study was to study genetic heterogeneity of nucleotide sequences of VSV phospholipid gene between various isolates of different hosts, collection date and countries.

Materials and methods. To analyze genetic heterogeneity 40 nucleotide sequences of VSV phospholipid gene were downloaded from NCBI Virus database (https://www.ncbi.nlm.nih.gov/labs/virus/vssi/#/). The sequences were selected according to their collection date, geographic location, host and serotype. The analysis was carried out using MEGA 10 program [3].

Results and discussion. Currently there are 1225 nucleotide sequences of VSV phospholipid gene are submitted to the NCBI Virus database (accessed on April 22, 2025). They represent several geographical regions: the most are from countries of Southern and Northern America, and several from Europe (Spain). The selected in the presented study sequences were combined in the groups based on the host: isolated from *Bos taurus* (21 sequences), *Equus caballus* (11 sequences), *Sus scrofa* (5 sequences) and insects (3 sequences); the followed countries were taken in the analysis: Argentina, Brazil, Costa Rica, Canada, Columbia, Ecuador, Honduras, Mexico, Panama and the USA; selected isolates were collected before 2000 and after 2013 year to compare the most temporary distinct samples.

Results of the comparative analysis revealed that the most diverse group of samples was isolated from *B. taurus* and the least – from insects (table 1). The genetic

variability between nucleotide sequences was defined as nucleotide polymorphisms (up to 4-nucleotide fragments), deletion / insertion (up to 8 nucleotide fragments).

Table 1. Percentage of informative sites in phospholipid gene sequences.

Isolation source (Host)	Nucleotide sites, %		
	Variable	Parsimony informative	Singleton
Bos taurus (n=21)	76	72	5
Equus caballus (n=11)	71	63	7
Sus scrofa (n=5)	64	40	23
Insects (n=3)	55	-	53

The highest level of singleton sites was detected for strains isolated from insects although it may be due to few samples analyzed. Totally, among all samples high level of nucleotide polymorphism was observed.

The dendrogram of genetic similarity based on nucleotide sequences of phospholipid gene revealed that differentiation between various strains was occurred in accordance with virus serotype – New Jersey, Indiana or none albeit the differentiation was not strict. The host, geographic location and collection date did not affect combining strains into clusters. It could suggest that observed genetic variability of VSV phospholipid gene does not associate with virus adaptation neither to different hosts nor to geographic regions. The differentiation of VSV strains according to serotype groups and geographic distribution based on variable regions of phosphoprotein and glycoprotein genes and whole genome sequences was shown in several studies [4, 5]. However, such studies were analyzed distribution of virus within countries, such as various states in the USA, and the authors indicated high level of genetic diverse between isolates of the same serotype.

Conclusions. The results obtained in the presented research showed high level of genetic variability of VSV phospholipid gene sequences among various strains. The differentiation of strains was connected with serotype but not the host, geographic location or collection date.

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