Comparative genome analysis of related *Lymantria dispar* nucleopolyhedrovirus isolates differing in virulence

Yu. Ilinsky^{1, 2, 3}, E. Lunev², S. Toshchakov^{2, 4}, J. Podgwaite⁵, V. Martemyanov^{6, 7}*

¹ Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

² Immanuel Kant Baltic Federal university, Kaliningrad, Russia

³ Novosibirsk State University, Novosibirsk, Russia

⁴ Winogradsky Institute of Microbiology, Moscow, Russia

⁵ USDA Forest Service, Hamden, USA

⁶ Institute of systematics and ecology of animals SB RAS, Novosibirsk, Russia

⁷ National Research Tomsk State University, Tomsk, Russia

* e-mail: martemyanov79@yahoo.com

Key words: nucleopolyhedrovirus, Lymantria dispar, NGS, genome, virulence

Motivation and Aim: Nucleopolyhedroviruses (NPVs, Baculoviridae) are specific viruses of insects that are used for pest control. High variation in virus virulence depends upon genetic factors [1]. Here we compare genomes of closely related genetic variants of *Lymantria dispar* multiple NPV (LdMNPV) that differ in virulence.

Methods and Algorithms: Five viral genotypes, differing in virulence, were isolated from the standard strain of NPV in the biopesticide "Gypchek" [2]. Complete genomes of these five genotypes were sequenced using Illumina technology by paired end sequencing of fragment genomic libraries, and assembled by SPAdes 3.9.0 [3]. Initial assemblies consisted of 1–3 scaffolds with a total assembly length of 159–174 kbp. Genome coverage was in range of 200x–850x. Closing of scaffold gaps was performed by Sanger sequencing of amplicons. To determine genetic relatedness among studied LdMNPV variants a phylogenetic tree was reconstructed based on a set of core loci. Comparative analysis of candidate genes was performed to reveal genetic determinates of variation in virulence.

Results: Phylogenetic analyses indicated recent divergence of LdMNPV-studied isolates from a common ancestor. We found a number of nonsynonymous nucleotide substitutions and *indels* in many genes. However, we could not find a locus that could be considered as the main effector of observed variation in virulence. This fact indicated a complex genetic nature of virulence variation among closely related virus isolates.

Conclusion: Variation in virulence among related LdMNPV isolates can be explained by the complex effect of different loci.

Acknowledgements: the study was supported by RSF (grant No. 17-46-07002).

References

- 1. Martemyanov V.V. et al. (2017) A comparison of the adaptations of strains of Lymantria dispar multiple nucleopolyhedrovirus to hosts from spatially isolated populations. Journal of Invertebrate Pathology. 146:41-46.
- 2. Podgwaite J.D. et al. (2013) Potency of Nucleopolyhedrovirus Genotypes for European and Asian Gypsy Moth (Lepidoptera: Lymantriidae). Journal Entomological Science. 48(4):332-344.
- 3. Bankevich A. et al. (2012). SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Computational Biology. 19(5):455-477.