

WHOLE GENOME SEQUENCING OF TWO HUNGARIAN RANAVIRUS STRAINS ISOLATED FROM BROWN BULLHEADS (*AMEIURUS NEBULOSUS*)

S.L. Farkas¹, A. Doszpoly^{1,*}, R. Borzak¹, K. Banyai¹, T. Juhasz²

^{1,*}*Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences, Budapest, Hungary*

²*National Food Chain Safety Office, Veterinary Diagnostic Directorate, Budapest, Hungary*

Members of the genus *Ranavirus* in the family *Iridoviridae* infect lower vertebrates: fish, amphibians and reptiles. Ranaviruses are known to cause acute, systemic disease and are often associated with mass mortality events. In brown bullheads (*Ameiurus nebulosus*) the disease is generally severe, pathologic/histopathologic changes are dominated by necrotic lesions in the kidneys and the spleen, and haemorrhages in the gills, the skin and internal organs.

In Hungary in the last decade ranavirus infection was frequently detected by virus isolation and virus specific PCR assays in connection with haemorrhagic syndrome and high mortality of brown bullheads. In order to obtain more information about the strains circulating in Hungary we decided to determine the whole genome sequence of isolates 13051/2012 and 14612/2012. Viruses were propagated in EPC and BF-2 cell lines. After freezing and thawing the infected cell culture PEG 6000 solution was used to concentrate viral particles, then DNA was purified and the samples were prepared for next generation sequencing. Sequencing was carried out on a 316 chip using Ion Torrent semiconductor sequencing equipment (Ion Personal Genome Machine_ [PGMTM], Life Technologies). The genome sequences were assembled applying the CLC Bio software (<http://www.clcbio.com>).

Nucleotide sequence analysis revealed 99.7 and 99.9 % identity to the European catfish virus (ECV; JQ724856) available in GenBank. We could identify all described ORFs of ECV in both studied genomes. The highest variability was observed in ORFs 105R and 105L giving the possibility for differentiation between strains within the same virus species, phylogenetic calculations and epidemiological follow-up.

Acknowledgements: "This study was supported by KTIA-AIK-12-1-2013-0017 Grant", the OTKA PD104315 and the Momentum program of the Hungarian Academy of Sciences (HAS).