

## MOLECULAR DETECTION AND GENOME ANALYSIS OF CIRCOVIRUSES OF EUROPEAN EEL (*ANGUILLA ANGUILLA*) AND SICHEL (*PELECUS CULTRATUS*) FROM LAKE BALATON, HUNGARY

**R. Borzák\*, B. Sellyei, Cs. Székely, A. Doszpoly**

*Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences, Budapest, Hungary*

The effect of the climate change on pathogen distribution is being examined in the framework of a national monitoring program 'Bioclimate' in Hungary. In the project freshwater fishes were screened for the presence of circoviruses, as well.

Circoviruses are small, non-enveloped viruses with a circular single-stranded (ss) DNA genome ranges about 1.3-2.3 kb in size. The genome contains at least two open reading frames (ORF), positioning in opposite directions and encoded replication (Rep) and capsid (Cap) proteins.

For the detection of circoviruses a broad-spectrum nested PCR was used targeting a conserved region of the Rep gene. In case of positive results inverse nested PCR or RCA were carried out to amplify the remaining part of the circular genomes.

Surprisingly, high prevalence of circoviral DNA was detected in the European eel (*Anguilla anguilla*) population in Lake Balaton. Nineteen out of 31 eels proved to be positive by PCR. Comparing the partial rep-like sequences, 11 of them have identical nucleotide sequences with the previously described European eel circovirus (EeCV) (Doszpoly et al., 2014). Eight samples were similar to the above mentioned ones with 96% nucleotide identity and were identical to the rep-like sequence originating from a sichel (*Pelecus cultratus*) caught also in Lake Balaton.

Until now, the complete genome sequencing of 11 eel and one sichel circoviruses were completed successfully. Ten of the newly sequenced eel circovirus genomes were identical with the formerly reported EeCV genome while the remaining eel circovirus and the sichel circovirus genomes showed 100% nucleotide similarity to each other.

Circoviruses were described as host-specific or narrow host range microorganisms. To the best of our knowledge, this is the first report about the detection of very similar circovirus related sequences (probably the same virus species) in various, distantly related fish species.

This study was supported by KTIA-AIK-12-1-2013-0017 and OTKA PD104315 grants and by the János Bolyai Research Scholarship of the Hungarian Academy of Sciences.