

FULL GENOME ANALYSIS OF FOUR CIRCOVIRUSES NEWLY DETECTED IN LOWER VERTEBRATES (FISHES, FROGS AND A TURTLE)

ZOLTÁN LÁSZLÓ TARJÁN, JUDIT J. PÉNZES, ANDOR DOSZPOLY, MÁRIA BENKŐ

Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences
Hungaria krt. 21, H-1143 Budapest, Hungary

In the past couple of years, members of the *Circoviridae* family have been demonstrated in representatives of a sharply increasing number of animal species worldwide. Moreover, the metagenomic approaches led to the discovery of numerous novel circoviral sequences in different environmental samples, such as sewage waters, fecal samples, raw meat products, as well as in novel vertebrate and invertebrate hosts. The first circoviruses found in fish have been described in Hungary recently. By screening of lower vertebrates, we detected several novel circovirus-like sequences in samples from fish, amphibians and a reptile. Here we report the full genomic sequence of the putative circoviruses, found in a common bream (*Abramis brama*), in a European eel (*Anguilla anguilla*), in two captive-bred green tree frogs (*Litoria caerulea*) and in a red-eared slider (*Trachemys scripta elegans*). Initial detection of the viruses was by a consensus nested PCR targeting the most conserved (~ 350-bp) fragment of the replication-associated protein gene (*rep*). For the acquisition of the entire genome, we used inverse nested PCRs with specific primers designed from the respective *rep* sequences. The full *rep* sequence of each of the four viruses showed clear homology to its counterparts in previously described circoviruses, however the putative capsid protein genes were more divergent. Accordingly, the size of the full genomes also showed considerable differences. In phylogenetic analyses, the two piscine and the frog circoviruses clustered into the *Circovirus* genus. However, the genome arrangement of the slider virus resembled that of cycloviruses, recently proposed as a novel genus of the *Circoviridae*. The eventual pathogenic role of these newly characterized viruses is unclear. The bream and the frogs seemed to be healthy. The eel showed typical signs of the so-called cauliflower disease. The red-eared slider had a concurrent adenovirus infection and one-sided bacterial otitis. Support: OTKA K100163.