

Molecular comparison of sturgeon alloherpesviruses

Andor Doszpoly, Igor, S. Shchelkunov, Thomas B. Waltzek

Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian

Academy of Sciences, Budapest, Hungary

Department of Infectious Disease and Pathology, College of Veterinary Medicine, University of Florida, Gainesville, USA

All Russia Research Institute for Veterinary Virology and Microbiology, Pokrov, Russia

Alloherpesviruses constitute a significant group of pathogens of cultured fish and therefore are of great veterinary importance worldwide. This study focuses on the molecular characterization of alloherpesviruses of sturgeon species in Eastern Europe and North America. One of the most important viral disease of sturgeon species in aquaculture is caused by the Acipenserid herpesvirus 2 (AciHV-2). The virus belongs to the *Ictalurivirus* genus within the family *Alloherpesviridae*, under the order *Herpesvirales*.

In North America, the herpesviral diseases of sturgeons were described decades ago from white sturgeon (*Acipenser transmontanus*). Later, novel AciHV-2 strains were found in shortnose sturgeon (*Acipenser brevirostrum*) and lake sturgeon (*Acipenser fulvescens*). In Russia, alloherpesviruses were isolated from Siberian sturgeon (*Acipenser baerii*) in the new millennium. An approximately 8000-bp-long fragment, between two well conserved genes, was amplified and sequenced from all genomes. In terms of position, orientation and size of the ORFs, the organization of the sequenced genome fragment was identical or very similar to the corresponding genome part of the firstly sequenced AciHV-2 isolated from white sturgeon. Serological comparison assays also suggest that these viruses belong to the same virus species, the *Acipenserid herpesvirus 2*.

Although, herpesviruses are considered to be host specific viruses, it seems that the AciHV-2 could cause disease in different sturgeon species. Besides the above mentioned species, the Russian sturgeon (*Acipenser gueldenstaedti*), the sterlet (*Acipenser ruthenus*) and some sturgeon hybrids seem to be susceptible to the AciHV-2. The closest relatives of AciHV-2 are *Ictalurid herpesvirus 1* and *2*. These viruses infect catfish species, and their genomes have balanced G+C content. However, the AciHV-2 genome has low G+C content, this fact and the high mortality caused by the virus suggest that the virus has not co-evolved with the sturgeons, but represents a host switch.

The financial support was provided by the grant OTKA PD104315.