Phylogenetic analysis of a Newly Discovered European Perch Herpesvirus and the Development of a Real-time Quantitative PCR Assay for its Detection

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European perch, *Perca fluviatilis,* can be infected by a disease that presents as white nodules on the skin. Histological studies and transmission microscopic images suggested a herpesvirus as the causative agent. PCR amplification and sequencing of a segment of the DNA polymerase gene from DNA extracted from nodules supported identification of the virus as a member of the *Alloherpesviridae* Family. A 79,727 base pair contiguous nucleotide sequence of the viral genome was generated by high-throughput sequencing. This study begins with the foregoing work completed. An annotation of the 79,727 base pair contiguous sequence identified several genes, including full-length sequences for the DNA polymerase catalytic subunit and the terminase gene. Phylogenetic reconstructions were generated by Maximum Likelihood, Neighbour Joining and Bayesian Inference methods, using nucleotide and amino acid sequences, for each gene separately and in concatemers, for full-length and for partial gene sequences. A total of 36 trees place the perch herpesvirus (PeHV-2) as sister-species to a cluster that infects catfish and sturgeon and distantly to those that infect carp. A real-time quantitative PCR assay targeting the terminase gene of PeHV-2 was developed as a tool to survey the presence and amount of virus in infected fish, and DNA extracted from different tissues of infected perch was subjected to the assay.