Viral haemorrhagic septicaemia virus (VHSV) genotype II isolated from European river lamprey Lampetra fluviatilis in Finland during surveillance from 1999 to 2008

We examined the occurrence of viral haemorrhagic septicaemia virus (VHSV) in the main spawning stocks of wild European river lamprey Lampetra fluviatilis in the rivers of Finland from 1999 to 2008. Pooled samples of internal organs (kidney, liver and heart or brain) from 2621 lampreys were examined for the presence of VHSV by standard virological techniques. VHSV was isolated from 5 samples from the rivers Lestijoki and Kalajoki, which flow from Finland into the Bothnian Bay of the Baltic Sea. The presence of VHSV was confirmed by immunofluorescent antibody technique (IFAT), ELISA and RT-PCR. Phylogenetic analysis based on the full-length VHSV glycoprotein (G) gene sequence revealed that the isolates were most closely related to the VHSV strain isolated in 1996 from herring Clupea harengus and sprat Sprattus sprattus in the Eastern Gotland Basin of the Baltic Sea, and were therefore assigned to VHSV genotype II. The partial G gene sequences obtained (nt 1 to 672–1129) of all 5 lamprey VHSV isolates were identical, and so were the entire G genes (nt 1 to 1524) of 2 isolates sequenced. The virulence of one of the lamprey isolates was evaluated by an experimental infection trial in rainbow trout Oncorhynchus mykiss fry. No mortality was induced postinfection by waterborne and intraperitoneal challenge, respectively, while 2 genotype Id isolates originating from Finnish rainbow trout caused marked mortality under the same conditions. The infection in the European river lamprey is thought to be independent from the epidemic in farmed rainbow trout in Finnish brackish waters, because the isolates from rainbow trout were of a different genotype. This is the first report of VHSV found in the European river lamprey. The role of wild river lampreys in maintaining the infection in the marine environment remains unclear.
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