European freshwater VHSV genotype Ia isolates divide into two distinct subpopulations - DTU Orbit (24/01/2019)

**European freshwater VHSV genotype Ia isolates divide into two distinct subpopulations**

Viral haemorrhagic septicaemia (VHS), caused by the novirhabdovirus VHSV, often leads to significant economic losses to European rainbow trout production. The virus isolates are divided into 4 distinct genotypes with additional subgroups including sublineage Ia, isolates of which are the main source of outbreaks in European rainbow trout farming. A significant portion of Danish rainbow trout farms have been considered endemically infected with VHSV since the first disease outbreak was observed in the 1950s. However, following a series of sanitary programs starting in 1965, VHSV has not been detected in Denmark since January 2009. Full-length G-genes of all Danish VHSV isolates that were submitted for diagnostic analyses in the period 2004–2009 were sequenced and analysed. All 58 Danish isolates from rainbow trout grouped with sublineage Ia isolates. Furthermore, VHSV isolates from infected Danish freshwater catchments appear to have evolved into a distinct clade within sublineage Ia, herein designated clade Ia-1, whereas trout isolates originating from other continental European countries cluster in another distinct clade, designated clade Ia-2. In addition, phylogenetic analyses indicate that VHSV Ia-1 strains have caused a few outbreaks in Germany and the UK. It is likely that viruses have been transmitted from infected site(s) out of the Danish environment, although a direct transmission pathway has not been identified. Furthermore, VHSV Ia-2 isolates seem to have been transmitted to Denmark at least once. Interestingly, one viral isolate possibly persisted in a Danish watershed for nearly 4 yr without detection whereas other subclades of VHSV isolates appear to have been eliminated, probably because of implemented eradication procedures.

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