Virulence of viral haemorrhagic septicaemia virus (VHSV) genotype III in rainbow trout

In general, viral haemorrhagic septicaemia virus (VHSV) isolates from marine fish species in European waters (genotypes GIb, GII and GIII) are non- to low virulent in rainbow trout. However, a VHSV isolation was made in 2007 from a disease outbreak in sea farmed rainbow trout in Norway. The isolate, named NO-2007-50-385, was demonstrated to belong to GIII. This isolate has attracted attention to assess which of the viral genome/proteins might be associated with the virulence in rainbow trout. In this study, we describe the difference of virulence in rainbow trout between the NO-2007-50-385 and 4p168 isolates as representatives of virulent and non-virulent GIII isolates, respectively. Rainbow trout were bath challenged with VHSV NO-2007-50-385 for 1 and 6 h, resulting in cumulative mortalities of 5 and 35%, respectively. No mortality was observed in the rainbow trout groups immersed with the genotype III VHSV isolate 4p168 for 1 and 6 h. The viral titre in organs from fish challenged with NO-2007-50-385 for 6 h increased more rapidly than those exposed for 1 h. By in vitro studies it was demonstrated that the final titres of VHSV DK-3592B (GI), NO-2007-50-385 and 4p168 inoculated on EPC cells were very similar, whereas when inoculated on the rainbow trout cell line RTG-2 the titre of the non-virulent 4p168 isolate was 3-4 logs below the two other VHSV isolates. Based on a comparative analysis of the entire genome of the genotype III isolates, we suggest that substitutions of amino acids in positions 118-123 of the nucleo-protein are candidates for being related to virulence of VHSV GIII in rainbow trout.

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