Virulence marker candidates in N-protein of viral haemorrhagic septicaemia virus (VHSV): virulence variability within VHSV Ib clones 

Four major genotypes of viral haemorrhagic septicaemia virus (VHSV), which have been isolated from many marine and freshwater fish species, are known to differ in virulence. While fast and low-cost genotyping systems based on monoclonal antibodies (MAbs) have been developed for typing of VHSV virulence, there is a need for supplementing the knowledge. In particular, 2 field isolates from viral haemorrhagic septicaemia (VHS) outbreaks in sea-reared rainbow trout Oncorhynchus mykiss in Sweden, SE-SVA-14 and SE-SVA-1033 (both genotype Ib), have yielded contradictory reactions. In the present study, upon cloning by limited dilution, both isolates appeared to be heterogeneous in terms of reactivity with nucleo (N)-protein-specific MAbs as well their gene sequences. Infection trials in rainbow trout further revealed differences in the virulence of these virus clones derived from the same primary isolate. Based on a comparative analysis of the entire genome of the clones tested, we suggest that the differences in virulence are tentatively linked to substitutions of amino acids (aa) in the N-protein region covered by aa 43-46 and aa position 168, or a combination of the two. The fact that such minor naturally occurring genetic differences affect the virulence implies that even low-virulent VHSV isolates in the marine environment should be considered as a potential threat for the trout farming industry. The described MAbs can represent useful tools for initial risk assessment of disease outbreaks in farmed trout by marine VHSV isolates.
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