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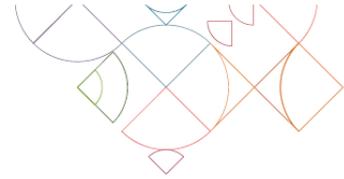
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Phylogeny of Viral haemorrhagic septicaemia virus (VHSV) based on full genome sequences

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Introduction: VHSV is a rhabdovirus with a negative sense, single strand RNA genome of about 11 kb. One of the most intriguing characteristics of VHSV is its ability to cross species boundaries, not only to cause sporadic infection, but also to create stable intra-species transmission in novel fish species. Indeed, since its first isolation from cultured rainbow trout in 1963, VHSV has been found in more than 90 different fish species in freshwater and marine environments. Molecular characterization of VHSV are mostly based on the sequence of the glycoprotein (G-gene). Although more than 800 full G-gene sequences are publicly available to date, it remains difficult to establish the phylogenetic relationships among the different sublineages within the largest genotype I.

Methodology: A dataset comprising more than 100 VHSV isolates were sequenced by NGS to obtain their full genome. Special emphasis was put in sequencing a large number of marine isolates, as these have been largely underrepresented in previous studies. To resolve the phylogenetic relationships among genotypes, analyzes were done both based on complete genome sequences and on individual genes.

Results: Congruency of trees topology based on different parts of the genome was evaluated, finding few strongly incongruent regions caused by chimeric consensus sequences resulting from mixed samples. After cleaning the dataset from ambiguous sequences, overall topology coincides with results obtained using the glycoprotein gene alone. However, some discrepancies among single gene analyses were confirmed, especially in the placement of genotypes Ia, Ib, Ic, and Iu. The phylogenetic tree based on full genome sequences provides a larger resolution in some areas of the tree. This is particularly true for some previously underrepresented marine isolates.

Conclusion: To our knowledge, this is the first phylogeny of VHSV based on full genome sequences, and including more than 100 isolates. This dataset could be used as a backbone to further test hypothesis of the tempo and mode of the genome evolution of VHSV.

Keywords: VHSV, phylogeny, virulence

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