

Wild fish are negligible transmitters of viral haemorrhagic septicaemia virus (VHSVId) in the VHS restriction zone in Finland

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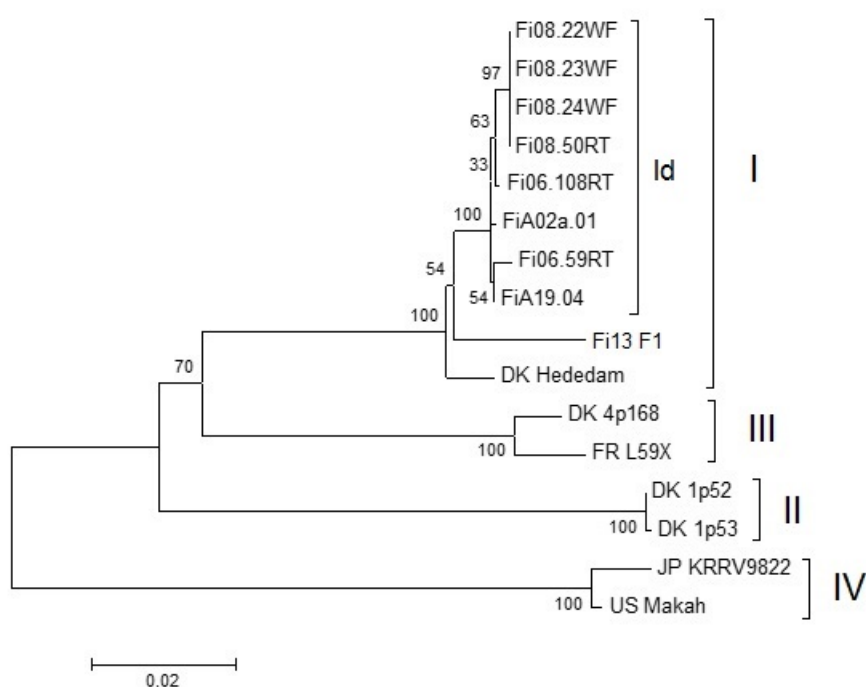


Fig. S1. Phylogenetic analysis of Finnish VHSV- strains isolated from white fish (Fi08.22WF, Fi08.23WF, Fi08.24WF) and rainbow trout (Fi08.50RT, Fi06.59RT, Fi06.108RT, FiA02a.01, FiA19.04) together with selected strains of VHSV belonging to genotypes I-IV. Tree is based on complete coding sequence of the glycoprotein (G) gene (1524 nt), and it was generated by using the neighbor-joining method in MEGA 4.1 software (Tamura et al. 2007). The reliability of the tree was determined by 1000 dataset bootstrap resampling; numbers on the tree represent percentage of bootstrap support. The scale bar indicate nucleotide substitutions per site. GenBank Accession numbers of the sequences used in the analysis are presented in Table 4.

Table S1. The percentage identities (upper right) and divergence (lower left) between paired G-gene sequences of Finnish VHSV- strains isolated from white fish (Fi08.22WF, Fi08.23WF, Fi08.24WF), rainbow trout (Fi08.50RT, Fi06.59RT, Fi06.108RT, FiA02a.01, FiA19.04) and selected strains of VHSV belonging to genotypes I-IV. Y18263 is the sequence of the VHSV strain Fi13 F1.

Percent Identity																		
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16		
1	█	100.0	100.0	100.0	99.4	99.7	99.7	99.7	89.4	89.2	91.6	98.5	91.2	86.2	86.7	97.4	1	Fi08.22WF
2	0.0	█	100.0	100.0	99.4	99.7	99.7	99.7	89.4	89.2	91.6	98.5	91.2	86.2	86.7	97.4	2	Fi08.23WF
3	0.0	0.0	█	100.0	99.4	99.7	99.7	99.7	89.4	89.2	91.6	98.5	91.2	86.2	86.7	97.4	3	Fi08.24WF
4	0.0	0.0	0.0	█	99.4	99.7	99.7	99.7	89.4	89.2	91.6	98.5	91.2	86.2	86.7	97.4	4	Fi08.50RT
5	0.6	0.6	0.6	0.6	█	99.5	99.6	99.7	89.5	89.4	91.3	98.4	91.1	86.2	86.7	97.5	5	Fi06.59RT
6	0.3	0.3	0.3	0.3	0.5	█	99.8	99.8	89.5	89.4	91.5	98.6	91.2	86.2	86.7	97.6	6	Fi06.108RT
7	0.3	0.3	0.3	0.3	0.4	0.2	█	99.9	89.6	89.4	91.4	98.7	91.1	86.2	86.8	97.6	7	FiA02a.01
8	0.3	0.3	0.3	0.3	0.3	0.2	0.1	█	89.6	89.4	91.4	98.7	91.1	86.2	86.8	97.6	8	FiA19.04
9	11.8	11.8	11.8	11.8	11.6	11.6	11.5	11.5	█	99.9	89.0	89.4	89.2	84.9	85.1	88.8	9	DK_1p52
10	11.9	11.9	11.9	11.9	11.7	11.7	11.6	11.6	0.1	█	88.9	89.3	89.1	84.8	85.0	88.6	10	DK_1p53
11	9.1	9.1	9.1	9.1	9.5	9.2	9.3	9.3	12.2	12.3	█	91.8	98.4	85.2	85.7	90.5	11	DK_4p168
12	1.5	1.5	1.5	1.5	1.6	1.4	1.3	1.3	11.7	11.8	8.8	█	91.5	86.2	86.7	97.4	12	DK_Hededam
13	9.5	9.5	9.5	9.5	9.6	9.5	9.6	9.6	11.9	12.0	1.7	9.2	█	85.1	85.4	90.1	13	FR_L59X
14	15.8	15.8	15.8	15.8	15.8	15.8	15.7	15.7	17.4	17.4	17.0	15.8	17.1	█	99.0	85.6	14	JP_KRRV9822
15	15.0	15.0	15.0	15.0	15.0	15.0	15.0	14.9	17.2	17.2	16.4	15.0	16.7	1.0	█	86.2	15	US_Makah
16	2.6	2.6	2.6	2.6	2.5	2.5	2.4	2.4	12.5	12.6	10.4	2.7	10.9	16.5	15.7	█	16	Y18263
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16		