Genetic and serological typing of European infectious haematopoietic necrosis virus (IHNV) isolates

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Infectious haematopoietic necrosis virus (IHNV) causes the lethal disease infectious haematopoietic necrosis (IHN) in juvenile salmon and trout. The nucleocapsid (N) protein gene and partial glycoprotein (G) gene (nucleotides 457 to 1061) of the European isolates IT-217A, FR-32/87, DE-DF 13/98 11621, DE-DF 4/99-8/99, AU-9695338 and RU-FR1 were sequenced and compared with IHNV isolates from the North American genogroups U, M and L. In phylogenetic studies the N gene of the Italian, French, German and Austrian isolates clustered in the M genogroup, though in a different subgroup than the isolates from the USA. Analyses of the partial G gene of these European isolates clustered them in the M genogroup close to the root while the Russian isolate clustered in the U genogroup. The European isolates together with US-WRAC and US-Col-80 were also tested in an enzyme-linked immunosorbent assay (ELISA) using monoclonal antibodies (MAbs) against the N protein. MAbs 136-1 and 136-3 reacted equally at all concentrations with the isolates tested, indicating that these antibodies identify a common epitope. MAb 34D3 separated the M and L genogroup isolates from the U genogroup isolate. MAb 1DW14D divided the European isolates into 2 groups. MAb 1DW14D reacted more strongly with DE-DF 13/98 11621 and RU-FR1 than with IT-217A, FR-32/87, DE-DF 4/99-8/99 and AU-9695338. In the phylogenetic studies, the Italian, French, German and Austrian isolates clustered in the M genogroup, whereas in the serological studies using MAbs, the European M genogroup isolates could not be placed in the same specific group. These results indicate that genotypic and serotypic classification do not correlate.

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