

Viral Diseases as a Possible Cause of Salmon Mortality in the North Pacific Ocean

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Keywords: IHNV, phylogeny, diversity, transmission

Many viruses have been isolated from wild fish species from marine ecosystems. Whether these viruses can initiate an infection, cause disease, and eventually cause mortality of fish in ocean environments is not well understood. However, mortalities linked to viral infections in cultured marine fish have been reported. Three major virus pathogens that have been associated with outbreaks of cultured fish in salt water include infectious salmon anemia, viral hemorrhagic septicemia virus, and infectious hematopoietic necrosis virus.

Infectious salmon anemia (ISA) is an established viral disease of cultured Atlantic salmon in the marine environment (Nylund et al. 1999). Outbreaks were first reported from Norwegian cultured Atlantic salmon (Thorud and Djupvik 1988), but reported mortalities due to ISA soon followed in Scotland (Rodger et al. 1998) and on the east coast of Canada (Lovely et al. 1999) in Atlantic salmon reared in salt water net pens. Wild fish in the waters near where the marine outbreaks occurred have tested positive for the virus, but do not exhibit any clinical signs of disease (Raynard et al. 2001).

Originally, viral hemorrhagic septicemia virus (VHSV) was identified in association with high mortalities of rainbow trout reared in fresh water culture facilities in central Europe. Since 1979, VHSV has been isolated from many species of fish present in salt water from the Atlantic Ocean near continental Europe, Baltic Sea, Kattegat, Skagerrak, and the North Sea (Mortensen et al. 1999). Most wild marine fish infected with VHSV show no clinical signs of disease though a few isolations were from skin lesions. However, there have been epizootics in cultured turbot reared in salt water from Germany, Scotland, and Ireland (King et al. 2001). In North America, VHSV was first isolated in 1990 from returning adult coho and chinook salmon (Eaton et al. 1991; Meyers and Winton 1995) and the virus is now known to be endemic to many north Pacific fish species (Meyers et al. 1994; Hershberger et al. 1999). No mortalities in wild or cultured fish from North America have been directly attributed to VHSV, but it has been speculated that VHSV infection may play a role in the population fluctuations observed in wild herring stocks in Alaska (Hershberger et al. 1999).

Infectious hematopoietic necrosis virus (IHNV) is the most significant viral pathogen of cultured salmonids in the Pacific Northwest. IHNV is primarily associated with epidemics in fresh water culture facilities (e.g. fish farms, hatcheries, and spawning channels) and can infect many species of Pacific salmonids (Bootland and Leong 1999). The virus is endemic to the waters of North America from Alaska to northern California and has been isolated from both wild and cultured fish in fresh water (Wolf 1988). In 1992 the first marine isolation of IHNV from an Atlantic salmon (*Salmo salar*) occurred during an outbreak at a salt-water net pen rearing facility near Vancouver Island in British Columbia, Canada (Armstrong et al. 1993). Subsequent IHNV outbreaks in neighboring facilities rearing Atlantic salmon have occurred intermittently (S. St-Hilare, University of Guelph, Guelph Ontario, Canada, personal communication). IHNV has also been isolated from a returning adult sockeye (*Oncorhynchus nerka*) in salt-water (Traxler et al. 1997), and four other species of ocean-harvested wild fish (Kent et al. 1998; S. St-Hilare, University of Guelph, Guelph Ontario, Canada, personal communication). The isolation of IHNV from wild and cultured fish in both salt and fresh water within the Pacific Northwest indicates that the virus is highly versatile in regard to host specificities and host environments during its infectious cycle.

In order to better understand the epidemiology of IHNV infections and their possible transmission patterns in both fresh and salt-water environments, a long-term project is underway to genetically characterize virus isolates throughout the entire geographic range of IHNV in the Pacific Northwest. The IHN virus RNA genome consists of 6 genes in the following order: the N, P, M, G, NV, and L, which code for the nucleoprotein, phosphoprotein, matrix protein, glycoprotein, nonvirion protein, and the polymerase, respectively (Kurath et al. 1995; Morzunov et al. 1995). We have extensively examined various genes of IHNV isolates from Alaska (Emmenegger et al. 2000), British Columbia (Anderson et al. unpublished data), Washington coastal rivers (Emmenegger and Kurath 2002), 12 mile region along the Snake River subbasin in Idaho (Troyer et al. 2000), the entire Columbia River basin (Garver et al. unpublished data), and watersheds from California and the southern Oregon coast (Kurath et al. unpublished

data). The virus isolates were characterized by nucleotide sequencing and comparing genetic fingerprints using the ribonuclease protection assay. The data presented is a comprehensive phylogenetic analysis of a 303 nucleotide region in the G-gene of IHNV isolates throughout its North American range over the last 35 years.

Phylogenetic analysis of the partial sequences indicated that IHNV isolates clustered into three major clades U, M, and L, with maximum genetic diversities of 3.0%, 7.6%, and 3.3% respectively. These analyses indicated that the three major genetic groups of the virus isolates correlated with both their geographic origin and the long-distance migration patterns of the salmonid host stocks. Interestingly, the U clade is the largest clade by numbers of isolates and by geographic range, occurring from approximately the Columbia River to the farthest northern IHNV isolation in Alaska, and yet it has the lowest genetic diversity. Genetic homogeneity within the viral U and L clades suggests that viral transmission may occur during the marine life stage of the hosts. Possible hypotheses that may explain IHNV genetic homogeneity within specific regions of its range include: species/stock migration patterns in the ocean, a marine reservoir or carrier state of the virus in saltwater, oceanic features (i.e. small or large gyres), fish culture practices, host specific factors, and differences in coastal versus inland salmonid migration distances. In association with other climatic or ecological stressors, marine virus transmission could result in epidemics. Further sampling of salmonids and other fish species during their ocean migration is required in order to determine if IHNV infection is highly prevalent and contributes to the mortality of salmon in the North Pacific Ocean.

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