Infectious hematopoietic necrosis virus (IHNV)

- IHNV is a significant viral pathogen that causes disease and death in Pacific salmon and trout in the Pacific Northwest.

- When IHNV infects hatchery fish juveniles experience high mortality and managers may decide to destroy them all to prevent spread of the virus.

- WFRC’s IHNV surveillance program offers genetic typing and epidemiological analysis of samples sent in by state, federal, and tribal partner agencies.

- There are three related but distinct genetic groups of virus. The groups are called U, M, and L, and they vary in geographic and host ranges.

- By analyzing the virus genetic type and the case details of a given virus outbreak, the IHNV technical assistance program provides partner agencies scientifically rigorous information on the possible sources of transmission and the risks of virus spread.

IHNV Types: Patterns of emergence and displacement

Recent genetic analysis provides clues that may help predict the rise of new strains of IHNV to dominance in local populations of steelhead trout. IHNV is an important fish virus that adapted to trout in the late 1970s, giving rise to the M group of IHNV, which has been detected in the Columbia River Basin for more than 30 years. Over time different strains of IHNV have dominated in the population, waxing and waning in prevalence due to ecological or evolutionary changes. During the last 30 years there have been three cycles of emergence and displacement of M group IHNV subtypes in the lower Columbia River Basin.

WFRC operates an IHNV technical assistance program to provide hatcheries and fish health agencies with rigorous information on the possible sources of IHNV transmission and risks of spread during outbreaks. All the virus types identified in the serial patterns of emergence/displacement have been associated with significant disease and death of young steelhead trout. All these types also traveled many miles after becoming dominant, and caused more widespread mortality in new populations of steelhead trout. These patterns have been detected due to the long term IHNV genetic and epidemiological surveillance program at WFRC. Keeping track of this ever-changing virus provides an unprecedented possibility of forecasting the next dominant strain of IHNV.
Historical IHNV Disease Dynamics

To date WFRC has tracked three cycles of emergence and displacement among the trout-adapted M group of IHNV in the lower Columbia region. The first was sequence type 007 M, which dominated from the time it emerged in 1980 until 1994. In 1994 007 M was displaced by 111 M which dominated until 1999. Type 110 M emerged in 2002 and has dominated since then. Also since 2002 two new types have emerged and persisted without overturning 110 M’s dominance. One of these types, 139 M, eventually traveled to the Washington coast and the lower Snake River where it became dominant. The second new type, 178 M, stayed within the local lower Columbia for years, but in 2012 was detected elsewhere. The patterns of emergence, persistence and recent spread of type 178M suggest that it has potential to become the new dominant strain in the Lower Columbia River Basin. If so, it will be detected by ongoing genetic surveillance.