

**An investigation into the epidemiology and genetics of erythrocytic
necrosis virus (ENV) in the coastal North Pacific Ocean**

by

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ABSTRACT

Viral erythrocytic necrosis (VEN) affects over 20 species of marine and anadromous fishes in the North Atlantic and North Pacific Oceans. However, the distribution and strain variation of its viral causative agent, erythrocytic necrosis virus (ENV), has not been well characterized within Pacific salmon. Here, metatranscriptomic sequencing of Chinook salmon revealed that ENV infecting salmon was closely related to ENV from Pacific herring, with inferred amino-acid sequences from Chinook salmon being 99% identical to those reported for herring. Sequence analysis also revealed 89 protein-encoding sequences attributed to ENV, greatly expanding the amount of genetic information available for this virus. High-throughput PCR of over 19,000 fish showed that ENV is widely distributed in the NE Pacific Ocean and was detected in 12 of 16 tested species, including in 27% of herring, 38% of anchovy, 17% of pollock, and 13% of sand lance. Despite frequent detection in marine fish, ENV prevalence was significantly lower in fish from freshwater (0.03%), as assessed with a generalized linear mixed effects model ($p=5.5e-08$). Thus, marine fish are likely a reservoir for the virus. High genetic similarity between ENV obtained from salmon and herring also suggests that transmission between these hosts is likely.