## IDENTIFICATION OF A NEW INFECTIOUS PANCREATIC NECROSIS VIRUS (IPNV) VARIANT IN ATLANTIC SALMON

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Breeding resistant Atlantic salmon against the infectious pancreatic necrosis virus (IPNV) has been one of the most successful stories in the history of fish breeding. It has been shown that fish with specific genetic variations on a narrow genomic region of chromosome 26 can be highly resistant to this virus. In this work, we present the discovery of a new IPNV variant that can cause mortality even in genetically resistant animals. By sequencing the whole genome of this variant, we describe unique mutations in this isolate and how it forms a phylogenetically distinct clade compared to other IPNV variants and strains. We further developed an infection model and challenged fish during different developmental stages, with both the common and the newly identified variant. While we found no evidence of mortality during the parr and smolt stages, the mortality following infection with the new variant was very high among the fry. We found the heritability of genetic resistance to the new variant to be significant but much lower than that of the standard strain. However, our data also shows that the resistance against the two variants has a positive genetic correlation, suggesting that the fish with higher resistance to the standard strain should perform better when infected with the new variant.