

**A novel salmonid bafinivirus with a putative sixth protein and wide in-vitro host range**

Frederick S. Kibenge<sup>1</sup>, Molly J. Kibenge<sup>1</sup>, Yingwei Wang<sup>2</sup>, Emma Moore<sup>1</sup>, Ashley V. McKibbon<sup>1</sup>, Alexandra Morton<sup>3</sup>; <sup>1</sup>*Department of Pathology and Microbiology, Atlantic Veterinary College, University of Prince Edward Island;* <sup>2</sup>*School of Mathematics and Computer Science, University of Prince Edward Island;* <sup>3</sup>*Raincoast Research Society;*

Studies suggest that coronaviruses are prevalent in freshwater cyprinids and salmonids but few isolates have been shown to fulfill the criteria for taxonomic classification. Fish coronaviruses are classified in the genus *Bafinivirus*, subfamily *Torovirinae*, family *Coronaviridae*, and order *Nidovirales*. During routine surveillance of samples from market-bought farmed Atlantic salmon *Salmo salar*, a novel cytopathogenic agent was isolated from two separate submissions, VT01292015-09 using ASK-2 cell line at 16°C and VT11052014-71 using KF-1 cell-line at 22°C. Here we performed extensive studies to characterize the viral isolates. Their ultrastructural and genomic characteristics place them in the genus *Bafinivirus* and we named them strains of Atlantic salmon bafinivirus (ASBV). Full genome sequence analysis of ASBV revealed nucleotide sequence identity of 99% to Chinook salmon bafinivirus (CSBV), but with a large deletion within the replicase polyprotein pp1a gene. The genome sequence analysis also revealed a putative sixth protein, a 60 amino-acid polypeptide, likely an envelope protein, not previously described in bafiniviruses. *In-vitro* cell culture susceptibility testing in various fish cell lines revealed a broad cell tropism, indicating that ASBV has a potentially very wide host range. The prevalence of ASBV and its impact on fish health in both farmed and wild fish remains to be further determined.