



University  
of Victoria

Graduate Studies

Notice of the Final Oral Examination  
for the Degree of Master of Science

of

**HOLLIE JOHNSON**

BSc (University of Victoria, 2010)

**“Northern Pike of North America: Population Genomics  
and Sex Determination”**

Department of Biology

Tuesday October 15, 2019

1:00 P.M.

Engineering Computer Science Building  
Room 128

Supervisory Committee:

Dr. Ben Koop, Department of Biology, University of Victoria (Co-Supervisor)  
Dr. John Taylor, Department of Biology, University of Victoria (Co-Supervisor)  
Dr. John Nelson, Department of Biology, UVic (Member)

External Examiner:

Dr. Chris Darimont, Department of Geography, UVic

Chair of Oral Examination:

Dr. Wanda Hurren, Department of Curriculum and Instruction, UVic

## Abstract

Northern Pike (*Esox lucius*) is an economically and ecologically valuable species with a circumpolar distribution across the Northern Hemisphere. Northern Pike have been shown to have low levels of genetic variation despite their great capacity to colonize new environments. Here, high-resolution resequencing data from 47 Northern Pike from across North America was used for SNP discovery and population analysis. Our analysis reveals an extraordinary lack of genetic variation among Northern Pike with observed heterozygosity ( $H_e$ ) of just 0.0835. Our analyses suggest that two major groups of Northern Pike exist in North America that are separated by the Great Continental Divide. Genetic variation associated with the stratification of these two groups resides across the genome particularly in gene regions with multiple copy number variants and functions related to immunity, tissue permeability, and development. Northern Pike from Alaska and the Yukon River harbour about two times more heterozygosity than Northern Pike east of the great divide with an average of one heterozygous SNP every 6,250 bases. Populations east of the Continental Divide possess a remarkable level of genetic homogenization with an average of just one heterozygous SNP every 16,500 bases.

We observed a recently described master sex-determining gene, *amhby*, in three western North American populations but not in populations east of the Continental Divide. We could not resolve any signals indicating a genetic sex determination system was present in populations from southern Manitoba or the St. Lawrence River. This may indicate that environmental sex determination is at play in these populations. We find evidence of a possible female heterozygous, male homozygous ZW-ZZ genetic sex-determination mechanism in New Jersey Northern Pike.

With the highest average of 181,268 heterozygous SNPs genome wide and the greatest observed  $H_e$  (0.3228) of all populations, as well as the presence of the sex-determining gene *amhby* indicate that Northern Pike from our Alaskan population are the oldest in North America. Fewer numbers of heterozygous SNPs (61,073), low observed  $H_e$  (0.0922), and the absence of *amhby* in Northern Pike east of the

Continental Divide suggests that these are relatively young populations and are descended from a small founding population. These results imply that Northern Pike first came to North America through Beringia and colonized its North American range from there, possibly via pro-glacial lake formation and drainage. However, from the data herein it was not possible to trace how re-colonization occurred after the final retreat of glaciers at the end of the last ice age.

This thesis provides a genetically high-resolution snapshot of Northern Pike population structure in North America. It demonstrates that organisms with largely homogenous genomes can be incredibly successful and resilient. Finally, it adds to the complex subject of sex determination in fish and provides insight into a sex determination system in transition.