



University
of Victoria

Graduate Studies

Notice of the Final Oral Examination
for the Degree of Doctor of Philosophy

of

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BA (University of Victoria, 2009)

**“Conserved Synteny in the Genomes of Teleost Fish Aids in the Rapid
Development of Genomic Tools to
Query Fundamental Biological and Evolutionary Questions”**

Department of Biology

Friday, December 1, 2017

9:00 A.M.

Clearihue Building

Room B017

Supervisory Committee:

Dr. Ben Koop, Department of Biology, University of Victoria (Supervisor)

Dr. John Nelson, Department of Biology, UVic (Member)

Dr. Steve Perlman, Department of Biology, UVic (Member)

Dr. Stephen Cross, Department of Geography, UVic (Outside Member)

External Examiner:

Dr. Kim Thomas Scribner, Department of Fisheries and Wildlife, Michigan State University

Chair of Oral Examination:

Dr. Andrew Marton, Department of Pacific and Asian Studies, UVic

Dr. David Capson, Dean, Faculty of Graduate Studies

Abstract

As two species diverge, much of their genomes begin to differentiate. In many lineages, however, the genomic structure remains remarkably intact, with orthologous gene content maintained across millions of years and vast changes to their biological characteristics. The maintenance of gene content is defined as conserved synteny while the preservation of gene order is defined as conserved linkage; the conservation of both can be incredibly informative when interrogating and comparing two genomes. In non-model organisms, conservation of linkage to a well-developed model allows informed, cost-effective and rapid answers to fundamental biological questions without the complete regeneration of equivalent resources. With the development of new model organisms, we can begin to discuss more fundamental evolutionary concepts, such as the maintenance of chromosomal gene content across larger evolutionary time-scales, or the reorganization that occurs in chromosomes following major genomic events such as whole-genome duplications. In this work, I utilized the rapid development of primary genomic resources in the non-model teleost sablefish (*Anoplopoma fimbria*) to demonstrate that conserved linkage to a model genomic reference can identify the gene most likely responsible for genetic sex-control. I then assembled the first genome for a non-duplicated member of the teleost lineage Protacanthopterygii, the northern pike (*Esox lucius*), and demonstrated the conservation of synteny between three major lineages of teleosts, the Protacanthopterygii, the Acanthopterygii and the Ostariophysi. I further showed that the genome of northern pike represents an ancestrally organized, pre-duplicated genome in comparison to the economically important Salmoniformes. Finally, with continued improvements of the genome to chromosome level, I demonstrated the degree of conserved linkage maintained between Atlantic salmon and northern pike and explained how conserved linkage through both genomes could be used to improve the genome assembly of the other, even with over 125 million years of separation. As genomic technology continues to advance and new genomic resources become available, the continued refinement of genome reorganization post duplication will be revealed, and this pre-duplication outgroup will continue to push our understanding of the effects of genome duplication, as we transition from genome organization to functional modifications of gene duplicates following duplication.