Development of a Genetic Linkage Map for Cisco (*Coregonus artedi*) to Facilitate Integrated Studies of Adaptive Diversity

Danielle Blumstein[1], Wendylee Stott[2], Wesley Larson[3]
[1]University of Wisconsin-Stevens Point, College of Natural Resources,
[2]U.S. Geological Survey, Great Lakes Science Center, [3]U.S. Geological Survey, Wisconsin Cooperative Fishery Research Unit

Introduction

Throughout their circumpolar range, species within the coregonine complex are ecologically and socioeconomically important. In the Laurentian Great Lakes, overfishing has left the abundance and diversity of ciscoes well below historic levels. Accurate identification of forms (Fig. 1) is critical for the development of effective restoration and management plans. Currently, form classifications are based on morphometric variation. However, the relative influence of phenotypic plasticity and heritable genetic differences in determining these forms is not well understood.

Objectives

1) Construct dense sex specific linkage maps for *C. artedi* (Fig. 2) from haploid and diploid individuals
2) Conduct QTL analysis for phenotypic traits from the sampled population
3) Align the *C. artedi* linkage map to closely related previously studied species

Fig. 2 *C. artedi* collected from Lake Huron during the spawning run.

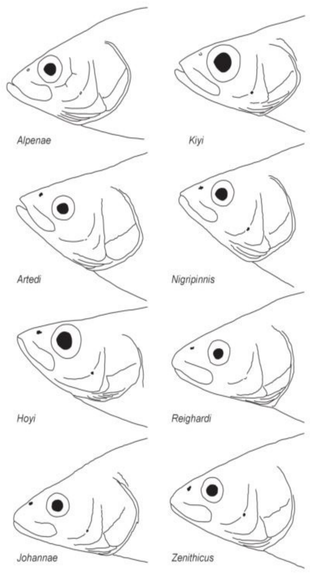

Fig. 1 Cisco forms present in the Great Lakes (Eshenroder et al. 2016).

Field Methods

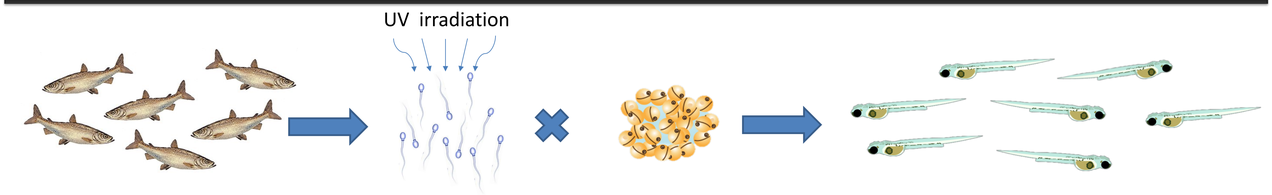

Fig. 3 Modified spawning method to create haploid individuals.

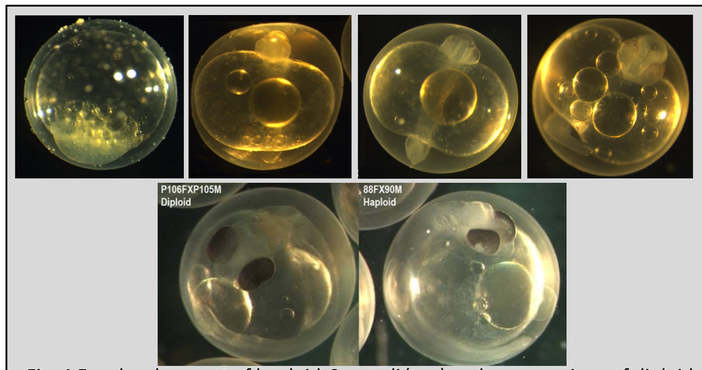

Fig. 4 Egg development of haploid *C. artedi* (top) and a comparison of diploid (bottom left) and haploid *C. artedi* (bottom right) ~50 days post fertilization.

- Spawning cisco will be collected from northern Lake Huron
- Fin clips from adults will be taken for genetic analysis
- UV irradiation of milt destroys DNA in sperm (Fig. 3)
- Irradiated sperm will be used to fertilize eggs to produce haploids (Fig. 4)
- Larvae will be collected at hatch for genetic analysis

Lab Methods

- DNA will be extracted from adults and embryos
- Genotyping will be performed by sequencing restriction site associated DNA (RADseq) (Fig. 5)
- Linkage map (Fig. 6) construction will be performed based on identified recombination events (Fig. 7)

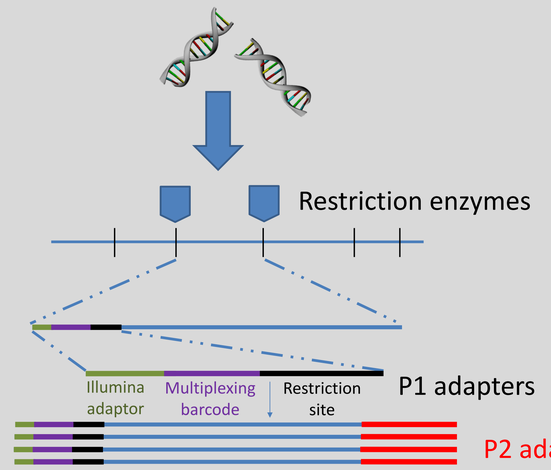

Fig. 5 RADseq workflow from Baird et al. 2008

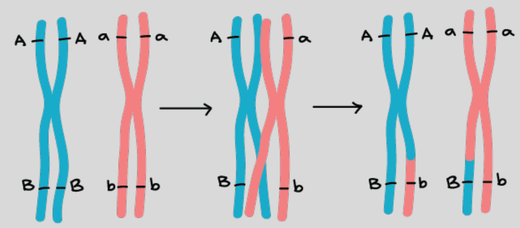

Fig. 7 Chromosomal crossing over during meiosis

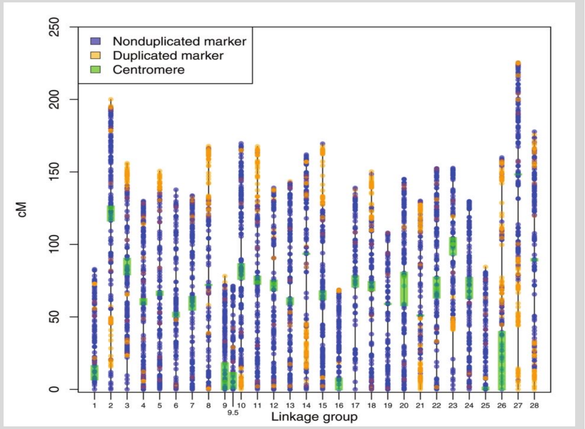

Fig. 6 Sockeye Salmon linkage map example (Larson et al. 2015)

Discussion

- The *C. atredi* linkage map will function as a genetic resource to facilitate research with the aim of determining the degree of heritable genetic differences among cisco forms
- Linkage map construction assists in understanding the genetic basis of adaptation and can provide important insights into how chromosomes interact in polyploid organisms
- Development of high-density linkage maps for less described salmonid species will contribute to the understanding of speciation and the evolution of genomes

Acknowledgments

We would like to thank USFWS crew members Chris Olds, Paul Haver, Kaley Genther, Steve Nimcheski, and Matt McLean for assistance in field sampling, USGS Great Lakes Science Center Aquatic Research Wet Lab for egg rearing, and Keith Turnquist from the University of Wisconsin- Stevens Point Molecular Conservation Genetics Lab for assistance in lab work.

Contact: Danielle Blumstein
dblum940@uwsp.edu @DaniBlumstien

References

- Baird NA, Etter PD, Atwood TS, Currey MC, Shiver AL, Lewis ZA, Selker EU, Cresko WA, Johnson EA (2008) Rapid SNP discovery and genetic mapping using sequenced RAD markers. PLoS One 3, e3376.
- Eshenroder RL, Vecsei, P., Gorman, O.T., Yule, D.L., Pratt, T.C., Mandrak, N.E., Bunnell, D.B., and Muir, A.M. (2016) Ciscoes of the Laurentian Great Lakes and Lake Nipigon [online].
- Larson WA, McKinney GJ, Limborg MT, Everett MV, Seeb LW, Seeb JE (2016) Identification of Multiple QTL Hotspots in Sockeye Salmon (Oncorhynchus nerka) Using Genotyping-by-Sequencing and a Dense Linkage Map. J Hered 107, 122-133.