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

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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.

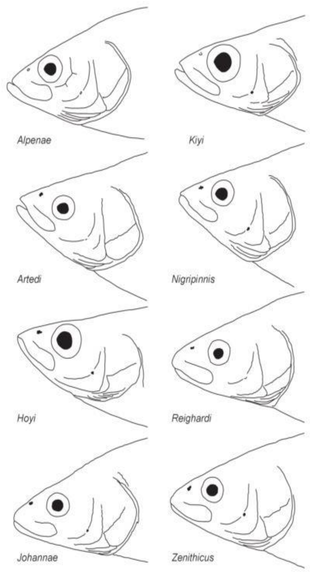

Fig. 1 Cisco forms present in the Great Lakes (Eshenroder et al. 2016).

Field Methods

- Spawning cisco will be collected from northern Lake Huron
- Fin clips from adults (Fig. 2) 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
- Larvae will be collected at hatch for genetic analysis

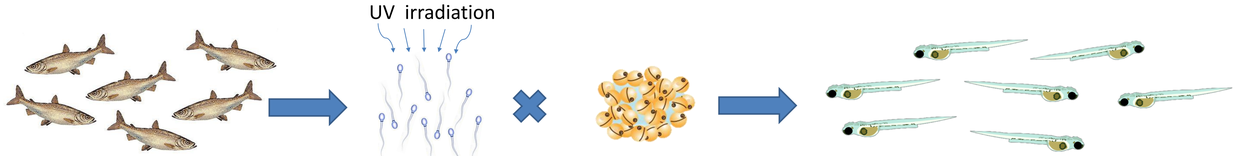

Fig. 3 Modified spawning method to create haploid individuals.

Lab Methods

- DNA will be extracted from adults and embryos
- Genotyping will be performed by sequencing restriction site associated DNA (RADseq)
- Linkage map (Fig. 4) construction will be performed based on identified recombination events (Fig. 5)

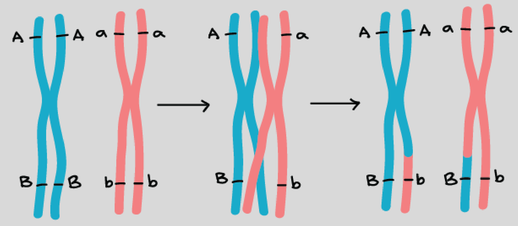

Fig. 5 Chromosomal crossing over during meiosis

Results

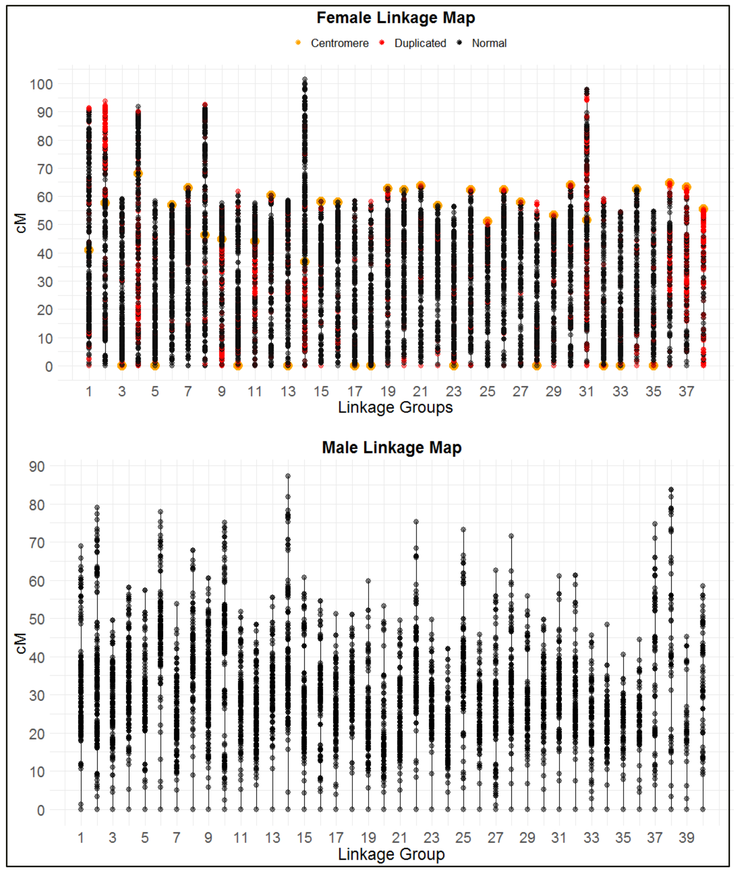

Fig. 4 Female (top) and male linkage maps (bottom) for cisco containing 20458 and 6340 loci (Table 1), respectively. Each dot represents a locus, and darker shading indicate higher density. Approximate centromere locations are placed on all LGs in the female map.

Linkage Group (LG)	% Duplicated	Length		# Markers		LG Type
		Female	Male	Female	Male	
1	0.13	91.36	68.95	837	278	M
2	0.33	93.56	78.98	711	248	M
3	0.04	58.96	49.49	564	204	A
4	0.33	91.73	58.07	867	219	M
5	0.02	58.38	57.23	569	195	A
6	0.04	56.93	77.82	566	184	A
7	0.05	62.90	53.67	585	181	A
8	0.08	92.45	67.80	595	194	M
9	0.28	57.72	60.40	685	204	M
10	0.05	61.85	75.08	570	213	A
11	0.26	57.56	51.62	721	170	M
12	0.05	60.19	48.36	567	224	A
13	0.10	58.57	55.39	525	162	A
14	0.29	101.35	87.14	722	224	M
15	0.06	58.00	60.69	531	213	A
16	0.06	57.79	54.44	471	141	A
17	0.05	58.28	51.08	484	161	A
18	0.06	58.09	50.91	475	147	A
19	0.14	62.66	59.74	527	140	A
20	0.05	62.25	53.19	505	160	A
21	0.07	63.72	49.41	548	165	A
22	0.04	56.56	75.17	497	177	A
23	0.04	56.37	49.57	480	146	A
24	0.05	62.16	42.08	471	136	A
25	0.05	50.97	73.21	456	171	A
26	0.05	62.25	45.80	480	153	A
27	0.04	57.78	62.64	419	149	A
28	0.07	57.76	71.50	413	141	A
29	0.06	53.16	55.82	427	122	A
30	0.04	63.98	49.68	509	152	A
31	0.51	97.77	61.11	778	159	M
32	0.07	59.04	61.23	419	142	A
33	0.05	54.45	45.50	351	117	A
34	0.23	62.45	48.26	414	121	A
35	0.14	54.74	40.54	296	81	A
36	0.47	64.53	44.47	509	92	A
37	0.69	63.18	74.69	570	80	A
38	0.76	55.54	83.66	344	62	M
39	0.00	0.00	45.13	0	41	M
40	0.00	0.00	58.46	0	71	M
total	0.20	2456.98	2357.97	20458	6340	

Table 1. Summary of male and female linkage maps for cisco. Linkage group type denotes acrocentric (A) and metacentric (M) Linkage groups.

Conclusion

- 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 (Fig. 6)

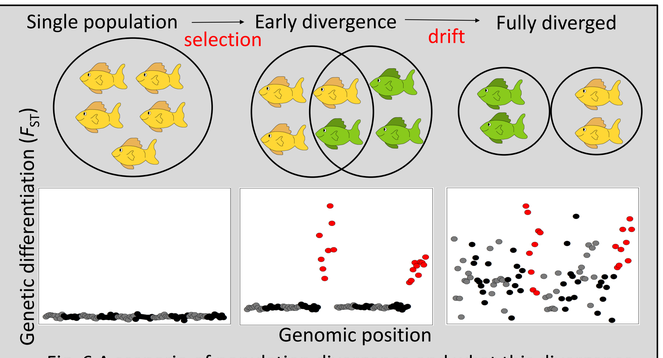

Fig. 6 A scenario of population divergence and what this divergence looks like across the genome.

Acknowledgments

We would like to thank USFWS crew for assistance in field sampling, USGS Great Lakes Science Center Aquatic Research Wet Lab for egg rearing, and the University of Wisconsin- Stevens Point Molecular Conservation Genetics Lab for assistance in lab work.

References

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