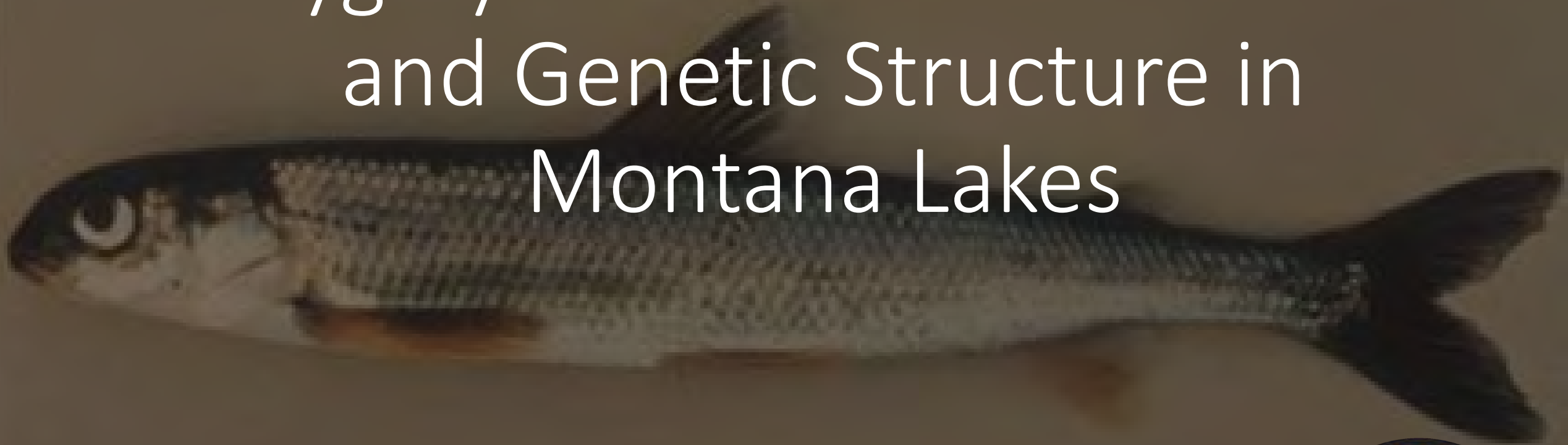
Pygmy Whitefish Distribution and Genetic Structure in Montana Lakes



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Montana Fish, Wildlife, & Parks

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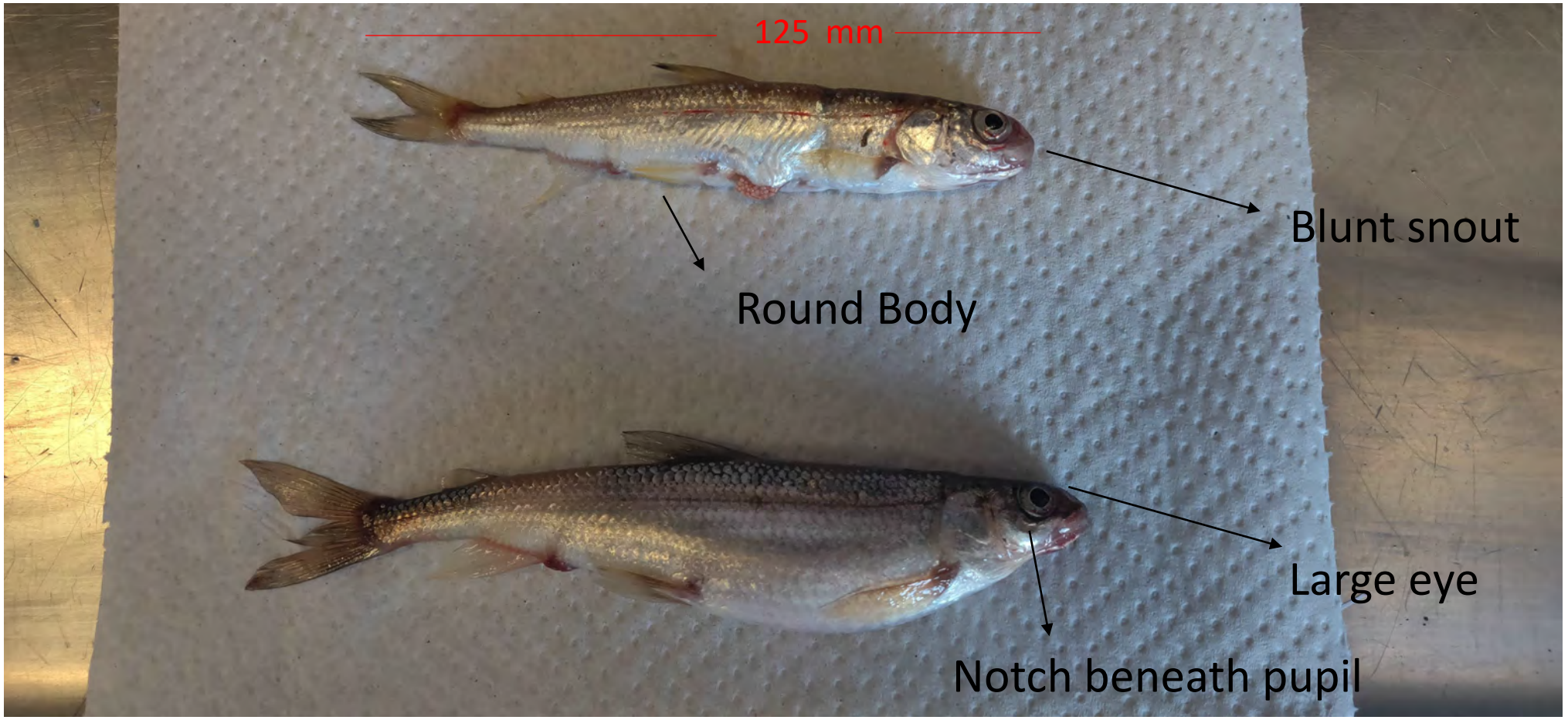
Pygmy Whitefish – *Prosopium coulterii*



Distribution

267

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NOTE

Morphological and genetic analyses identify a new record of a glacial relict: pygmy whitefish (*Prosopium coulterii*) from northwestern Ontario

P.J. Blanchfield, E.B. Taylor, and D.A. Watkinson

Abstract: The pygmy whitefish (*Prosopium coulterii* (Eigenmann and Eigenmann, 1892)) is a glacial relict species with a disjunct North American distribution that, apart from its most easterly known location in Lake Superior, is predominantly found in northern and western regions of Canada. Here we report on a new finding of pygmy whitefish from Winnange Lake in northwestern Ontario that extends the range of this species ~320 km from its most easterly distribution in Lake Superior and almost 1500 km east of the closest previously known western localities. Genetic analyses confirmed that the fish from Winnange Lake were most closely related to the lineage that includes fish from Lake Superior and likely also originated via postglacial dispersal from a refugium in the upper Mississippi – Missouri river system.

Key words: pygmy whitefish, *Prosopium coulterii*, disjunct distribution, clades, refugia.

Résumé : Le ménomini pygmée (*Prosopium coulterii* (Eigenmann and Eigenmann, 1892)) est une espèce relique de l'ère glaciaire de répartition nord-américaine disjointe qui, outre sa présence la plus orientale connue dans le lac Supérieur, est principalement présente dans les régions du nord et de l'ouest du Canada. Nous faisons état de la découverte de ménominis pygmées dans le lac Winnange, du nord-ouest de l'Ontario, qui élargit l'aire de répartition de l'espèce à ~320 km du lac Supérieur, sa localité la plus à l'est connue à ce jour, et à près de 1500 km à l'est des localités occidentales les plus proches déjà connues. Des analyses génétiques confirment que les poissons du lac Winnange s'apparentent le plus étroitement à la lignée qui comprend les poissons du lac Supérieur, et qu'ils sont vraisemblablement issus de la dispersion postglaciaire à partir d'un refuge dans le réseau hydrographique supérieur de la rivière Missouri et du fleuve Mississippi.

Mots-clés : ménomini pygmée, *Prosopium coulterii*, répartition disjointe, clades, refuges.

Introduction

Pygmy whitefish (*Prosopium coulterii* (Eigenmann and Eigenmann, 1892)) have a disjunct distribution in North America. West of the Continental Divide, native populations are widely distributed in portions of the Columbia River system in Montana, Idaho, Washington State, and British Columbia; north in the Fraser, Skeena, and Yukon river systems in Canada; and the Chignik and Ugashik river systems in southwestern Alaska (Scott and Crossman 1973; McPhail 2007; Page and Burr 2011; Witt et al. 2011). East of the Continental Divide, they are known to occur in northerly regions that include Lake Athabasca, Great Bear Lake, Elliot Lake (in the Peel River drainage), lakes in the Liard and Peace river systems, the Athabasca River, and most recently Bluefish Lake on the Yellowknife River (Lindsey and Franzin 1972; Scott and Crossman 1973; McPhail 2007; Page and Burr 2011; Alberta Sustainable Resource Development and Alberta Conservation Association 2011; Witt et al. 2011; Vecsei and Panayi 2014). Waterton Lakes in southwest Alberta represent the southern extent of the eastern range of pygmy whitefish. The third, and most easterly, area of this disjunct North American distribution is Lake Superior (Eschmeyer and Bailey 1955). A single population has also been recorded in Ekityki Lake on the Chukotski Peninsula in northeastern Russia (Chereshnev and Skopets 1992).

Recently, Witt et al. (2011) investigated the degree of phylogeographical divergence within pygmy whitefish and the origin of these three disjunct populations within North America. Using mitochondrial and nuclear DNA sequence variation, they found the species is composed of two monophyletic mitochondrial clades in North America. One consists of populations in Alaska, in the Chignik, Ugashik, and Alsek river watersheds and Aishihik lake. The second consists of remaining portions of the distribution in Cascadia and Mackenzie (Peace) river watersheds and Lake Superior. The authors propose that the most likely explanation for the current range disjunctions of pygmy whitefish in North America was from a combination of isolation, genetic divergence, and selective dispersal from the Beringia and Cascadia Pleistocene glacial refugia, as well as more recent isolation and dispersal from an upper Mississippi refugium (Witt et al. 2011).

Pygmy whitefish is a glacial relict species, and a common habitat feature among the disjunct areas of their distribution is their presence only in cold, well-oxygenated lakes. Similar to other glacial relict species, such as deepwater sculpin (*Myoxocephalus thompsonii* (Girard, 1851)), lake trout (*Salvelinus namaycush* (Walbaum,

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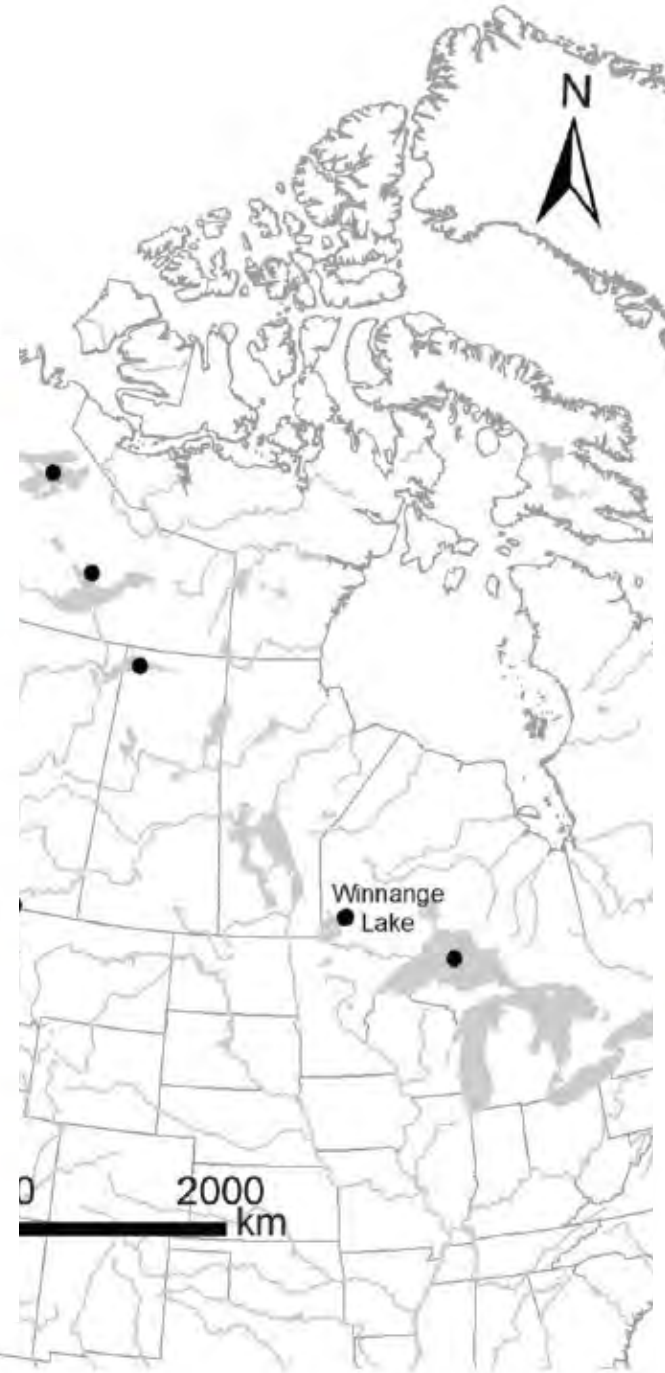

diversity

MDPI

Article

Phylogeny, Distribution, and Biology of Pygmy Whitefish (*Prosopium coulterii*) in the Beringia Region (Chukotka)

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Abstract: The pygmy whitefish *Prosopium coulterii* (C. H. Eigenmann & R. S. Eigenmann, 1892) is a freshwater fish with a highly disjunct distribution ranging from the middle part of North America to Chukotka. There is still no consensus regarding its phylogeny and dispersal history due to limited information from the Chukotkan part of the range. We investigated 22 lakes over Chukotka and found a much broader distribution than it was previously thought. Pygmy whitefish was found to be a common species in the lakes that belong to rivers draining into the Arctic. Cytochrome B, cytochrome oxidase subunit 1, and ATP synthase F0 subunit 6 mitochondrial sites were analyzed from 25 samples to reconstruct the phylogenetic history of pygmy whitefish. Two haplogroups belonging to the east and west Chukotkan ranges were identified; both groups are closely related to Alaskan pigmy whitefish and distant from the Cascadia-Mackenzie (Peace) populations. Combining the distribution patterns, phylogenetic network topology, and the contemporary knowledge on the glaciation history of the region, we suggest a possible colonization pathway over Beringia region and beyond it. The basic biological characteristics (fork length, number of gill rakers, and pyloric caeca, age structure, and feeding) are also presented to characterize the populations over the investigated range.

Keywords: glacial refugia; migrations reconstruction; cytochrome B; cytochrome oxidase subunit 1; ATP synthase F0 subunit 6; Coregoninae

check for updates

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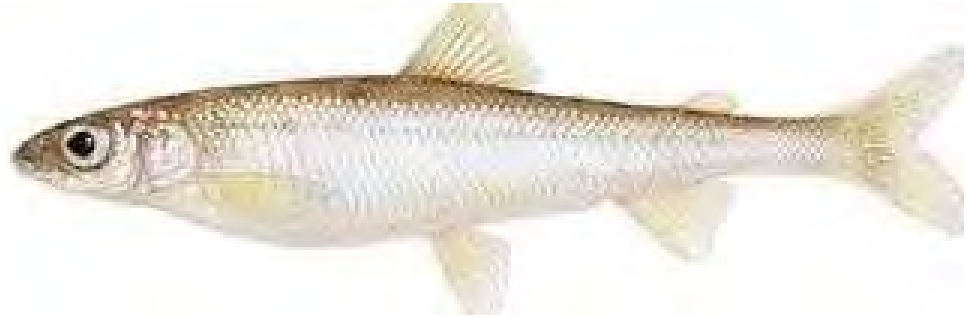
1. Introduction

The diversity and distribution of the fish fauna inhabiting high latitude freshwaters is globally shaped by quaternary climatic cycles. The advancing of multiple glacial shields caused a dramatic reduction and fragmentation of ranges, while the glacial melting and warming led to global hydrological transformations, giving rise to broad opportunities of ecosystem colonization far beyond the boundaries of refugia [1–4]. The Beringian refugium, considered as a vital region for the origin of contemporary fish fauna in the northern North America and easternmost Asia, is one of the least studied sites even in the zoogeographical aspects. Several strictly freshwater species, particularly *Dallia pectoralis* Bean, 1880, *Catostomus catostomus* Forster, 1773, *Coregonus pidschian* Gmelin, 1789, *Cottus cognatus* Richardson,

Blanchfield et al. 2014

Pygmy Whitefish in Montana

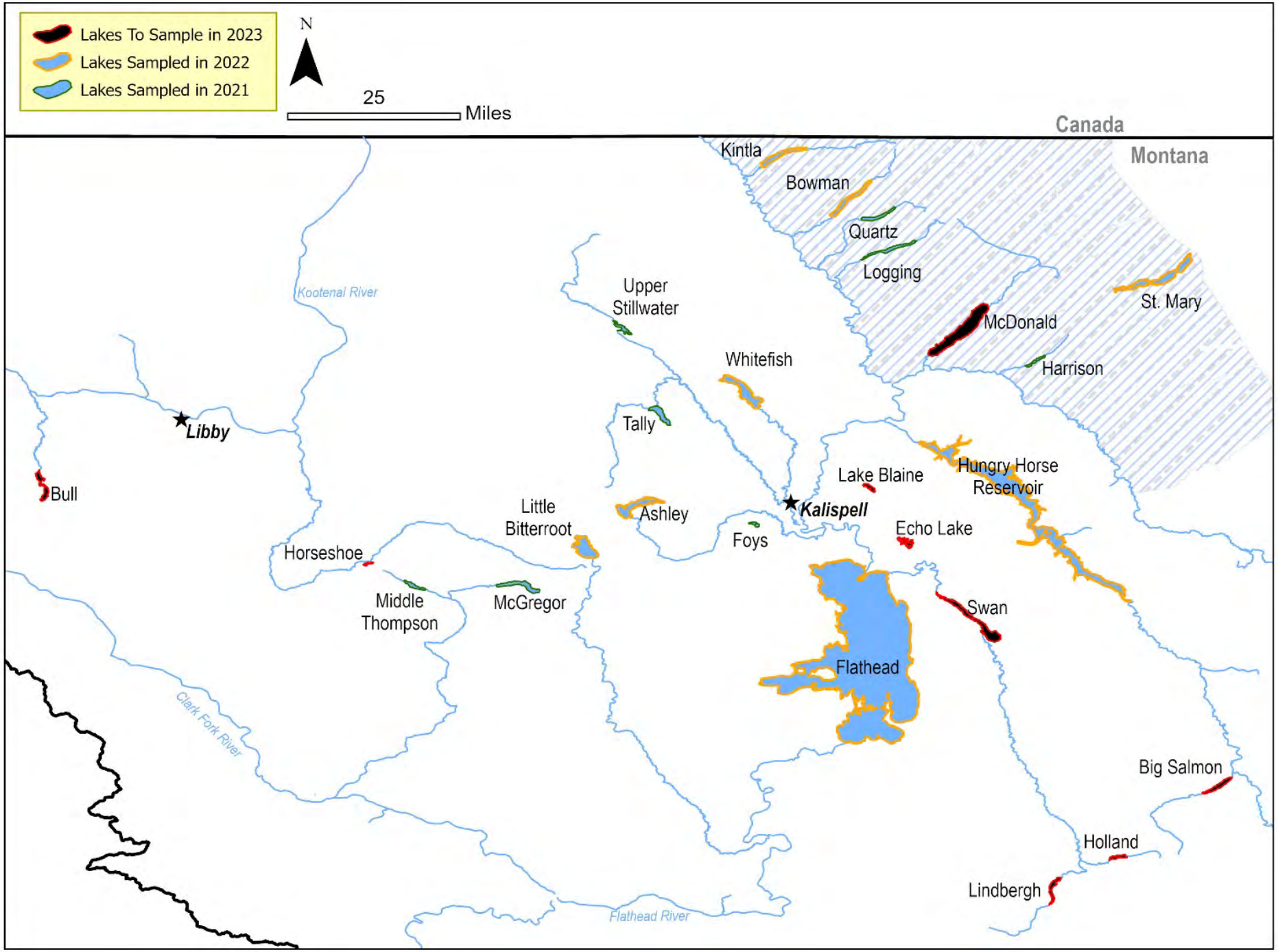
- Understand their distribution in Western Montana
- Length and age
- Investigate genetic structure for relatedness, connectivity, adaptive potential
- Food web characterization using stable isotopes



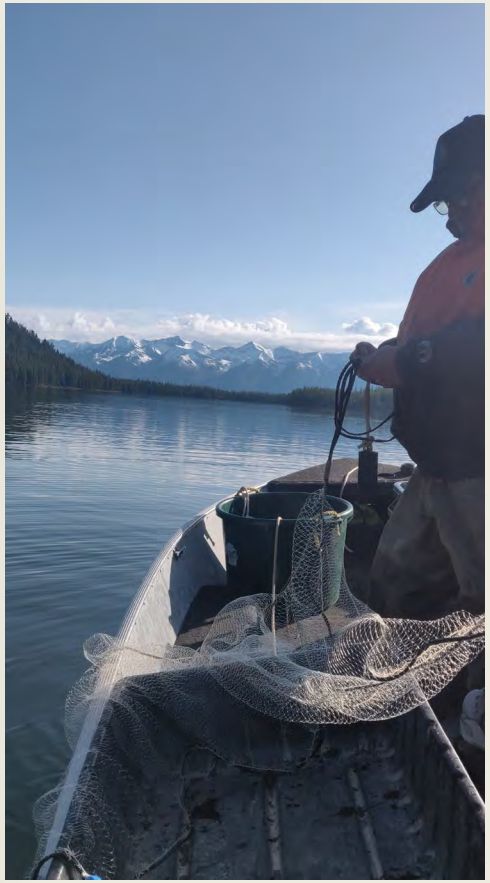
2021 N =5

2022 N =9

2023 N =7



Lindbergh Lake 2023



- 6 gill nets / night
- 5/8 and ½ inch gill net bar
- 50- 150 feet deep
- Littoral drop offs

Big Salmon Lake, Bob Marshall Wilderness 2023

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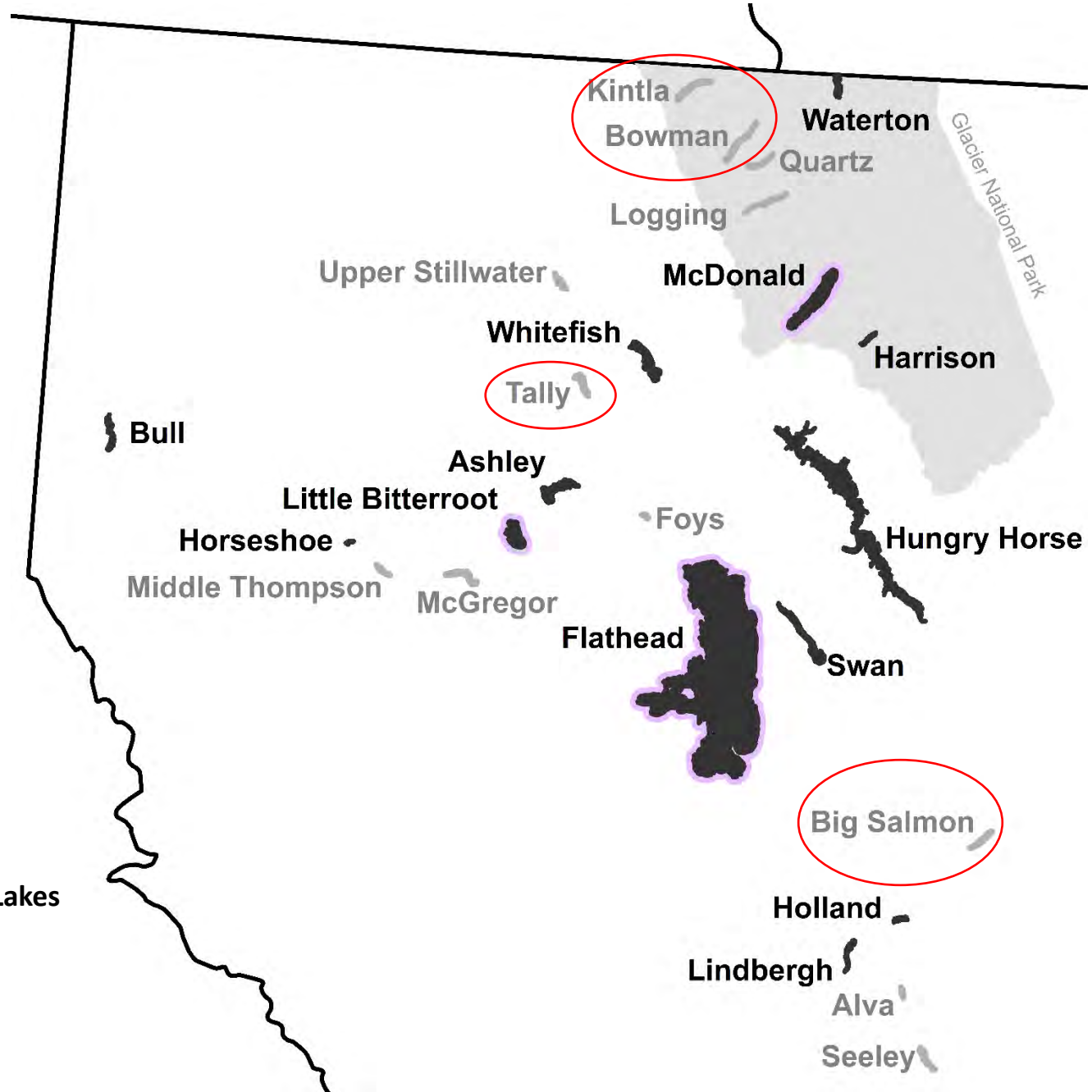
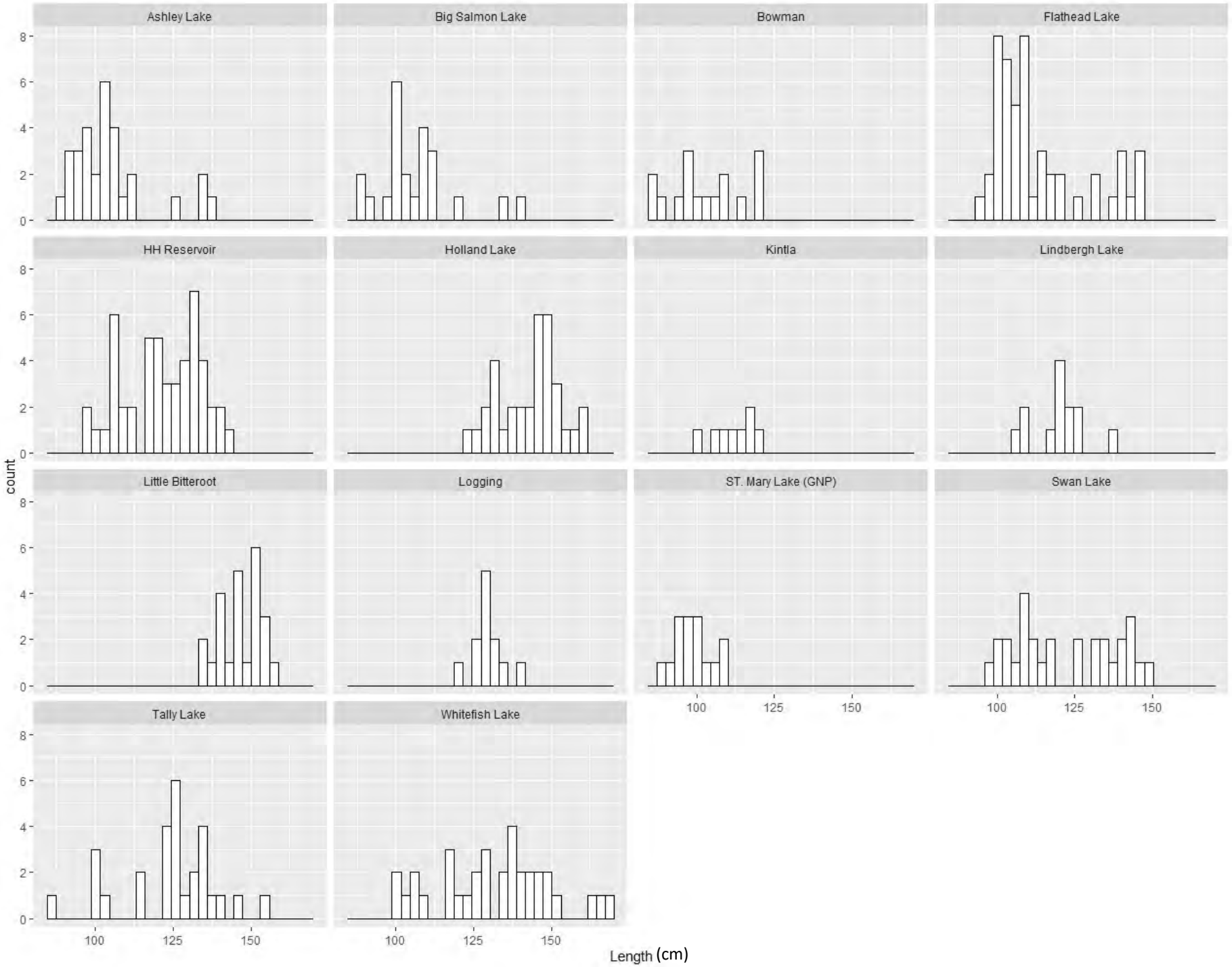
THE **OUTSIDE** IS IN US ALL.

Biologists Discover Rare Native Fish in Two Northwest Montana Lakes



Results

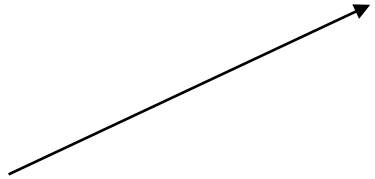
Length



Preliminary Results

Genetic diversity within populations

Population	Num	Eff_num	Ho	Hs
Tally Lake	6.333	3.984	0.611	0.595
Whitefish Lake	8.444	5.389	0.707	0.669
Ashley Lake	7.333	4.322	0.658	0.612
Hungry Horse Res.	7.556	3.836	0.567	0.572
Little Bitteroot Lake	7.556	4.942	0.675	0.644
Flathead Lake	9.222	5.215	0.68	0.668
St. Mary Lake (GNP)	2	1.265	0.2	0.163



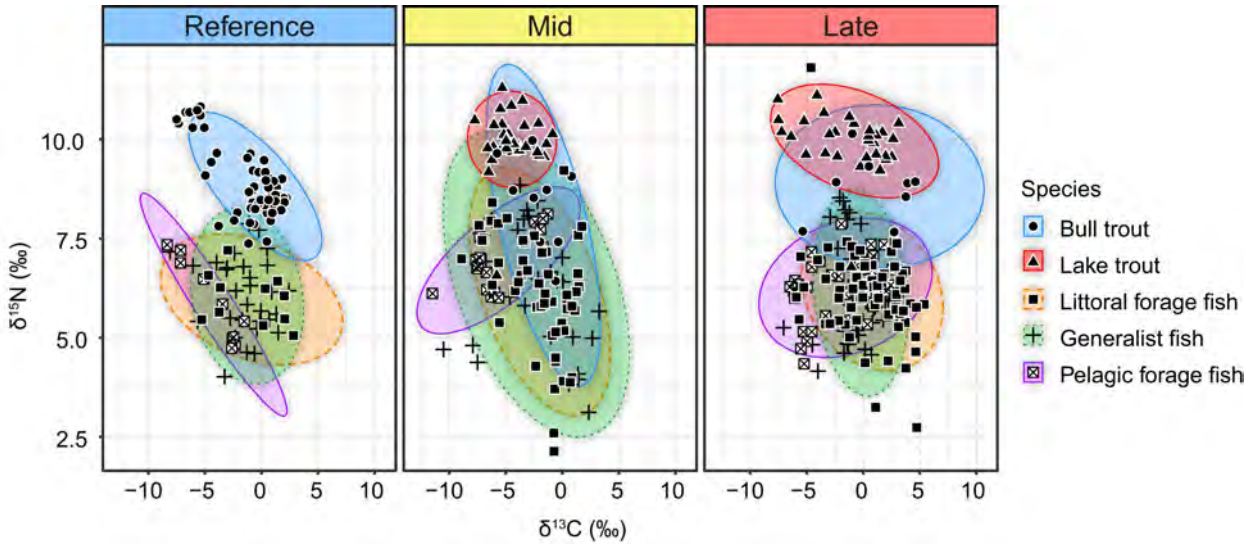
Ho = Observed Heterozygosity – genetic variability ranging from 0 - 1

Preliminary Results
Genetic differentiation among populations

Fst Statistic Table						
Populations	Tally	Whitefish	Ashley	Hungry Horse	Little Bitterroot	Flathead
Whitefish	0.0301					
Ashley	0.1767	0.1558				
Hungry Horse	0.1128	0.0413	0.2026			
Little Bitterroot	0.1117	0.1096	0.0453	0.1171		
Flathead	0.0882	-0.0022	0.1828	0.0378	0.127	
St Mary	0.7081	0.7435	0.8073	0.8189	0.8137	0.7648

Future Work – Food Web Analysis

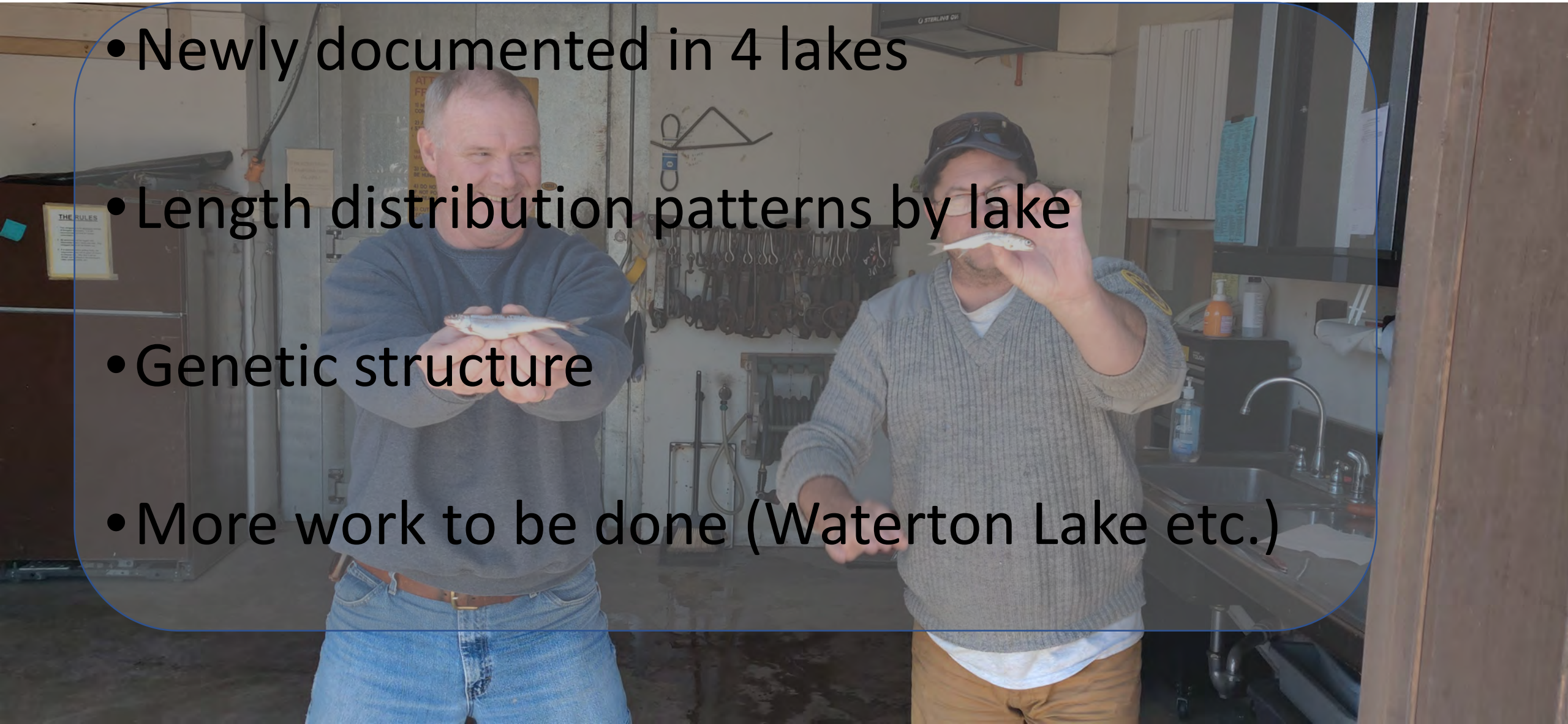
Lake Name	Surface Elevation (m)	Surface Area (ha)	Max Depth (m)	Invasion Phase
Kintla	1221	1039	120	Invaded
Bowman	1228	910	77	Invaded
Lower Quartz	1277	80	19	Invaded
McDonald	961	2760	144	Invaded
Lindbergh	1369	329	36	Invaded
Grace	1208	52	30	Reference
Trout	1189	114	50	Reference
Big Salmon	1340	393	42	Reference
Hungry Horse Reservoir	1112	9630	149	Reference
Logging	1161	581	60	Remediated
Swan	940	1335	43	Remediated
Quartz	1345	352	84	Remediated



Wainwright et al. 2021

Conclusions

Conclusions



- Newly documented in 4 lakes
- Length distribution patterns by lake
- Genetic structure
- More work to be done (Waterton Lake etc.)

Questions?

Little Bitterroot Lake, 10 inch, 2010 State Record