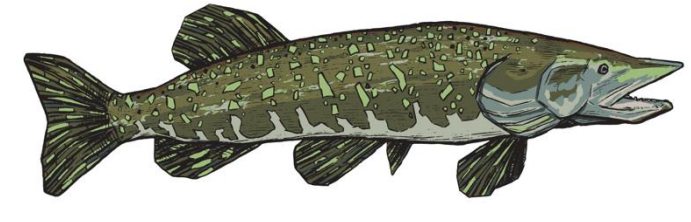


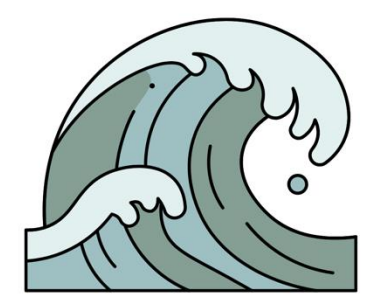
Using genomics to determine origins and dispersal patterns of invasive northern pike (*Esox lucius*) in southcentral Alaska

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Background



Invasive species significantly threaten local ecosystems, economies, and native cultures; however, little is known about the mechanisms, especially genetic mechanisms, that predispose some species to becoming successful invaders. One such invader, the northern pike (*Esox lucius*), is native to the northern and central Alaska, but was introduced to southcentral Alaska in the 1950s (Figure 1). Since introduction, invasive pike have dramatically altered native fish communities, especially local salmonids, negatively impacting the local economy and local ecosystems.

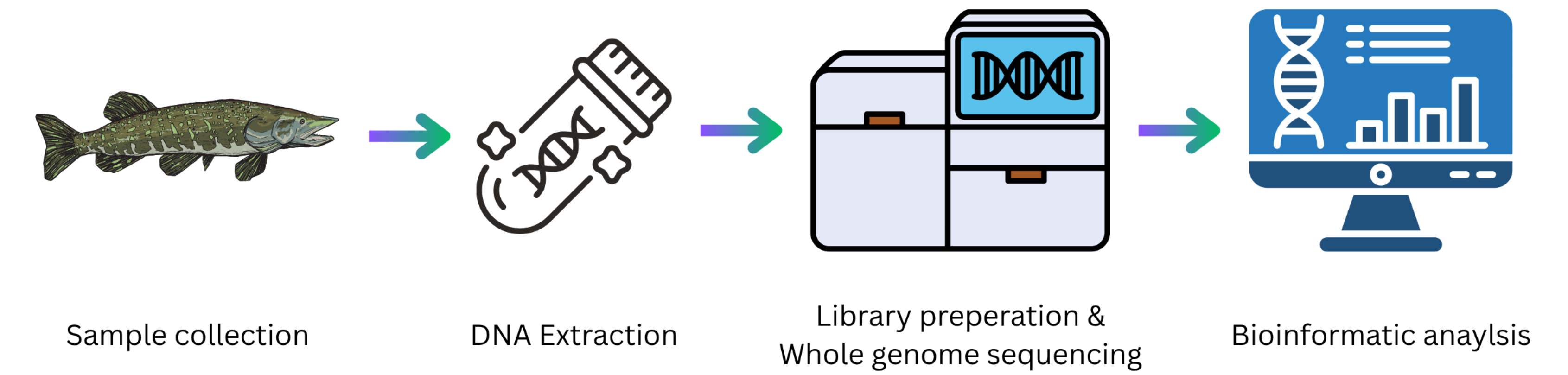


Until recently, North American pike were considered a freshwater species unable to survive in seawater. However, otolith microchemistry analyses suggest they spend some degree of time in marine environments in Alaska, suggesting they may be able to occupy and disperse through the marine environment to colonize new watersheds. Understanding salinity tolerance mechanisms is critical for predicting dispersal routes and developing effective management strategies.

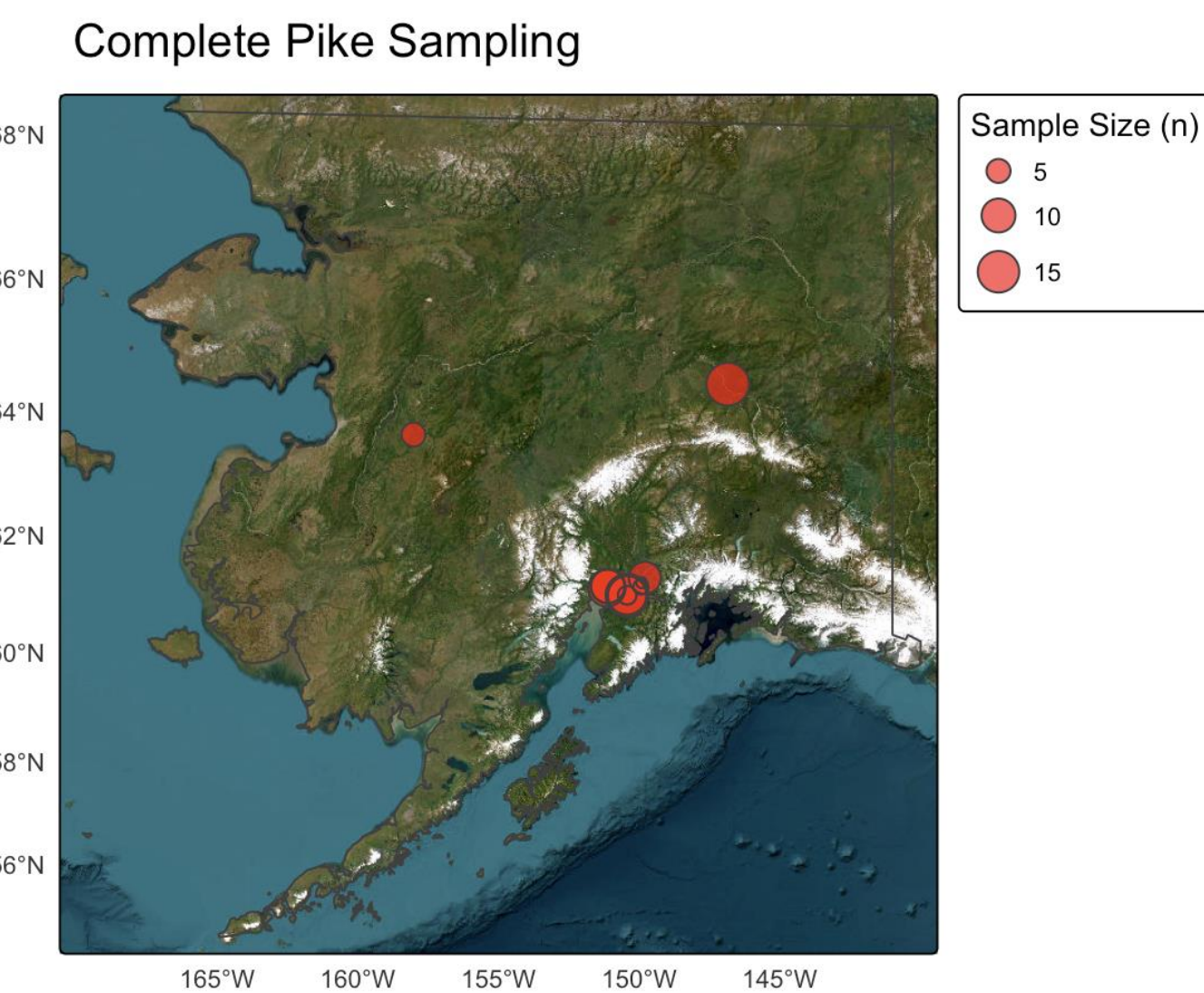
Research Questions

- 1) Is there a genetic adaptation to marine dispersal in invasive pike?
- 2) What populations of pike have the genetic component that allows them to disperse?

Methods

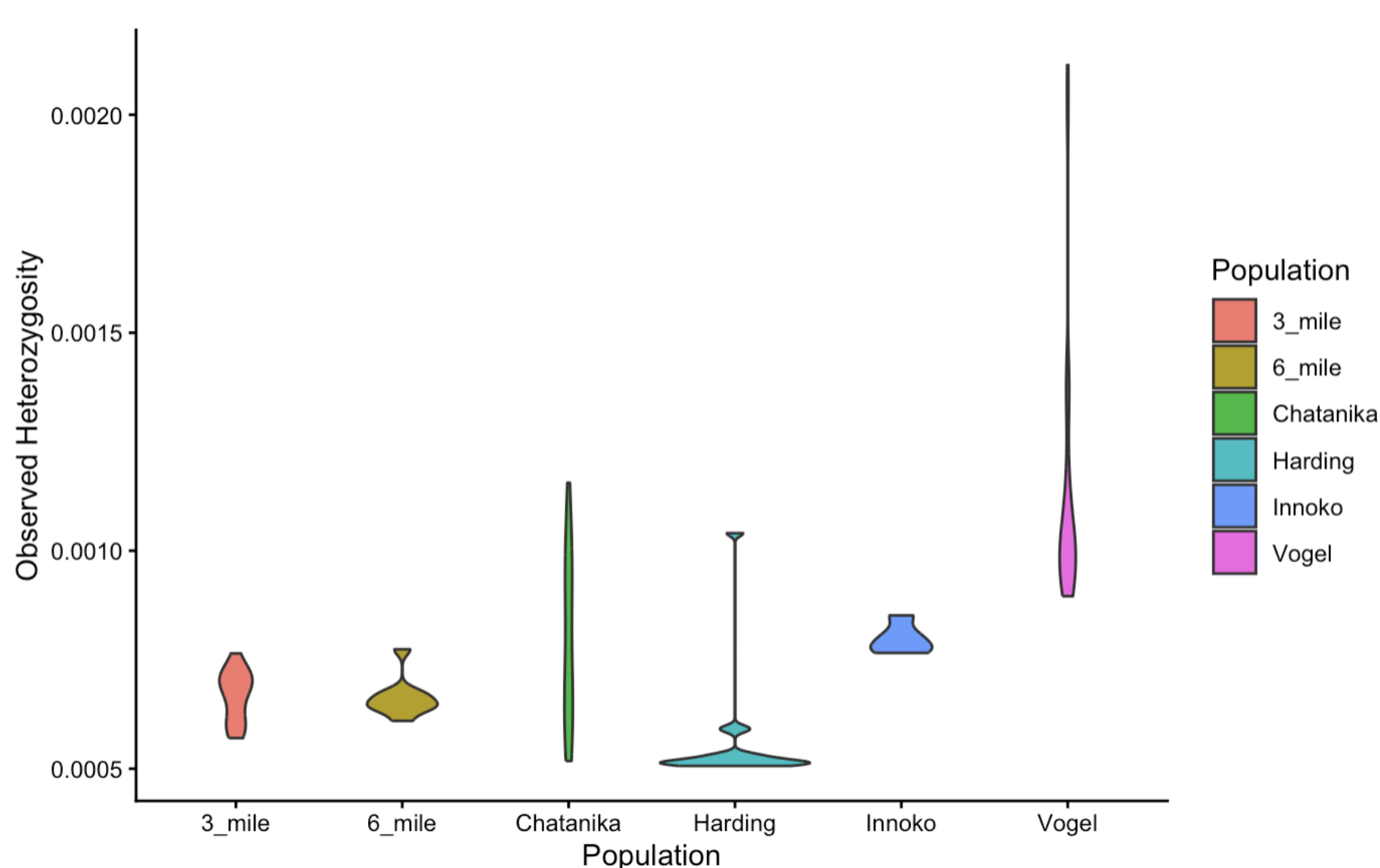
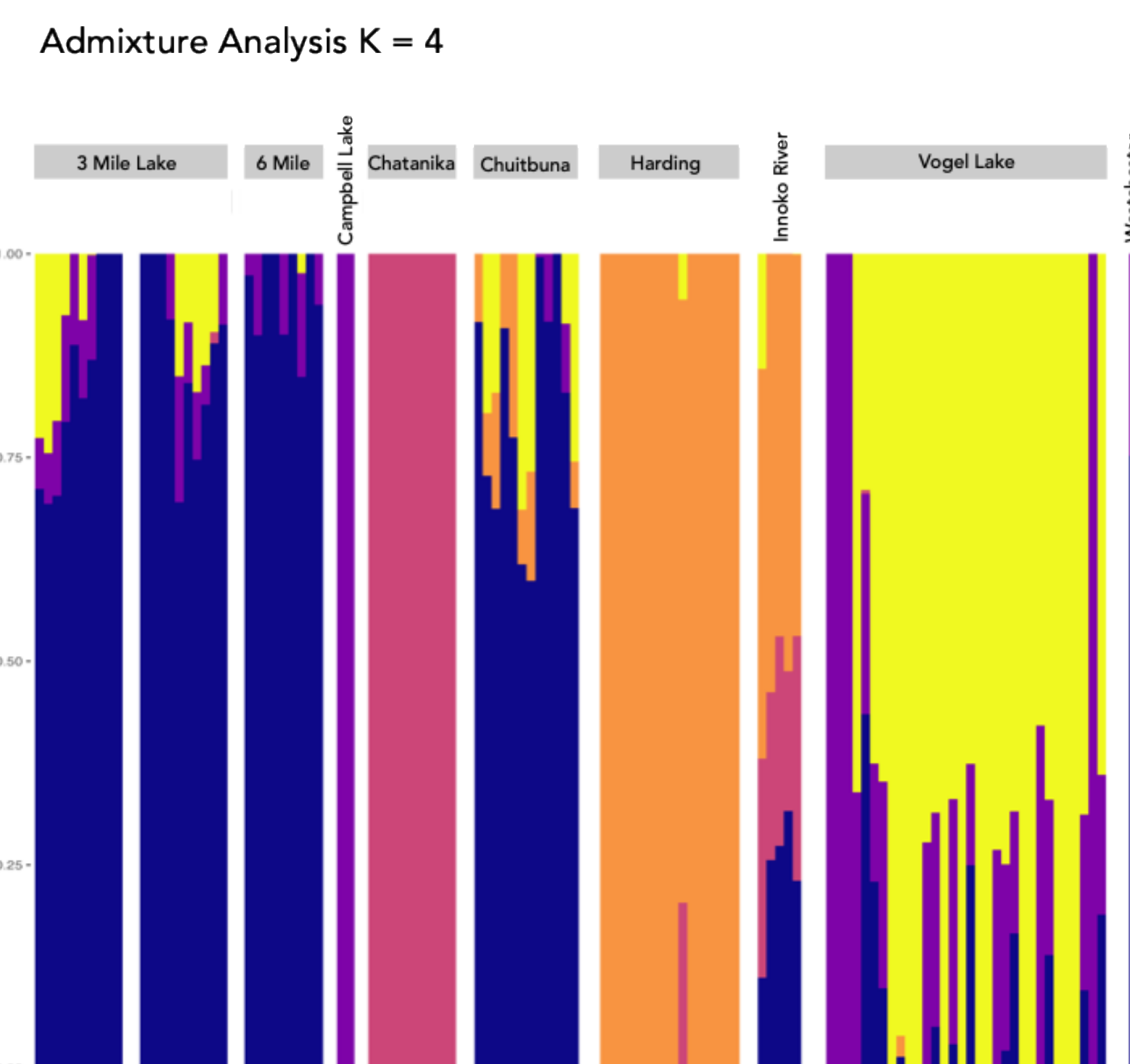
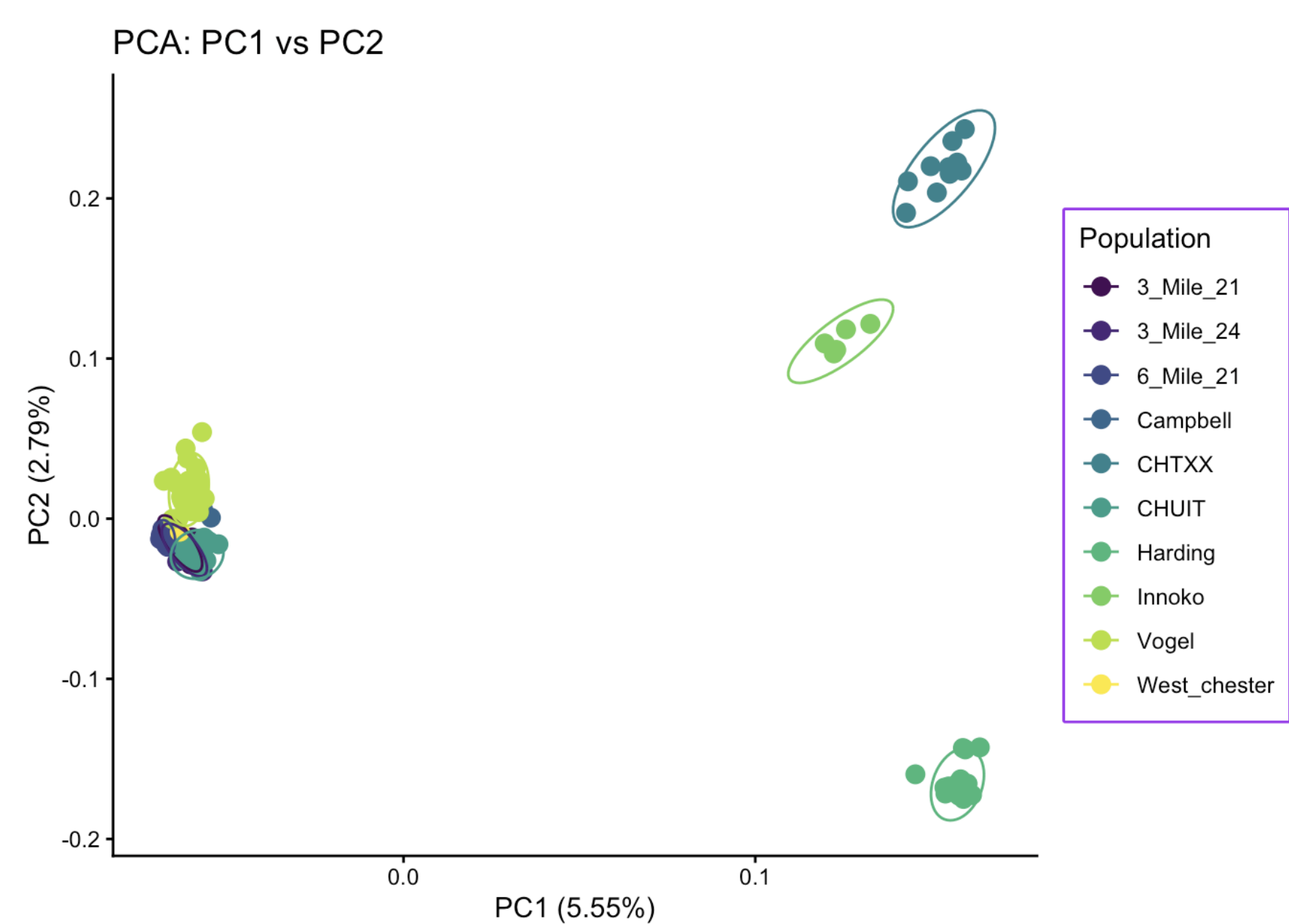


	Population	n
Native Populations	Chatanika River	10
	Harding Lake	16
	Innoko River	5
Invasive Populations	3 Mile Lake	20
	6 Mile Lake	9
	Campbell Lake	2
	Chuitbuna Lake	12
	Vogel Lake	32
	Westchester Lagoon	1
		N = 107



Results

Population Structure



	Chuitbuna	3 mile	6 mile	Harding	Chatanika
Chuitbuna					
3 mile	0.012				
6 mile	0.036	0.030			
Harding	0.227	0.236	0.262		
Chatanika	0.210	0.214	0.228	0.171	
Vogel	0.040	0.051	0.067	0.236	0.193

Conclusions & Future Chapters

Funding and Acknowledgments

