Bull Trout (*Salvelinus confluentus*) Population Structure and Extent of Hybridization with Brook Trout (*S. fontinalis*) Across Alberta's Eastern Slopes

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Abstract: Biodiversity loss on Earth is increasing, primarily from anthropogenic (human) impacts and the threat of climate change. Native bull trout (*Salvelinus confluentus*) is one species in Alberta that are currently threatened and require conservation action to survive. To aid in species management goals, we performed a genetic analysis on fish samples across the province. This was performed to determine the extent non-native hybridization, and the genetic population structure of bull trout across Alberta.

Introduction

Bull trout (*Salvelinus confluentus*) is a species of freshwater charr native to Canada and the USA. Currently, bull trout face population decline, due to climate change, habitat loss, river fragmentation, over-fishing and increased competition and hybridization with non-native brook trout (*S. fontinalis*). Though limits on stocking brook trout have been implemented since 2011, naturalized populations still exist in Alberta, which threaten the native bull trout's persistence. While hybridization exists between these two species, little is known on this risk in AB; to investigate this, I performed genetic analysis on n=1200 samples, collected by Alberta Environment and Protected Areas (AEPA) staff, with the objective of determining the extent of hybridization on bull trout with brook trout, and to also observe the genetic population structure of bull trout across Alberta.

Methods

Genetic loci known as Single Nucleotide Polymorphisms (SNPs) were used to investigate samples from 24 Hydrologic Unit Code (HUC) 8 watersheds (i.e. regional AB watersheds). These 24 watersheds are found along the Eastern Slopes of Alberta. The diagnostic SNPs, developed by the Montana Conservation Genomics Group (see: Amish et al. 2022), were used to determine the percentage of bull trout or brook trout ancestry in each of our samples. To determine population genetic structure, ADMIXTURE ancestry analysis (Alexander et al. 2009) were performed, which looks at different population clusters based on ancestry estimates. These were then plotted on QGIS to observe the landscape genetics of bull trout across Alberta.

Results

We found that hybridization outcomes vary site-to-site, and also between nearby watersheds; essentially, hybridization between bull trout and brook trout was limited beyond F1 generations, indicating that while the F1 hybrids remain fertile, low amounts of backcrossing into post-F1 generations exists; of the 1200 samples, only 42 hybrids were found, and of these, only 7 were post-F1 generation. In regards to genetic population structure analyses, a clear population split exists between bull trout in either of the two continental basins; this corresponds to COSEWIC's designation of bull trout in two Designatable Units (DUs) (COSEWIC 2009) and suggests the presence of two distinct populations in northern and southern Alberta. Within-watershed diversity was also observed, indicating a high amount of local diversity, resulting in a 'nested metapopulation structure'.

Discussion

Hybridization appears dependent on brook trout abundance; thus, management of non-native brook trout may be beneficial in reducing unwanted hybridization on bull trout. Two clear genetic populations at the broadest level validates the notion that two genetically different bull trout populations exist (i.e. the two Designatable Units); we, therefore, suggest that Alberta requires distinctive management between the north and south populations as a means of protecting evolutionary significant genetic lineages. We also suggest management at a local scale consider finer genetic structure, as a means of protecting local adaptations and the overall genetic integrity of discrete bull trout sub-populations.

References

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