

TITLE: STABLE ISOTOPE AND GENETIC ANALYSIS OF ABOVE-BARRIER, BELOW-BARRIER, AND IN-LAKE BROOK TROUT POPULATIONS WITHIN MINNESOTA WATERS OF LAKE SUPERIOR AND ITS TRIBUTARIES

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COSTS: \$53,000 (\$33K FIELD OPS + \$20K GENETICS) **PROJECT DATES:** Jan. 1, 2021 – December 31, 2023

RATIONALE: The Lake Superior Partnership Working Group's recommended science and monitoring priorities includes rehabilitation efforts for species of conservation such as Brook Trout. Genetic, ecological, and behavioral studies that describe past and present Coaster Brook Trout stocks in Lake Superior compared with resident populations are limited (Newman and Dubois 1996; Newman et al., 2003), especially in Minnesota waters (Miller et al. 2016). Minnesota provides a distinctive opportunity for such studies due to the steep topography and waterfall barriers near Lake Superior on almost all tributaries, which limits stream habitat below barriers and isolates above-barrier Brook Trout populations. The degree to which below-barrier populations are sustained by migrants from above or reproduction below barriers is unknown, as is the origins of individuals in the lake. Previous studies indicate that microsatellite DNA markers should have sufficient power to address questions of origins and gene flow (D'Amelio and Wilson 2008, Miller et al. 2016). Coasters are a life-history variant derived from resident populations, but the contribution of genes and the environment to migratory behavior is uncertain (D'Amelio and Wilson 2008; Elias et al. 2018). Combining isotope data on lake residence time with genomic data [i.e., single-nucleotide polymorphisms (SNPs), Elias et al, 2018; M. Meek, Michigan State University, unpublished data], can further determine whether genetic variants are associated with the Coaster ecotype. Finally, the ancestry of above-barrier populations is uncertain. Eddy and Underhill (1974) indicate that brook trout were likely absent above barrier falls in most Minnesota tributaries. Current populations may descend from transfers of local fish or stocking of Eastern U.S. hatchery lineages. Remnant populations or life-history variants of Brook Trout (i.e., Coasters) need to be protected, where they exist.

Brook Trout have a longstanding, important role in the Lake Superior food web, so understanding the interactions and role of Brook Trout in the food web of Lake Superior and its tributaries is critical. Our results will support on-going sampling efforts and collaborations to collect and analyze stable isotope data to determine food web interactions and life-history diversity among Lake Superior fish populations, and help reach population goals for Brook Trout outlined in MN DNR's [Fisheries Management Plan for the Minnesota Waters of Lake Superior](#) and in the lake wide Lake Superior Brook Trout Rehabilitation Plan. Our project will also support a lake-wide Brook Trout microchemistry study being proposed for CSMI funding by the Lake Superior Technical Committee/Aquatic Community Committee for which MN DNR will also collect and contribute samples to. The compilation of all of this work will provide managers with information needed to better understand the possible units for conservation and management and where to focus future Brook Trout rehabilitation efforts.

OBJECTIVES: Define metapopulation dynamics (movement) and genetic structure (gene flow) of Brook Trout among the three known ecotypes (above barriers, below barriers and in-lake) with stable isotopes and genetics.

METHODS: Brook Trout will be sampled from approximately twenty tributaries to Lake Superior and twelve in-lake locations (target N=50 per sample) in Minnesota waters partnering with the Grand Portage Band of Lake Superior Chippewa to share staff and equipment resources. MN DNR/GPB staff will collect fin tissues for stable isotope and genetic analysis. Stable isotope analysis will be completed by Dr. Joel Hoffman at the USEPA Mid-Continent Ecology Division Laboratory. Microsatellite genetic analysis will be completed by Dr. Loren Miller at the University of Minnesota Aquatic Genetics Laboratory to assess origins of and gene flow among Brook Trout ecotypes. He will also identify populations and individuals best suited for further higher-resolution genomic analysis (no funding requested in the proposal), likely through collaboration with Dr. Mariah Meek (Michigan State University), who is currently applying SNPs to many of these same

questions about population genetic structure and origins of coaster and resident Brook Trout across Lake Superior, but with small representation of Minnesota populations. MN DNR will also continue (and possibly expand) our [Coaster Genetics Project](#) with anglers to increase collections from Lake Superior tributary habitats that are difficult to sample with traditional electrofishing gear, increasing genetic sample size at no additional cost.

RELEVANCE: This project is relevant to Annex 2, 7, 8, and 10 of the Great Lakes Water Quality Agreement and Great Lakes Restoration Initiative, Action Plan III Focus Area 4 by providing scientific information pertinent to management, protection, and restoration of native species.

DELIVERABLES/PRODUCTS: We will identify a subset of samples with known histories of lake use suitable for genomic analysis of gene flow, ancestry and genetic variants associated with the Coaster ecotype. A final report will be made by the project end date. We expect to publish at least one paper in a scientific journal within a year of the completion of the study. In addition, as results are obtained throughout the study they will be presented to Great Lakes Fishery managers and to other agencies that are interested in these data.

D'Amelio, S., Wilson, C., 2008. Genetic population structure among source populations for coaster brook trout in Nipigon Bay, Lake Superior. *Trans. Am. Fish. Soc.* 137:1213–1228.

Eddy, S., and J.C. Underhill. 1974. *Northern Fishes, With Special Reference to the Upper Mississippi Valley*. third ed. University of Minnesota Press, Minneapolis (414 pp.).

Elias, A., R. McLaughlin, R. Mackereth, C. Wilson, K.M. Nichols, 2018. Population structure and genomic variation of ecological life history diversity in wild-caught Lake Superior brook trout, *Salvelinus fontinalis*, *J. Great Lakes Res.* 44:1373-1382.

Miller, L.M., D.R. Schreiner, J.E. Blankenheim, M.C. Ward, H.R. Quinlan, S. Moore. 2016. Effects of restrictive harvest regulations on rehabilitation of coaster brook trout in Minnesota's portion of Lake Superior, *J. Great Lakes Res.* 42:883-892.

Newman, L. E., and R. B. DuBois. 1997. Status of brook trout in Lake Superior. Prepared for the Lake Superior Technical Committee by the brook trout subcommittee. Great Lakes Fishery Commission.

Newman, L. E., R. B. DuBois, and T. H. Halpern, editors. 2003. A brook trout rehabilitation plan for Lake Superior. Great Lakes Fishery Commission, Miscellaneous Publication 2003-03, Ann Arbor, Michigan.