Effective fisheries management and restoration requires reliable estimates of abundance and population trajectories through time. However, absolute population estimates are extremely difficult to obtain in large systems due to the prohibitively high sample sizes required by most approaches. Close-kin mark-recapture (CKMR) is a new technique that can obviate this hurdle by using the observed kinship within a sample to estimate the true adult abundance. We are developing a CKMR model for lake trout (*Salvelinus namaycush*) in Lake Champlain in order to evaluate the size of the parental population contributing to the recently-observed (and much celebrated) wild recruitment. In addition to providing information for managing Champlain’s population, the resulting analysis pipeline will be designed with enough flexibility for application to other systems and species.

Despite evidence of sustained wild recruitment, Lake Champlain’s lake trout population in still primarily a stocked fishery. While the drivers behind the recent recruitment success are unknown, shifts favoring the survival of wild fish could similarly affect stocked juveniles, suggesting that the current stocking strategies may produce different results than they have in the past. Until 2022, Champlain was stocked with ~82,000 fish annually that came from either New York (33% of total, “Seneca strain” fish stocked at age-1 in the spring) or Vermont (66% of total, “Champlain strain” fish stocked at age-0 in the fall). With the onset of wild recruitment this stocking has been adjusted downwards by eliminating the New York portion. However, the relative survival and performance of the two stocking components are unknown. We designed a sequencing-based genetic marker panel to identify the origin of stocked fish in the lake. In combination with an archived tissue samples from 2000+ fish and maxillary aging, we are conducting a mixed-stock analysis in order to inform future stocking adjustments.

Burbot (*Lota lota*) is the only freshwater cod species and has the widest distribution of any freshwater fish, inhabiting cold lakes and rivers throughout the northern hemisphere. Although the species is likely an important component of the food web in many northern lakes, most populations are largely unstudied. In Lake Champlain, the construction of several causeways in the 1800s has potentially isola

Anthropogenic habitat fragmentation can isolate segments of populations and lead to genetic differentiation. Fragmentation is common in terrestrial systems (e.g., by roads) and rivers (by dams), but rare in lakes. Lake Champlain is naturally structured by several large islands, and construction of several causeways in the 1800s isolated three large basins from the Main Lake. Our objective was to determine whether the causeways have contributed to genetic differentiation of fish species within and among the lake basins. We focused on burbot (Lota lota), a circumpolar freshwater cod species that occupies deep lakes and rivers; populations have declined throughout much of their range due to commercial harvest and dams. Burbot were collected from a tributary, two regions of the Main Lake separated by approximately 12 km, and the Inland Sea, an isolated basin connected to the Main Lake only through narrow, shallow openings. Because burbot are a coldwater species, they would not have access to the causeway openings except in winter. We used low-coverage whole-genome sequencing and principle components analysis to assess genome-wide differences among samples.

Observed variation in nuclear DNA indicated isolation by distance between fish captured in the two regions of the Main Lake, and genetic separation among fish captured in the Main Lake, its tributary, and the Inland Sea. Mitochondrial DNA data indicated at least three maternal lineages, all of which are shared between the Main Lake and Inland Sea. Lack of differentiation in the much smaller mitochondrial genome supports the hypothesis that isolation between the lake basins is a recent phenomenon. The river population apparently arose from one Main Lake maternal lineage and has diverged from the lake population since colonization of the tributary. The presence of genetic structure suggests that human activities have fundamentally altered the population dynamics of this top predator, with implications for both burbot conservation and the larger food web.