

Genetic Research on Brook Trout and Lake Trout in Algonquin Park

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Advances in genetic technology over the past two decades have provided a variety of molecular genetic marker systems that are enabling new insights into the historical and contemporary processes that influence fish biology. Genetic research on brook trout (*Salvelinus fontinalis*) and lake trout (*Salvelinus namaycush*) in Algonquin Park is allowing us to examine issues ranging from the phylogeographic history of these species to the effectiveness and effects of past stocking efforts and reproductive success of individual fish.

Phylogeographic analysis of brook trout populations within the Park using mitochondrial DNA (Danzmann and Ihssen 1995) showed that the mitochondrial structure and diversity of Park populations primarily reflects post-glacial recolonization events, despite intensive stocking throughout most of the 20th century. By contrast, analysis of these same populations with polymorphic isozyme markers shows that past stocking events have had major impacts on native populations of brook trout (Ihssen *et al.*, unpublished data). Most of the extant brook trout populations within the Park contain at least some hatchery genes, which vary by watershed and proximity to the Highway 60 corridor. This mixed ancestry may have a direct influence on population-level fitness and life history characters, as growth rates within populations vary with the extent of hatchery ancestry (P. Ihssen, pers. comm.). Evidence from experimental stocking may also indicate variable fitness of mixed-ancestry (hatchery / native) brook trout, based on the extent of wild versus hatchery genes (Quinn and Wilson, this volume). This has obvious implications for management of brook trout populations within the Park, and the development of a Dickson Lake brook trout broodstock for stocking in the Park. Other current research is examining the metapopulation dynamics of brook trout populations in the Park, using microsatellite DNA markers and tagging data to evaluate movement among streams and lakes, the importance of tributary streams to lake populations, and connectivity among habitats.

Recent work on brook trout in Scott Lake has examined the behavioural genetics and reproductive success of individual fish during spawning, using microsatellite DNA (Blanchfield *et al.*, in prep). Despite observed attempts by multiple males to spawn with individual females, the majority of broods were fathered by single males. Male reproductive success varied with body size, over one third of the observed broods resulted from fertilization by two of the largest males. Smaller female brook trout showed no preference for mating with related versus unrelated males, whereas larger brook trout only mated with unrelated males.

Populations of lake trout within the Park primarily originated from a Mississippian refugium after the last deglaciation event (Wilson and Hebert 1996, 1998). Isozyme analysis of Park populations has so far failed to detect additional populations of the Haliburton 'glacial relict' lake trout (Ihssen *et al.* 1988), but have detected some unique biodiversity elements. Investigation of a unique 'silver' morphotype in Kingscote Lake has confirmed the genetic uniqueness of this population, despite intensive stocking between 1925 and 1985 (Yott 2000). Current research efforts are focused on identifying other unique

biodiversity elements and using molecular markers to quantify the historical demographics of lake trout populations in relation to carrying capacity and management practices.

References

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