

Mitigating fisheries-induced evolution in lacustrine brook charr in southern Quebec

Kenichi Okamoto

*Department of Ecology and Evolution,
University of California, Los Angeles, USA*

Goal

To develop a comprehensive fisheries management policy that mitigates fisheries-induced evolution in lacustrine brook charr populations in southern Quebec.

Background and motivation

Size-selective mortality due to fishing can impose strong selection on harvested fish populations, causing evolutionary changes in key life-history traits such as size at maturation (e.g., Swain et al. 2007). Understanding and predicting harvest-induced evolutionary change is crucial for the long-term maintenance of sustainable fisheries (e.g., Jørgensen et al. 2007). In this project, I will investigate optimal management strategies for an evolutionarily sustainable fishery of the lacustrine brook charr (*Salvelinus fontinalis*) in southern Canada. Brook charr inhabit a series of lakes, some of which are harvested, while some are not (Magnan et al. 2005). This provides an ideal model system for investigating harvest-induced evolutionary changes and developing management strategies that mitigate such changes. Using data collected over the years on brook charr ecology by the Research Group on Aquatic Ecosystems at l'Université du Québec à Trois-Rivières, I parameterized an eco-genetic model (akin to the approach of Dunlop et al., submitted) with the aim of investigating the effects of harvesting on life-history variation in brook charr populations. The important next step will be to elucidate optimal management strategies for the brook charr populations.

Research questions

The goal of this research project is to develop a comprehensive fisheries management policy to slow down or reverse ongoing and past evolutionary change due to harvesting practices, and to minimize the risk of future change by improving these practices. More specifically, we will address the following questions:

- How can fisheries managers manage fishing effort to minimize future evolutionary change in brook charr populations?
- How does the translocation of individuals with late-maturing genes from unharvested to harvested lakes curtail ongoing evolutionary change in the latter?
- How can these two strategies be effectively combined?

Methods and work plan

Akin the approach of Dunlop et al. (submitted), the eco-genetic model for this project will follow an individual-based implementation (e.g., DeAngelis and Mooij 2005).

Ecological model

I will consider a population of brook charr that inhabit a single lake with a single dynamic resource (e.g., zoobenthos). While the charr are modeled individually, the resource is not, and in each lake the resource density grows according to a logistic growth curve in the absence of charr predation. The charr consume the resource, and thus grow in both weight and length. Somatic growth is density-dependent, and thus slows down when resource availability is low. A proportion of mature individuals reproduce once a year, depending on whether they consumed enough food during the year to allocate energy reserves to gonadal mass. Brook charr are iteroparous, and reproduce two to three times after they mature. An individual's size at maturation is a function of both genetic and environmental effects. Following the approach described in Dunlop et al. (submitted), I will assume that maturation is governed by a probabilistic maturation reaction norm (PMRN; Heino et al. 2002), describing the weight- and age-specific probabilities of maturation in a given season. At the beginning of a given mating season, the probability that an individual of age a , sex g , and size w_a is mature is given by $p_m = [1 + \exp(-(w_{a,g} - w_{p50,a,g})/d)]^{-1}$, where $w_{p50,a,g} = i_g + as_g$ describes the PMRN midpoint (i.e., the weight at which 50% maturation probability is reached) at age a for sex g , and d is a constant that describes how steeply p_m changes around the midpoint. The quantities i_g and s_g are sex-specific evolving traits (see below). Sex is assigned randomly at birth. All individuals suffer a size-specific risk of fishing mortality and natural mortality, with the latter representing both density-independent mortality (e.g., predation by aquatic birds such as cormorants) and density-dependent starvation mortality.

Genetic model

Each individual charr carries a diploid genome. An individual's evolving trait values are determined by the additive effect of between 1 and 25 autosomal loci. All loci are weighed equally, with the initial allelic values at each locus for the evolving traits i_g and s_g being drawn randomly between 0 and M_i/n or M_s/n , respectively, where n is the number of loci. All loci are freely recombining, although the number of loci can be interpreted as characterizing tight linkage groups. To assess the effects of neutral processes such as genetic drift on the evolving populations each locus will have a neutral counterpart that has the same initial allelic value and is subject to the same mutation rate, but plays no part in determining the individual's phenotype, and thus does not affect fitness. Time permitting, I will also examine the sensitivity of the model's predictions to the genetic architecture of the evolving traits determining the PMRN: in particular, I will consider the effects of epistasis and dominance (e.g., Roff 1997). Mature males and females are paired up at random, with individual males being able to pair up with more than one female during the mating season (e.g., Thériault et al. 2006). Prior to reproduction, each parent produces a haploid gamete that contains, at random, half the parental alleles. With a small mutation probability (ca. 10^{-6}), the allelic value at a locus changes by a random amount drawn from a normal distribution with zero mean and a standard deviation that is proportional to M_i/n or M_s/n , with allelic values being bounded from below by 0. The gametes of each parent fuse to determine the genotype of the offspring. This approach follows the model of Strand et al. (2002) and the individual-based implementation of van Doorn

and Dieckmann (2007). For the sake of simplicity, I will assume that life-history traits other than size at maturation (such as offspring size, maternal investment in gonadal mass, and rates of somatic growth) are not subject to evolutionary change.

Model analysis

I will run the model for 2000 years to allow populations to attain their demographic and evolutionary equilibrium. Subsequently, I will compare the predicted evolving traits i_g and s_g to those observed in the field (e.g., Hendry 2003). This allows a direct comparison of the predictions of the eco-genetic model in the absence of harvesting to values observed in nature, thereby providing a measure of the model's capacity to mirror the system's ecological and evolutionary processes. Afterwards, I will run the model for a further 50 years with a given harvesting strategy. I will also run the model for entire 2250 years without harvesting in order to characterize its baseline behavior.

The first management policy I will investigate is based on harvesting that optimizes annual fishing effort. This is the level of fishing effort that maximizes the number and size of individuals harvested each year, while minimizing the risk of harvest-induced evolutionary change. Since increasing fishing yield is bound to increase harvest-induced evolutionary change, the goals of this policy imply a trade-off. I will employ a genetic algorithm (e.g., Taylor and Hastings 2004) to determine the optimal harvest strategy that strikes the best balance between these competing objectives. Considering a 50-year time frame, I will examine 100,000 harvest strategies initially sampled from a multivariate uniform distribution. Each harvest strategy is characterized by five parameters, $\{\alpha, \beta, a, b, c\}$. The first two parameters determine the size-dependence of harvesting. Specifically, selectivity at weight w is assumed to be proportional to $p_f = [1 + \exp(\alpha + \beta w)]^{-1}$. The last three parameters determine the density-dependence of harvesting. In particular, the total allowable catch in year t is assumed to be given by $Y_t = a + bH_t + cH_t^2$ (Eikeset et al., in preparation), where $H_t = \sum_i w_{i,t} p_{f,i,t}$ is the harvestable biomass in year t , with the sum extending over all fish i . The fishing season is assumed to lie between the growing season and the mating season. The annual probability of a fish at weight w to get harvested is thus given by $p_f Y_t / H_t$. This probabilistic treatment implies sampling variation in annual catches Y_t .

At the end of each simulation for a harvest strategy, I will calculate the strategies success as $Y/(1 + \delta/\delta_0)$, where $Y = \sum_t Y_t$ is the biomass of fish captured over all years, δ is the average relative amount of evolutionary change the evolving traits, and δ_0 determines the sensitivity of this success measure to changes in δ . Thus, when there is no evolutionary change, so that $\delta = 0$, a strategy's success is measured by its cumulative yield, while evolutionary change amounting to $\delta = \delta_0$ implies that the strategy's success is halved. I will then rank the harvesting strategies according to their success to determine the 100 best strategies, and generate 100,000 permutations of these 100 best strategies with free "recombination" between the five parameters determining the strategies. I will iterate this process until no better harvesting strategy can be generated.

Time permitting, I will use this modeling framework to examine a second management policy that involves the translocation of individuals with larger-maturing genes from unharvested to harvested lakes. I will subject the harvested lake to the optimal harvesting strategy determined from the analysis described above. I will then

begin to analyze translocations from a single unharvested lake into a harvested lake. While gene flow between populations mitigates the potential for local evolutionary divergence, conserving genetic resources requires minimizing the amount of artificial genetic contamination. I will use the eco-genetic model to determine (i) the degree to which translocations allow brook charr populations to recover intra-population allelic diversity at the loci controlling for maturation probability, should such diversity have been lost to harvesting, and (ii) the degree to which translocations promote genetic homogenization across populations at loci for traits other than the maturation probability. This policy once again implies two competing objectives. As before, I will utilize a genetic algorithm, now to optimize a strategy's success $h/(1 + \delta/\delta_0)$, where h is a measure of genetic homogeneity (such as F_{st}) between the two lakes at neutral loci.

Relevance and link to EEP's research plan

Characterizing and predicting the extent of fisheries-induced adaptive change is a main goal for the research project on *Evolutionary Fisheries Management* of the Evolution and Ecology Program at IIASA. Linking existing theoretical approaches to data is crucial if we are to generate comparative predictions on the evolutionary effects of different fishery-management strategies. This work aims to develop a general framework that can be readily be used by stakeholders and other policy-makers to design a wide range of strategies that manage the risk of fisheries-induced adaptive change.

Expected output and publications

I anticipate the results of this work to be presented as co-authored research articles. They will also be used as a chapter in my PhD dissertation.

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