

Special Seminar

Genetic effects of aquaculture and hatchery release on wild populations: extending our understanding to minimize them

High precision monitoring program for evaluating anthropological effects on bio-diversity, Tokyo University of Marine Science and Technology

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To minimize unintended fitness consequences of hatchery fish on wild populations, should you make them as similar as possible or as different as possible?

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For hatcheries that are focused on production rather than supplementation, two alternative management strategies might help minimize unintended fitness consequences on natural populations: (1) reduce selection in captivity as much as possible to reduce fitness load (keep them similar), or (2) create a divergent population to reduce captive-wild interactions as much as possible (make them different). The first strategy attempts to minimize consequences of individual mating events (which, however, might be very common), while the second strategy attempts to minimize the number of H-W matings (each of which, however, might be very detrimental). The net effect on natural populations thus depends in some complex way on the product of the number of H-W matings and the severity of each. Many biologists and managers have strong opinions about which strategy is better, but to date no one has conducted a rigorous analysis of the inherent tradeoffs involved. We attempted to do that with a coupled demographic-genetic model that incorporates a variety of relevant processes and dynamics: selection in the hatchery, assortative mating based on the trait under selection, and different life cycle events related to hatchery release, density dependence, natural selection, and reproduction. Model results show that the worst scenario is one in which the H fish are genetically different but still similar enough to successfully reproduce in the wild. The more extreme 'different' strategy is a potentially viable alternative, provided that an opportunity for purging selection occurs after

hatchery release but before reproduction. In this case, the appropriate approach depends on the feasibility of each strategy and the demographic goal (e.g., increasing natural abundance, or ensuring that a high proportion of natural spawners are naturally produced). In addition, the fitness effects of hatchery release are much greater if hatchery release occurs before (vs. after) density-dependent interactions. Given the logistical challenges to achieving both the similar and different strategies, evaluation of not just the preferred strategy but also the consequences of failing to achieve the desired target is critical. In a related study, we evaluate the genetic consequences of different patterns of escapes from aquaculture operations: continual leakage of small numbers of individuals, or rare episodes of large escapes.

Japan marine stock enhancement program and concerns of fitness decline of hatchery fish

Shuichi Kitada (Tokyo University of Marine Science and Technology)
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The Japan marine stock enhancement program was initiated in 1963 to increase coastal fishery production. The primary focuses were producing juveniles at lower costs and releasing them with high survival rates. Evaluation of the recapture rates was crucial and tag experiments were conducted from late 1970s to early 80s. However, non-reporting and tag shedding were very large and resulted in biased estimates. To overcome the problem, sampling surveys of commercial landings to count the number of recaptured fish identified by the natural marks were conducted nationwide for red sea bream and Japanese flounder in late 1980s. A general method to estimate the total landings of released and wild fish was developed for two stage sampling schemes, which enabled the unbiased estimation of the stocking effectiveness. While, concerns about ecological and genetic effects of hatchery fish on wild populations have increased since the 1980s against the background of salmon supplementation and aquaculture. To investigate the genetic effects of marine stock enhancement, we conducted genetic monitoring on red sea bream and Pacific herring. Losses of rare alleles and haplotypes were found for the red sea bream in Kagoshima Bay, but the genetic effect on stocked population was very small in terms of F_{ST} . Recently, using microsatellite parentage assignments, data suggesting considerable reduction in the reproductive success (RS) of hatchery-reared steelhead in the wild was accumulated. To extend our understanding for the results of the relative reproductive success (RRS) of the steelhead in the Hood River, USA (Araki et al. 2007 a, b, 2009), we estimated the posterior distributions of RRS. While the average level of RRS implied the reproductive decline of hatchery fish and wild-born hatchery descendants,

we could not reject the null hypothesis that the chance that hatchery fish and their descendants have smaller RS than wild fish is the same as the chance that hatchery fish and descendants has larger RS than wild fish. We hypothesize that the reduction in RS of hatchery-reared steelhead was caused by the fast growth in hatcheries until smolt. We discuss on enhanced growth and reproductive performance of hatchery fish based on gene expressions and maturation data of transgenic, non-transgenic and wild strains of salmon.

Genetic effects of aquaculture on wild populations: A case study of the red sea bream in the western Japan

Kaori Nakajima (Tokyo University of Marine Science and Technology)

Red sea bream (RSB, *Pagrus major*) is distributed widely along coastal waters of Japan, the East China Sea. This species is one of the most important coastal fishery resources and especially used on auspicious occasions in Japan. The total annual catch of wild RSB is 14,947 tons in 2010 and has been stable for three decades, while that of aquaculture rapidly increased since around 1980 and reached the historical maximum of 87,232 tons in 1999. Annual marine fish aquaculture production is 245,712 tons in Japan and RSB has been the top species using artificially produced seeds over the past 30 years. Fast growing individuals were selected for many generations to produce seeds for aquaculture. In fact, farm fish can grow very fast and spawn at ~1.5-2.0 years old age in net cages before shipping. The genetic effects of spawning and escapement of RSB from net cages have been a matter of concern, however no study investigated this problem. To investigate the genetic impacts of the farmed fish on wild populations, we took four geographical samples of wild RSB from the western coast of Japan and one farmed fish sample. We measured 199 wild and 50 farmed fish for morphometric analysis and genotyped 367 wild and 100 farmed fish using five microsatellite loci (Pma1,2,3,5 and GA2A). The mitochondrial DNA D-loop control regions of 163 wild and 94 farmed fish were also sequenced. In addition, we reanalyzed 180 sequences of two wild and one hatchery-released samples taken from the Kagoshima Bay (KB) (Hamasaki et al. 2010). The correspondence analysis found the distinct morphology of farmed fish from wild samples. The wild sample from Uwakai (UK), Ehime prefecture, the major aquaculture area, showed slightly different morphology. Genetic diversities of farmed and hatchery-released fish were very low, while those of wild fish were much higher except for the inner KB sample. Our result suggested that the genetic impact of RSB aquaculture was much smaller than releases of hatchery-reared juveniles in KB. This should be caused by the small survival rates of eggs of farmed fish in the wild compared with those of

hatchery fish released at ~7cm in total length. The culture nets of RSB in Uwakai were usually closed and sunk in the sea to avoid high waves and typhoons except feeding times, which might be effective to prevent escapements of farmed fish.

Directed graphical modeling of gene expression profile underlying salmonids reproductive behavior

Reiichiro Nakamichi (Tokyo University of Marine Science and Technology)

Complex traits may be determined by the expression levels of a number of genes and their interactions. Microarray data enables high throughput approach to measure the correlations between transcripts and phenotypes. Biologically meaningful message may be obtained by correlations between the phenotypes and the sets of known pathways. Here, we propose a likelihood-based graphical modeling approach to get the system-biological ground view of molecular mechanism behind the variation of phenotype. The geometry of the graph is selected based on AIC. From the local structure around the phenotype-node, it is possible to estimate the direct effect. By tracing a series of the hubs from the phenotype-node towards the center of the graph, it is possible to estimate the hierarchical module structure controlling the phenotype.

We applied our method to a public data of sockeye salmon (*Oncorhynchus nerka*) and estimate the gene expression network. A total of 80 individuals of sockeye salmon were captured following their spawning migration stages, and expressions of 16006 genes were measured using white muscle tissues. Estimated gene network shows that sexual hormones drive the spawning migration, and the environmental stress in the process of migration activates glycolysis and muscle growth. By integrating the phenotype, expressions and marker genotype data, it is possible to quantify the direct and indirect causal effect of genetic perturbations. Our method will elucidate the mechanisms of the genetic effects of hatchery supplementation and aquaculture on wild populations.