

USES AND LIMITATIONS OF CONTEMPORARY GENETIC ANALYSES IN DELINEATING BIOLOGICAL POPULATIONS FOR STOCK ENHANCEMENT

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A critical first step in effective resource management is to identify and delineate operational units for assessment, rule enforcement, etc. To sustain fisheries at maximum harvest levels, stock-assessment scientists would ideally identify ‘unit stocks’ as groups of fish for which demographic dynamics (i.e., recruitment rates, fishing and natural mortalities, etc.) are largely independent of other such groups. In contrast, when the goal is the preservation and maintenance of the genetic health and future adaptive integrity of natural populations, hatchery scientists seek operational units for which the genetic dynamics are largely independent, at least for relevant time periods. Although useful for some purposes (e.g. estimating migration rates and divergence times), genetic studies typically rely on selectively neutral markers to compare estimated levels of gene flow or divergence in light of putatively “homogenizing” levels. However, genotypic distributions at neutral loci represent only a portion of the genetic information contained in gene pools. Critical adaptive genetic differences can exist among individuals that are homogeneous with respect to surveyed neutral alleles. Thus, during genetic risk assessment and monitoring, managers should consider the relevant operational units to be the gene pools of natural populations and when forecasting potential genetic impacts, they should ideally rely on evolutionary models that jointly consider the processes of mutation, selection, drift and migration – not just the latter two.

Managers of stock enhancement programs may have dual needs with respect to unit-stock identification. They most certainly will want to define units for genetic management. At other times, hatchery scientists, like stock-assessment scientists, may need to know when groups of fish are demographically independent (or nearly so), particularly when investigating displacement or forecasting the potential for stocking to impact catch rates and spawning stock biomass. Unfortunately, the temporal and spatial boundaries of genetic and demographic units may not be congruent. Why? The short answer is because it only takes very low rates of sustained immigration over time to homogenize neutral allele frequencies. Following a discussion of the differential impact of migration on demographic and genetic dynamics, I review the relatively new suite of marker types and of analytical approaches that can be used to identify genetic stocks. I then describe an example of where a rigorous study of genetic stock identification, for the above stated reason, has so far failed to meet the needs of hatchery managers who seek a concrete description of demographic stock boundaries.

Briefly, tests of genetic homogeneity among sample localities almost always include exact tests of allele and genotype distributions, estimation of a fixation index θ , and perhaps an analysis of molecular variance or AMOVA. With increased computing speed,

advanced statistical approaches, principally maximum likelihood and empirical Bayesian estimation, have been applied to θ and other genetic parameters to improve power. More recently, individual-based population assignment methods have been employed to examine first- and second-generation migration. Some assignment methods are based simply on inter-stock differences in allele distributions. Other methods use genetic-based Bayesian models, which can be used to identify discrete clusters (genetic stocks) within the total data and to assign individuals to a cluster most consistent with their multilocus genotype. The first step usually involves the estimation of the most plausible number (K) of distinct clusters in the data, based on deviations from HWE and linkage equilibrium. Upon estimating K, individuals can then be assigned into each of K stocks. Still, even these analyses require sufficiently high levels of genetic heterogeneity between stocks (relatively large values of θ) for precision.

Scientists at Mote Marine Laboratory, Florida are stocking the common snook, *Centropomus undecimalis*, into estuarine waters of southwest (Gulf of Mexico) Florida. As well as optimizing snook breeding/release methods, they are studying displacement and are trying to assess the contribution of snook released for the popular recreational fishery. Extensive, long-term mark-recapture studies indicated that >99.9% of common snook in the Florida Gulf inhabit a single estuary for their entire lives. Snook in the Florida Atlantic tend to stray further north and south. There is little movement between and Gulf and Atlantic waters. Spawning tendencies seemingly preclude long-distance dispersal of snook larvae. A recent survey of 1,600 specimens, genotyped at 24 highly polymorphic microsatellite loci, has confirmed the existence of genetic structure between Gulf and Atlantic stocks. Assignment analyses based solely on allele frequency differences (e.g., Figure 1) correctly classified ~86-90% of individuals to their respective Gulf/Atlantic stocks. Bayesian methods improved this rate to 98%. However, despite the apparent natal fidelity exhibited by Gulf snook, there was no evidence of genetic structure within the Gulf stock, not even the commonly observed pattern of isolation-by-distance. Consequently, if Mote hatchery scientists inferred demographic stock boundaries for snook just using genetic data, they might incorrectly conclude that localized stocking in a single Gulf estuary could influence catch rates, hatchery/wild ratios, etc. along the entire Gulf coast. Generally, for these purposes, alternative methods (e.g., tagging/tracking, otolith microchemistry) may be more suitable for demographic unit-stock identification.

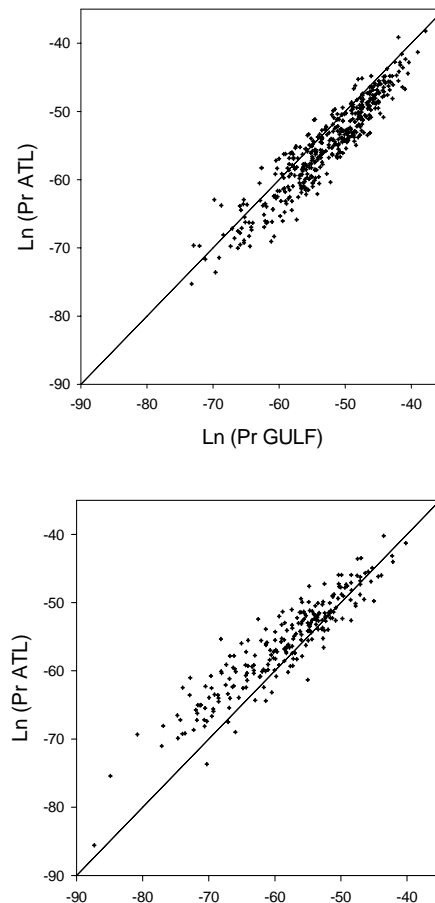


Figure 1: Population assignment for individual snook using the Ranalla and Mountain resampling algorithm.