

GENETIC CONSIDERATIONS DURING THE EXPERIMENTAL AND EXPANDED PHASES OF BLUE CRAB STOCK ENHANCEMENT IN THE CHESAPEAKE BAY

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A responsible approach to marine stock enhancement requires that potential negative impacts upon the gene pools of wild populations be mitigated through the use of genetically sound breeding and release protocols. There are numerous ways in which cultured organisms can have a direct genetic impact on recipient stocks. According to the Ryman/Laikre model reductions in effective population size (N_e), if severe, can result in substantial allelic and genotypic frequency changes over time and, depending upon future population abundance, excessive loss of genetic diversity. In order to adopt an effective broodstock selection approach for our blue crab *Callinectes sapidus* enhancement project, the genetic structure of this population must be assessed at the enhancement sites. Using mtDNA NADH dehydrogenase subunit II (NAD2) gene sequences and microsatellite loci as markers, the population structure of the blue crab population at our release site have been studied for 3 consecutive years (2003-2005). The local blue crab population is highly genetically diversified (haplotype diversity >0.7 ; lack of common haplotype; microsatellite heterozygosity varies from 40-97%, depending on loci). Based on mtDNA data, significant yearly variation of genetic composition was observed ($p < 0.005$), despite a low F_{st} value (< 0.03), suggesting local population genetic structure changes from year to year. Distinguishing hatchery from wild crabs based on the NAD2 haplotype is highly reliable but clearly impacts the local genetic structure at the release site. Given these findings our current approach is to use wild caught inseminated females from the mouth of the Bay, induce them to spawn in captivity, and not use them again for hatchery production.