GENETIC ANALYSIS OF YEAR CLASS FORMATION IN SHORTBELLY ROCKFISH (SEBASTES JORDANI)

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by
Richard W. Julian
San Francisco, California
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I analyzed the 1994 year class of shortbelly rockfish to determine if it comprised a small portion of the adult spawn that had unusually good survivorship. The polymerase chain reaction (PCR) enabled the amplification of the mitochondrial DNA (mtDNA) control region from larval, juvenile and adult samples collected off central California. The PCR amplification permitted the classification of haplotypes using denaturant gradient gel electrophoresis (DGGE). Direct nucleotide sequencing confirmed base pair differences between haplotypes. The juveniles collected in abundance off the Farallon Islands in June most likely represent the majority of the 1994 year class. Monte Carlo simulations of Chi-Square contingency tests yielded significant differences (p < 0.05) in haplotype frequency distributions between these juveniles (i.e. new recruits) and both adults and young larvae (i.e. spawning population). These abundant Farallon juveniles had a lower level of genetic diversity (H = 0.5532) than both adults (H = 0.6844) and young larvae

(H = 0.7355), as well as relatively high levels of genetic differentiation between adults (G = 0.0677) and young larvae (G = 0.0572). Furthermore, this reduction in genetic diversity occurred during the pelagic period, after parturition of the larvae. These results support Hedgecock's Sweepstakes-Chance Matching Hypothesis, since the reduction in genetic diversity of these abundant juveniles occurred in a manner consistent with bottleneck effects generated by temporal and spatial variability in environmental conditions during the pelagic period.

I certify that the Abstract is a correct representation of the content of this thesis.

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