Genetic stock structure and life History of euthynnus affinis cantor (1849) and scomberomorus commerson lacepede (1800) fishes in the northern coastal waters of Tanzania

Johnson Mshana Grayson
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University of Dar es Salaam, Institute of Marine Sciences, 2016

The population genetic structure and life history traits of Kawakawa Euthynnus affinis Cantor (1949) and Narrow barred Spanish mackerel Scomberomorus commerson Lacepede (1800) in the northern coastal waters of Tanzania, Western Indian Ocean were studied using sequence analysis of mitochondrial DNA (mtDNA) control region. A 475bp and 500bp segment of the control region was sequenced and analyzed (38 and 46 samples of Narrow barred Spanish mackerel and Kawakawa, respectively). The study revealed high levels of haplotype and nucleotide diversities. Analysis of molecular variance (AMOVAL), nearest neighboring statistic ($S_n$) and exact test of genetic differentiation did not show evidence for population subdivision ($p>0.005$); hence a null hypothesis that studied fish species constitute a single genetic stock in the northern Tanzania coastal waters could not be rejected. The Tajima’s D and Fu’s $F_s$ models showed a significant deviation from neutral condition ($p<0.005$), indicative of a recent population expansion. The study revealed a single clade of individual fish species, suggestive of similar genealogical history. The genetic data were also supported by life history traits, which revealed geographical similarities in the spawning patterns, size at maturity and fish condition. In addition, number and size of eggs ($\mu$m) for females collected from Dar es Salaam was not statistically higher than those from Pangani ($p>0.005$). The Presence of genetic similarities for studied fish species was a result of gene flow, short geographical distance (IBD) and homogeneity in environmental distances (IBED, $p>0.005$). A single-stock model and regional shared management along with further similar research covering the whole Indian Ocean is therefore recommended.