STOCK ASSESSMENT OF COMMERCIALLY IMPORTANT FISHES IN THE BAY OF BENGAL THROUGH MOLECULAR MARKERS: MANAGEMENT POLICY IMPLICATIONS

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Abstract

Stock (population) identification is very crucial both in the context of monitoring and conservation of the fish species of marine and open water habitats. The present research was conducted accordingly in the BoB aiming to determine and categorize the population of some commercially important marine fish species. In this study, about one hundred samples of each species of ten marine fishes namely, *Pampus chinensis, Pampus argenteus, Euthynnus affinis, Auxis thazard, Megalaspis cordyla, Lates calcarifer, Setipinna tenuifilis, Sillaginopsis panijus, Polynemus paradiseus* and *Coilia dussumieri* were collected between October 2020 and April 2022 mainly from coast and rivers of two ecological regions of Bangladesh coast: the South - west (Borguna-Khulna-Patuakhali, KP) coastal zone and the South - east (Chattogram-Cox's Bazar, CC) coastal zone based on different physico-chemical characteristics of habitat (KP: high brackish water area with dense clayed particle in river and estuaries; CC: sandy area with more clear saline water river and estuaries) and biology of species (e.g. migratory, amphidromous, anadromous etc.). For amphidromous or anadromous fish, samples were collected from coastal rivers. Fish/tissue samples or DNA sequence data of other seas in the Indian Ocean region (e.g. Southern BoB, Andaman Sea, Arabian Sea, Persian Gulf etc.) and South-west Pacific (e.g. South China Sea, Gulf of Thailand etc.) were collected from different researchers and scientific studies. For genetic diversity and stock study, sequence variations in different mitochondrial DNA gene regions such as COI, Cytb, and noncoding control region (d-loop) were examined Polymerase Chain Reaction (PCR) was used to amplify the target mtDNA region and sequenced by sequence analyzer. Lastly, the variation in the obtained DNA sequence data of different geographic locations were analyzed using different bioinformatic softwares such as Geneous, ARLEQUIN, MEGA-6; TCS etc. For all the genes in every sampling locations of Bangladesh, the nucleotide diversities (π) were very low (0.0001 ~ 0.05) but the haplotype or gene diversities (h) were relatively high, 0.5 ~ 1.0 (i.e. $h > 0.5$) indicates that the studied fishes have experience population expansion after a period of low effective population size, except two species, *M. cordyla* and *L. calcarifer* for which the gene diversities were also low (0.14 ~ 0.263). This result

implies that these two fish species of Bangladesh have experienced recent bottleneck. Immediate conservation measures should be immediately taken for these two species, such as limiting catch, banning on fishing season, making long term sanctuary or protected area etc. Neutrality tests such as Tajima's D and Fu's F_S statistics also suggested that most of the studied fish species of Bangladesh populations have undergone the demographic history of population expansion. Interestingly, the population statistic F_{ST}, and exact test of population differentiation revealed two different scenarios for two group of fishes. The first group contains six fish species namely *P. chinensis, P. argenteus, E. affinis, A. thazard, M. cordyla, L. calcarifer*. Fishes of this group have similar characteristics. These fishes are mostly oceandromous, pelagic and highly migratory. They are widely distributed throughout the Indian Ocean and South-West Pacific (or, Indo-west Pacific). These fish showed no significant population genetic structuring indicating that these six species have single genetic stock and these are panmictic (random mating among populations) throughout Bangladeshi marine water. Bangladesh should manage these species as a single conservation unit. Further, these six migratory fish showed its own genetic structure (F_{ST} P ≤ 0.05) within the BoB when compared with other neighboring seas such as Arabian Sea, Andaman Sea, Gulf of Thailand, South China Sea etc. So, the BoB countries should manage and conserve these vital and shared marine species through cooperation with each other. On the other hand, the second group consists of four species *S. tenuifilis, S. panijus, P. paradiseus* and *C. dussumieri* is relatively distributed to the narrow or localized geographic area mostly in the BoB and Andaman Sea. These fishes are mostly off-shore or coast dwelling and amphidromous (i.e. migrate between fresh and marine water but not to breeding purpose). For these species, pairwise F_{ST} values of mtDNA markers among fish samples of different sampling rivers showed significant differences ($P \leq 0.05$) in most of the cases. Different rivers showed their own genetic stock for different fish such as Bishkhali, Kirtankhola and Boleshwar river for *P. paradeseus* and *S. panjius*; Naf and Pashur river for *C. dussumieri*; Matamuhuri and Bishkhali river for *S. tenuifilis* etc. Based on this result, it is recommended that different river populations of studied fish having unique genetic structures (i.e. genetic stock) require separate monitoring and management strategies for conservation because the population of each river is genetically distinct and overfishing in any of the rivers may cause extinction of its fish stock. So, it is needed to maintain good water flow and direction such as by regular dredging and also needed to control water pollution for the good ecosystem to safeguard these fish species.

Keywords: BoB, population, stock status, molecular marker, fisheries management