

Genetic diversity, population structure, and demographic history of *Auxis thazard* (Perciformes), *Selar crumenophthalmus* (Perciformes), *Rastrelliger kanagurta* (Perciformes) and *Sardinella lemuru* (Clupeiformes) in Sulu-Celebes Sea inferred by mitochondrial DNA sequences

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ABSTRACT

Aside from having an important ecological role in the ocean food web, small pelagic fishes have become the major food source in the Sulu-Celebes Sea (SCS) bordered by Indonesia, Malaysia and Philippines. Because the people living within and around the SCS are highly dependent on these resources, conservation and management of these fishes are of prime importance, though basic biological information, especially relating to genetic diversity, population structure, and demographic patterns are often deficient. In this study, population genetic methods were used to investigate the population structure and historical demography of four ecologically and economically important small pelagic fishes in SCS: frigate tuna, *Auxis thazard* (AT); Bali sardine, *Sardinella lemuru* (SL); Indian mackerel, *Rastrelliger kanagurta* (RK); and bigeye scad, *Selar crumenophthalmus* (SC). Fishes were collected from 5 geographic locations (Philippines: Zamboanga, Tawi-Tawi and Palawan; Indonesia: Manado; and Malaysia: Kudat) around the SCS and muscle samples were sequenced for mitochondrial DNA control region (D-loop) marker (n=150, 231, 169 and 224 for AT, SL, RK, and SC, respectively). Low overall F_{ST} values, high genetic diversity and highly mixed clusters from BAPS analysis indicate no distinct genetic structure for these four marine pelagics in SCS. Furthermore, neutrality tests (Tajima's D and Fu's F_S), mismatch analysis and Bayesian skyline plots suggest population expansion for all species. Generally, the high genetic diversity and the wide haplotype distribution for all exploited pelagic fish populations indicate that the four marine pelagic species are very resilient over evolutionary timescales.