Early life history and stock identity of horse mackerel (LMR/PEL/09/09

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Abstract

Two species of horse mackerel are found off the Angolan coast, Cunene horse mackerel *Trachurus trecae*, typical of the Angola Current ecosystem, and Cape horse mackerel *T. capensis*, mostly associated with the cold Benguela current. The two species show a strong North-South seasonal migration, and they mix on fishing grounds in the Cunene – Benguela area. They are also shared with Namibia. The objective of the project was to investigate the genetic diversity within and between population of *Trachurus trecae* and *Tachurus capensis* and to study the spatial and temporal variability of horse mackerel maturation patterns, in order to incorporate the results on the management strategy for this fishery. The genetic population structure of the Angolan populations of the two horse mackerel, species were studied based on the amplification of a fragment of mitochondrial cytochrome b. A total of 748 Cunene horse mackerel and 390 Cape horse mackerel were collected from 18 sample sites in Angola and 5 in Namibia during the transboundary survey by the R/V "Dr Fridjof Nansen" carried out in 2010. The genetic composition of the populations of horse mackerel in the Northern, Central and Southern regions of the coast was compared based on genetic variability. Genetic variability was estimated using the nucleotide (π) andhaplotype (Hd) diversities and the number of polymorphic sites (S).For the *Trachurus trecae* samples the nucleotide diversity ranged from 0.44% to 0.55%, which are below the usual range of mitochondrial DNA diversity for marine fish ($\pi = 0.8\%$ to 3.20%). The observed values of haplotype diversity for the northern and central regions are also below the usual variation of mitochondrial DNA for marine fish (Hd = 0.7 to 1.0) while for the southern region it is within the range(0.55%). For *Trachurus capensis* the nucleotide diversity measured is within the range of the mitochondrial DNA diversity for marine fish. The populations of both species of horse mackerel seems to be classified as a population with high haplotype diversity and low nucleotide diversity (Hd> 0.5 and π <1.0%). Such patterns are typical for large populations which have recently expanded rapidly from a small population, so allowing the retention of new mutations without sufficient time for the accumulation of large differentiation among haplotypes. For both species, the hierarchical AMOVA analysis shows a large genetic variation within each (Northern, Central and Southern) population and no genetic differentiation was found between populations. Based on this result it is not possible to conclude that these populations are structured genetically. Considering the role of

these species in the Benguela ecosystem it is important to develop mitochondrial markers anchored in the region of the mitochondrial D-loop as well as specific microsatellite loci for the two species. As regards the maturation dynamics, analyses of the data from the INIP database (2005–2010) indicated that the GonadoSomatic Index (GSI) varied within and between areas for *T. trecae*, and the areas north of Lobito have relatively higher average GIS. This is more notable for 2007-2008 and high values are recorded from March to July. varied between to 23 and 14.3cm showing an evidence of an overall increase in the percentage of small Cunene horse mackerel mature