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Preliminary results of the Indian Ocean Swordfish Stock Structure Project – IOSSS – focus on the population genetic approach

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Abstract

Fisheries managers have as one of their primary objectives the need to ensure resources sustainability and to avoid population crashes. Associated to classic approach such as long term bioecological indicators, fisheries time series data and spatial dynamic approaches, genetic analyses have much to offer to fisheries managers, especially in the provision of complementary tools assessment of stock structure of heavily exploited marine resources. The swordfish *Xiphias gladius* is one of the most widely distributed species of pelagic fishes, commonly found in the tropical and temperate zones of the Atlantic, Indian and Pacific Oceans. On the basis of the 2010 stock assessments and indicators, the Indian Ocean Tuna Commission (IOTC) concluded that the level of catches in 2009 (about 22 000 t) was not globally overfished. However, assessment models using catch rate data from the Southwest and Northwest Indian Ocean suggest that overfishing of swordfish might occur in localized areas. Consequently, management measures should be considered for a sustainable exploitation in a near future.

The present study shows the population genetic results associated to classic biological data at a spatio-temporal scale of a large project undertaken in the Indian Ocean and targeting the swordfish *Xiphias gladius*. From 2009 to 2010, dedicated scientific at sea campaigns and national observers programs allowed measuring 5520 swordfishes caught by pelagic long liners (1645 in 2008, 2026 in 2009 and 1840 in 2010), collecting 2535 genetics samples (1263 in 2009 and 1272 in 2010), 1682 gonads, 515 isotopes samples, 305 stomach contents and 665 otoliths from 12 large areas in the IO and bordering Oceans. Samples collection and genetic laboratory procedures were done under a Quality Process in order improve data quality and reliability. Preliminary genetic structure has been

identified on the basis of ND2 mitochondrial DNA sequencing (n=1500) as well as microsatellite genotyping at 19 loci (n=1650), from samples collected in all Indian Ocean and in the adjacent Atlantic and Pacific Oceans.