

**MARKED GENETIC DIFFERENCE BETWEEN THE NORTH AND SOUTH  
ATLANTIC STOCKS OF THE SWORDFISH (*XIPHIAS GLADIUS*) REVEALED BY A  
SINGLE NUCLEOTIDE POLYMORPHISM AT CAM INTRON LOCUS**

Seinen Chow<sup>1</sup>

SUMMARY

*Recent molecular genetic analyses based on variation in mitochondrial (mtDNA) and nuclear (nDNA) DNA have indicated that the global population of swordfish (*Xiphias gladius*) may be subdivided into at least four populations (Mediterranean Sea, north Atlantic, south Atlantic and Indo-Pacific). In spite of the wider geographic range, little signal for population subdivision has been observed in the Indo-Pacific region. In contrast, the swordfish population in the Atlantic realm is notably structured. MtDNA analysis revealed not only genetic heterogeneity between the Mediterranean and Atlantic populations but also no exogenous immigrants entering the Mediterranean Sea. MtDNA analyses, however, appear to have little power for delineating genetic differentiation between the north and south Atlantic populations.*

*Variation observed in the 4<sup>th</sup> intron of the swordfish calmodulin gene (CaM) is a single nucleotide polymorphism (SNP) and much less variable than those detected in the mtDNA control region and nuclear microsatellite DNA. Yet, to date the CaM marker may be the best option for elucidating genetic differentiation between the north and south Atlantic swordfish stocks and for locating the boundary between the stocks. Although ICCAT has managed the north and south Atlantic swordfish stocks on the basis of a separation at 5° N, results obtained from the CaM locus indicate the actual boundary is located farther to the north than this ICCAT working hypothesis.*

*Two alleles (designated A and B) at the CaM locus are unambiguously determined by a single restriction digestion (Bst UI). The frequency of the A allele in five sampling events (n=16 to 64 samples each, 153 in total) in the northwest Atlantic (20°N-40°N, 45°W-90°W) ranged from 37.5 to 51.7 %, while much higher frequencies of the A allele (84 to 91.7 %) were observed in seven sampling events (n=22 to 68 samples each, 347 in total) in the mid to south Atlantic (10°N-33°S, 2°E-50°W)(Fig. 1). All samples were in Hardy-Weinberg equilibrium, and no notable differences in allele and genotype frequencies were observed between samples within these two regions. The marked genetic difference between these two regions has been maintained over a long period of time (1990 to 2002). Genotype frequency delineates another aspect of genetic difference between the regions. Although 25 % of individuals from the northwest Atlantic were BB homozygote, this genotype was observed to be very rare (1.5 %) in the mid to south Atlantic. These results indicate that not only the gene flow but also individual migration between the regions is considerably restricted.*

*Since few Japanese vessels operate in the range of 10°N to 20°N of the Atlantic, few swordfish samples from this range are available to Japanese scientists. So far, samples from only two sampling events in the area of 10°N to 15°N have been obtained. One (n=18) was collected by the RV Shoyo-Maru at 14°N, 48°W in October 2002, and the other (n=26) was from Japanese longline vessels operating at 12°N to 15°N and 28°W to 34°W in February to April 2002. Frequencies of A allele (66.7 %) and BB homozygote (11 %) observed in the former sample appear to be intermediate between the north and south Atlantic stocks, while frequencies of A allele (92.3 %) and BB homozygote (0 %) of the latter were similar to those of mid to south Atlantic samples. These results suggest that the boundary between the north and south stocks may be located in the range of 10°N to 20°N but may shift spatiotemporally. In addition, individuals from the north and south stocks may intermingle around the boundary. However, the small number of individuals collected in this very narrow area has hindered further speculation. If intensive Atlantic-wide sampling of swordfish in the area around 10°N to 20°N is realized, it*

<sup>1</sup> National Research Institute of Fisheries Science, Nagai 6-31-1, Yokosuka, Kanagawa 238-0316, Japan. E-mail: chow@affrc.go.jp

may be possible to determine the location and spatiotemporal dynamics of the boundary using the simple but diagnostic *CaM* marker.

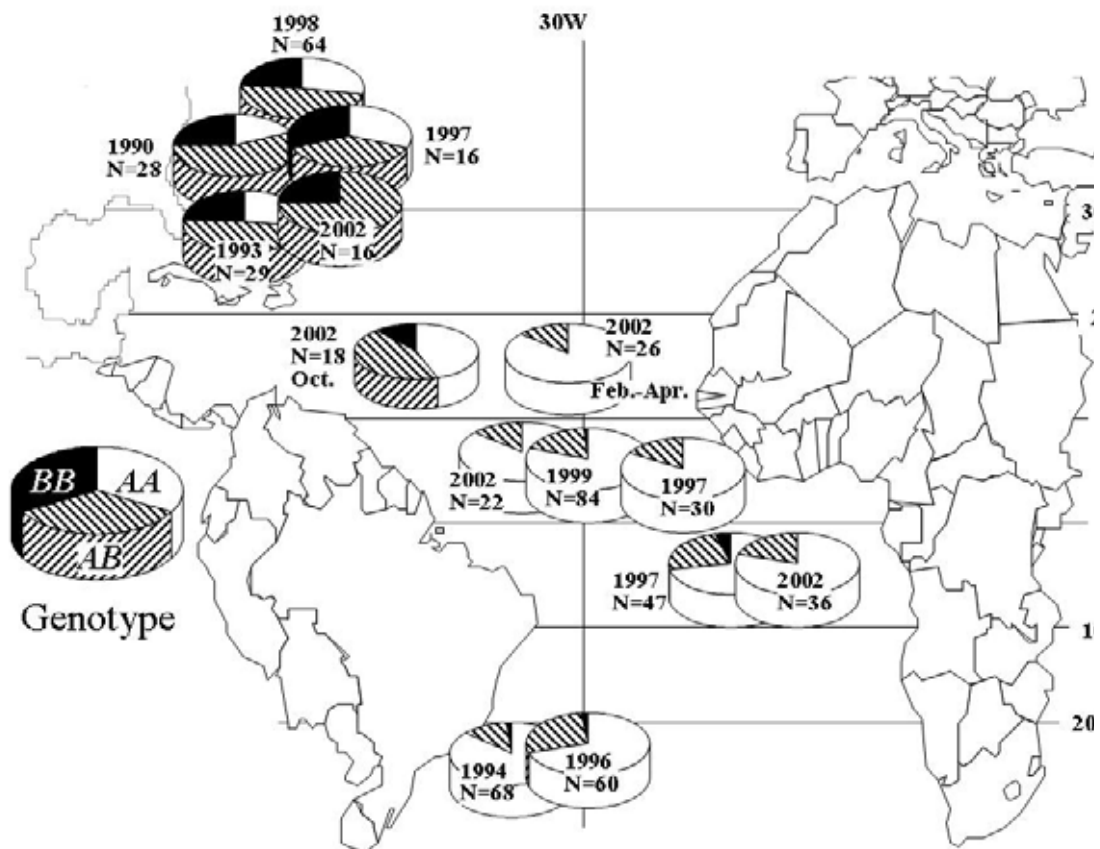


Fig. 1. Genotype frequencies at the swordfish *CaM* gene locus in samples from the north and south Atlantic.