D. SILVER HAKE STOCK IDENTIFICATION

SARC COMMENTS

Objectives

The SARC provided technical review of Phoel et al. (2002, SARC WPD1) and provided advice on the implications of the results for the management of the silver hake stock.

Part I. Silver Hake Abundance and Mid-Atlantic Bight Bottom Water Temperatures

Based on descriptive analysis of survey information, WPD1 concludes that:

1. Both commercial landings and survey catches confirm the decrease in silver hake abundance in the Mid-Atlantic Bight (MAB).
2. There is a trend toward warmer bottom water during the spring, albeit only about 1°C increase in the 33 years studied.
3. In both spring and fall, temperatures lie well within the preferred temperature range published for this species.

Despite the lack of hypothesis testing and limitations with temperature data, the conclusions are supported by temporal patterns in observed survey temperature and biomass indices. However, the SARC questioned whether the increase in temperature was significant.

Part II. Stock identification of silver hake following Mendelian inheritance and Hardy-Weinberg equilibrium of a microsatellite DNA locus heterogeneity with P^2 test for goodness of fit.

Major technical problems with genetic analyses, selection of characters and statistical analyses invalidate the conclusions stated in WPD1: "each sample appears to represent a separate silver hake population." Silver hake were sampled from the Mid-Atlantic Bight, southern Georges Bank, northern Georges Bank, the Gulf of Maine and the Scotian Shelf. Sample sizes were 14-15 fish from each area. Genotype frequencies at a single locus were compared to Hardy-Weinberg (H-W) expectations of pooled (combined-area) samples to test for genetic differences among areas using P^2 tests (i.e., differences from pooled H-W expectations were used to test that heterogeneous samples were pooled).

Interpretations of allelic frequencies at "locus 4" from PCR images are not appropriate. Primarily, the use of a null allele should be avoided, unless the presence of a such an allele can be confirmed through testing. Analyses should be based on several (4-10) loci with clearly defined bands and several to many alleles from many more spawning fish (40-100) for each spawning ground. Secondarily, the statistical tests used in WPD1 are inappropriate and associated interpretations are incorrect. Using H-W comparisons to detect group differences is unconventional and inefficient, because there are many sources of deviation from H-W equilibrium. More conventional analyses that test for differences among areas should be applied. Other more appropriate analyses may include genetic distance matrices, molecular variance and phylogenetic trees, such as the analyses presented to the SARC by P. Straub.

The samples from each putative stock should be collected over an adequate geographic and temporal range to represent each spawning group in order to more closely conform to the assumption of randomness in the statistical analysis. Existing samples may be available in NMFS archives with associated location, date and maturity condition.

SARC CONCLUSIONS

Given the deficiencies that were identified in the study, such as the use of a single locus with a null allele and unrepresentative samples, the SARC concluded that the data were inadequate to form reliable interpretations. Accordingly, the preliminary finding of significant genetic differences among samples should be disregarded. Management units of silver hake should be based on interdisciplinary analysis of published stock identification information (e.g., Almeida 1987, Helser et al. 1995, Bolles and Begg 2000). Further research should address the technical deficiencies of the genetic analyses, sampling design and statistical methods.

SOURCES OF INFORMATION

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