Striped Bass Technical Committee

June 21, 2006 Providence, RI

Meeting Summary

Participants

Doug Grout, Chair-NH Gary Nelson - MA Gary Shepard - NMFS Rob O'Reilly - VA Alexei Sharov - MD Vic Vecchio -NY Laura Lee - RI John Hoenig - VMIS Des Kahn - DE Vic Crecco - CT Brandon Muffley - NJ Charlton Godwin - NC Mike Brown - ME

ASMFC Staff Nancy Wallace

Patrick Kilduff

<u>Guests</u> Ed Cooke

Meeting Summary

Tagging Catch Equation

Gary Shepard gave a presentation *(Appendix A)* describing the concerns he had with use of Baranov's catch equation for estimating natural mortality, fishing mortality, and population abundance as described in the ASMFC 2005 Striped Bass Assessment Report. Des Kahn (chair of the Tagging Committee) discussed the tagging Committee's rational for using Baranov's catch equation in the most recent assessment

The Technical Committee determined that the equation should be included for peer review with the next stock assessment and that they should move forward with it. However, there are ways to improve this equation.

The Technical Committee recommended that confidence intervals should be developed for F and population estimates. The tagging subcommittee should work on developing these intervals at their next meeting.

There is also a need for a program that can calculate the catch estimates using just one model, which will help with consistency. Surviv can give you estimates of F and M, but it will be very cumbersome. A more user-friendly model is Avocado, but it needs to be updated to include catch and release data.

The first step is to develop a spreadsheet program to calculate variances and down the road Avocado can be updated.

It seems there was general agreement that:

- The general approach to using the catch equation to generate estimates of fishing and natural mortality is mathematically sound; this is an example of a general strategy for estimating the components of mortality from two functions of the fishing and natural mortality, generally the exploitation rate and the survival rate.
- The issue is in the particular implementation for striped bass
- Natural mortality of Maryland striped bass may well have gone up in the late 1990s
- It is clear that the catch equation approach, and similar approaches, relies heavily on knowing the tag reporting rate. Consequently, this should be a priority for research on striped bass.
- The properties of the catch equation approach should be studied. For example, how are errors in the inputs (i.e., the estimates of u and S) propagated to the estimates of F and M? Similarly, how are estimates of u and S correlated if they come from a Brownie model or an instantaneous rates model and how does this correlation affect the estimates of F and M?
- It would be good if an integrated analysis of available data could be done. This is what is done in the analysis by Jiang et al. (in review-distributed to SBTC by John H. prior to meeting) where one analysis of the tagging data provides the estimates of F and M, in contrast to the catch equation method previously used in which u and S are estimated separately and then combined to give estimates of F and M. It is felt that an integrated analysis should give a more precise estimate.
- Efforts should be made to determine the precision (i.e., variance or standard error) of the estimates obtained by the catch equation approach.

The recommendation was made to update the Management Board at each meeting on the progress of the stock assessment instead of giving them all of the information after the assessment is completed. This will keep them up to date on the process.

Fishery Dependent Data Survey

Gary Nelson reviewed the results from the survey that each state filled out describing their fishery dependent surveys. This data includes the commercial, recreational, and volunteer angler surveys that occur in state waters.

The ACCSP puts together a biological sampling matrix each year. The Striped Bass Technical Committee should weigh in on how many samples should be collected each year. Gary Nelson will develop a table of each state, the gear types that are used, the number of samples by year from 2000- present. He will send this out to the TC members to fill out the relevant information. He will also create a recreational table of length and age, by year and gear type samples by quarter.

The Technical Committee decided that an additional data workshop would not be needed.

Addendum I

The Technical Committee discussed the revised Addendum I to Amendment 6 to the Striped Bass FMP. This document has been revised to include recommendations for monitoring bycatch and discards of striped bass. The Technical Committee determined that an ideal sampling effort is optimally allocated, both seasonally and spatially, among directed and non-directed fishing that have a strong likelihood of generating striped bass bycatch.

The first step is to conduct an analysis on the number and type of all fishing trips from each state, by gear, season, and area if possible. Initial observer coverage can then be allocated across all fisheries at a level of 2-5 per cent coverage. Once this base line information has been gathered, sea sampling coverage can be targeted at fisheries determined to have a high probability of discarding striped bass during specific in specific areas and/or areas. It was also suggested that some kind of monitoring system for area fished be incorporated in the program (i.e. aerial over flights, VMS, etc.).

The Technical Committee felt trawls should be the highest priority for discard mortality studies.

ASMFC staff will incorporate the recommendations from the Technical Committee into the draft Addendum I for public comment for Board Review at the August 2006 meeting week.

Multispecies Presentation

Patrick Kilduff gave a presentation on the Multispecies model developed by the ASMFC. The ISFMP Policy Board charged the Technical Committee with identifying technical and management issues relating to multispecies management. Their comments included the following:

- There is a need to get a lot of gut samples from the predator species on a regular basis
- Transparency of model is poor because of complexity; this is more opaque than most models and it will be difficult to explain to the public and managers so they can understand an issue
- Temporal/Spatial variation depending on species abundance (i.e. bluefish expand range as abundance goes up)

- Should include predators feeding on each other
- This is a very data demanding model
- The model should be used as a learning/teaching tool
- There are too many assumptions which increases the uncertainty
- Need to have better estimates of alternative prey populations

Appendix A:

Examination of the Catch Equation model for estimating Natural Mortality as described in the ASMFC 2005 Striped Bass Assessment Report

Gary Shepherd and Christopher Legault

National Marine Fisheries Service Woods Hole, MA 02543

A report to the ASMFC Striped Bass Technical Committee

June 21, 2006

The basic catch equation model used for calculating M, as described in the 2005 Striped Bass stock assessment report, was:

$$F = u/A *Z$$
 eq. 1

The mixture of variable types make it difficult to evaluate the equation. However, since

$$u = F/Z^{*}(1-exp(-Z))$$

and $Z = F + M$
and $A = 1-(exp(-Z))$,

equation 1 can be translated into an instantaneous rates model as:

$$F = \frac{F/(Z)(1-\exp(-Z))}{1-\exp(-Z)} * (Z)$$
eq. 2

or further expanded as:

$$F = \frac{F/(F+M)(1-\exp(-(F+M)))}{1-\exp(-(F+M))} * (F+M)$$
eq. 3

Since the values for u come from the tagging R/M analysis and A and Z were derived in *MARK*, we can subscript them with 1 for R/M components and 2 for Mark components:

$$F = \frac{F_1/(F_1+M_1)(1-\exp(-(F_1+M_1)))}{1-\exp(-(F_2+M_2))} * (F_2+M_2)$$
eq. 4

In solving for F, the 1-exp(- (F_1+M_1)) terms in the numerator and the denominator cancel, leaving us with:

$$F = \frac{F_1}{(F_1 + M_1)} * (F_2 + M_2)$$
 eq. 5

And since $(F_1 + M_1)$ and $(F_2 + M_2)$ also cancel, we are left with the solution:

$$\mathbf{F} = \mathbf{F}_1$$
 eq. 6

which is a logical conclusion. Returning to equation 4, M is derived using the original Z parameter from the *MARK* model such that:

$$(\mathbf{F}_2 + \mathbf{M}_2) - \mathbf{F} = \mathbf{M}$$

As noted in earlier correspondence, if F_1 and F_2 are not equivalent, they do not cancel within the equation and F or subsequently M has no exact solution. Since F_1 and F_2 are contained within the *u* and Z terms, the required equality of these two parameters (*u* and Z) is implied. However, the circularity of the argument becomes that one cannot directly evaluate the equivalency of Z and *u* without prior knowledge of M (or F). If there is a difference between the two values, the accompanying residual gets masked as the difference between F and Z, which is also the calculated M. And around and around it goes.

The relationship between the S (which is ultimately transformed to $F_2 + M_2$ in equation 4) and u can be examined using simulated data. Since the estimates derived in the tagging models and used to calculate M are estimated with error, we can look at the influence of estimation error on the determination of M. Using 100 randomly generated combinations of S and u with a mean M of 0.15, then deriving the M using the above equations, it becomes apparent that there is a negative correlation between S or U and M. If U or S is under-estimated, then the calculated value of M becomes overestimated, and vice versa.





Another approach to evaluate the method is to examine the M estimates calculated using the catch equation method and incorporate variance estimates for u and Z derived from the tagging data. The 95% CI of F was provided in the 2005 tag report, therefore confidence bounds around Z were available (since F was simply Z - 0.15). One thousand values were randomly selected from within those confidence bounds for each annual estimate. The variation around u was calculated using a Monte Carlo approach. Randomly drawing from a normal distribution of reporting rates (with a mean of 46% and 95% CI between 28% and 63%) and catch and release mortalities (8% mean with 95%CI from 0% to 17%), the original harvest values where used to estimate 1000 modified R/M values ([# recaps harvested + (# recaps released alive * release mortality)/ reporting rate] / # marked) for Chesapeake Spawning stock >28" release and recapture data time series (1998 to 2004). The distributions of Z and u were used to calculate 1000 values of M (using M = Z - ((U/A) *Z). The mean M + 95% CI are shown below. Although the trend in the point estimates implies that M has been increasing in recent years, the variability around the estimates is large enough to prevent making that conclusion with a high degree of certainty.





A general assumption for Chesapeake Bay striped bass is that once they reach larger sizes (>28") they become part of the coastal migratory stock and the time spent in the Bay is usually limited to the spring spawning period. In the 28+ category, striped bass on the coast are generally mixed among stocks and should all be subjected to the same basic sources of natural mortality. Variability in M within each program was calculated using the 95% CI of F (+ 0.15 to create Z) from the 2005 stock assessment report and an annual estimate of exploitation rate without variability. One assumption was that each programs representation of survival was equivalent. Results indicate a wide variability among programs with M ranging between -0.4 and 0.4 with no ability to determine any trend.



The resident striped bass in the 18-28" range would be the fish most likely to be subjected to conditions in the Bay. Using the same approach as previously described, the results for the 18-28" fish also show a trend of increasing M until 2000, then a decrease, albeit remaining at a higher level than the 1990s. The 95% confidence bounds around the point estimates since the late '90s makes is difficult to identify a trend with reasonable confidence. It is also interesting that the increase in the average M coincides with the expansion of the fishery beginning in 1995.





As initially suggested, all of these estimates imply comparability between the r/m results and the MARK model results.

The conclusion from these analyzes is that the method of determining M from tag data is appropriate but is subject to bias if the results from the two models providing input data are not equivalent. Additionally, evaluating the equality of the two estimates require prior knowledge of M or F for comparison, thus it becomes a circular argument. Using this approach to estimate natural mortality of striped bass tagged in the MD spawning survey suggests an increase in M either in recent years or throughout the time series. However, the variability within and among tag programs is sufficiently large that is would be difficult to draw conclusions from point estimates with any certainty. The M estimates for fish in the 18-28" range have a similar increasing trend in M but the variability in the recent estimates precludes drawing any conclusions regarding natural mortality.