Collaborative biological sampling of highly migratory species

Michael J. Kinney, Joseph O'Malley

Pacific Islands Fisheries Science Center, National Marine Fisheries Service, 1845 Wasp Boulevard
Honolulu, HI 96818.

Working document submitted to the ISC Billfish Working Group, International Scientific Committee for Tuna and Tuna-like Species in the North Pacific Ocean, January 30–February 3, 2020, in Taipei City, Taiwan. Document not to be cited without author's permission.

Abstract

For highly migratory species such as tuna and billfish, basic biological processes like growth and reproduction are notoriously difficult to accurately estimate. The Billfish Working Group (BILLWG) indicated that improved estimates of these basic biological processes were key components in efforts to reduce model uncertainty in the assessment of such animals. Here, the United States, as a member of the BILLWG, propose a collaborative biological sampling effort in order to improve estimates of growth, maturity, and stock structure by allowing analyses of more representative sample sets collected in a uniform manner from multiple nations across the North Pacific. Our current proposal is only an outline of a general sampling strategy, designed to help establish agreement on a collaborative approach, while also identifying key players who can serve as lead scientists. These leads will ensure adherence to a sampling design, as well as undertake specific areas of life history research utilizing the samples collected during the collaborative effort.

Introduction

For highly migratory species such as tuna and billfish, basic biological processes like growth and reproduction are notoriously difficult to accurately estimate. This can be due to a myriad of factors, but often is simply the result of a single study's inability to access samples from across the species range. Sampling limitations among highly migratory species commonly result in regionally specific studies, sometimes with conflicting biological parameter estimates. Issues can arise when stock assessments, with their associated assumptions of stock structure, are combined with regionally specific life history studies which do not match the stocks assumed range.

Such is the case with striped marlin (*Kajikia audax*) in the Western and Central North Pacific (WCNPO), where various studies have independently produced estimates for the species basic biological parameters, such as length at 50% maturity (L_{50}) and asymptotic size (L_{inf}). Samples collected from the Taiwan Tungkang, Singkang, and Nanfangao fish markets from 2004–2010 resulted in an estimated L_{50} of 181 cm eye-to-fork length (EFL) (Chang et al. 2018), which was used in the most recent assessment of striped marlin. Alternatively, samples collected from the Hawaiian longline fishery from 2008–2011 indicated a much lower L_{50} of 161 cm EFL (Humphreys & Brodziak 2019). Asymptotic size also varied among studies, indicating a larger L_{inf} from waters off Taiwan [228.7 cm EFL converted from lower jaw fork length (Sun et al. 2011)] from 2004–2010, compared to waters off Hawaii [181.7 cm EFL (Fitchett 2019)] from 2003–2010. These disparate estimates from individual studies were investigated with various sensitivity analyses during the striped marlin assessment (ISC 2019); however, in the end a single parameter had to be selected for the base case model. From a biological perspective, it is difficult to determine if these differences reflect true natural spatial variability in life history attributes or represent different sampling designs or analytical methods.

The International Scientific Committee for Tuna and Tuna-like Species in the North Pacific Ocean (ISC) Billfish Working Group (BILLWG) indicated that changes to L_{inf} had a greater modeling impact then changes to L_{50}. However, models with different L_{50} parameters displayed convergence issues in the last assessment (ISC 2019), indicating that both parameters were important. The 2019 assessment sensitivity analyses identified growth and maturity as key sources of uncertainty, and the BILLWG specifically identified growth (growth curve and associated parameters) and size at maturity (L_{50}) as parameters in need of more research prior to the next assessment in 2024.

In order to make meaningful progress on these identified issues, we propose a collaborative biological sampling program, which would allow participating countries to pool their biological samples in order to produce more representative estimates of key biological parameters. This not only allows us to conduct analysis on a sample set that more closely resembles the assumed spatial structure of the stock, but it will also reduce the burden of extensive sample collection and analysis for individual countries by spreading responsibilities amongst member nations. Additionally, by combining samples, study leads can be identified by the BILLWG to undertake specific areas of life history research that interest them, or where they have particular expertise.

Materials and Methods

The ability to make inferences about a population that are suitable for stock assessment and management purposes is highly dependent on sampling design. Essentially, a balance must be achieved for a sufficient number of samples—too few and estimates will be inaccurate and imprecise whereas too many may be too costly to collect and process. Two sampling designs are typically utilized to collect biological samples for growth and mortality estimation: random or size stratified sampling. Size stratified sampling entails ‘filling’ pre-determined size bins with a fixed number of samples. Several studies indicate that random sampling of fishery catch is not cost efficient due to the amount of samples necessary to collect suitable numbers of the least abundant age classes, something which typically leads to further oversampling of the more common age classes (Brouwer & Griffiths 2005, Chih 2009). In some cases, specific individuals are then targeted to supplement the least abundant classes (i.e., typically the lower and upper tails of the size distribution), leading to an amplification of biases (Goodyear 2019). Goodyear’s (2019) simulation study demonstrated this using striped marlin as an example species. Furthermore, the ability to impose a truly random sampling design on fishery−collected samples is far from simple, with size-selective gear, shifting fisheries practices, and the fish themselves not being randomly distributed, all complicating issues (Lee et al. 2017).

Lacking the ability to collect truly random samples, size stratified sampling is the preferred option. There are many different approaches for determining the appropriate number and size of length bins in a size stratified sampling approach. More work is needed to determine an appropriate sampling strategy for striped marlin in the North Pacific; however, general guidance on the number of size bins and samples per size bin indicate that these numbers can depend on the number of age classes and the maximum size of the species of interest (Goodyear 1995, Brouwer & Griffiths 2005). Coggins et al. (2013) suggest computing $L_{inf}/30$ as an approach to determine the number of size bins. For striped marlin with an L_{inf} estimate of 214 cm EFL (Sun et al. 2011, ISC 2019), this equates to 31 total size bins, at 7 cm each. Ten to 15 samples per size bin appears to be a suitable number to produce reliable estimates of quantities of interest (Ketchen 1950, Kritzer et al. 2001, Brouwer & Griffiths 2005, Mandado & A.Vázquez 2011), which results in 465 total samples.

With concerns of spatial variability in life history parameters for striped marlin, it is likely that a spatial component will need to be considered and ultimately augment the above outlined general sampling approach. It may be necessary to split the Pacific into areas and conduct uniform size stratified sampling within each area. The key is that the sampling approach be uniform across the North Pacific, with sampling guidelines clearly established.

Discussion

Current evidence of disparate life history parameters (e.g., maximum size, age at maturity) among striped marlin caught in the western, central, and eastern North Pacific could be evidence of different stocks; however, without a consistent sampling methodology it is unclear whether these differences are truly evidence of stock structure or simply the result of differences in sampling and analysis. Improved collaborative sampling for biological parameters can help inform this issue of stock structure through the analysis of a more representative sample set, while also providing an improved sample set for genetic analysis, an important component in any investigation of stock structure, mixing, and breeding.

With the improvement of key biological parameters and stock structure identified as research priorities for the upcoming striped marlin assessment in 2024, we see a unified collaborative biological sampling program as a foundational step in our efforts to reduce uncertainty concerning growth, maturity, and stock structure of striped marlin in the North Pacific. As we discussed above, a general framework will need to be established; what has been presented here is merely an example. However, just as important as the design of the sampling approach is the support and participation of each contributing nation. A collaborative sampling effort requires engaged individuals from each participating nation to ensure adherence to the sampling design, as well as take on components of the life history research. Since a collaborative sampling effort is likely to produce extensive sample collections, study leads will need to be identified to undertake specific areas of life history research (Table 1). An added benefit of this approach will be to allow for a single standardized approach in individual areas of life history research. With individual labs focusing on specific projects with standardized approaches, we can more clearly address biological issues with reduced uncertainty resulting from sampling bias or inter-laboratory practice disparities.

The ISC BILLWG is the ideal vehicle with which to develop and carry out an internal collaborative biological sampling program for highly migratory species, with its range of experts from various nations, each able to contribute to the work. We used striped marlin here as an example species due to their status (overfished with overfishing occurring) and the pressing need for improved biological parameter estimates; however, this sampling approach is not intended exclusively for striped marlin and can be expanded to other species if desired.

Developing a thought-out, well designed collaborative biological sampling program that allows participating countries to pool their samples in order to produce more representative estimates of key biological parameters for highly migratory species is a fundamental step in order to make meaningful progress on reducing key sources of uncertainty in the assessments of these species. As we work to build a refined collaborative sampling approach, a key step forward will be the commitment of interested nations in contributing to the sample collection, as well as the identification of study leads to undertake specific aspects of the work.

References

Brouwer SL, Griffiths MH (2005) Influence of sample design on estimates of growth and mortality in *Argyrozona argyrozona* (Pisces: Sparidae). Fish Res 74:44-54

Chang H-Y, Sun C-L, Yeh S-Z, Chang Y-J, Su N-J, DiNardo G (2018) Reproductive biology of female striped marlin *Kajikia audax* in the western Pacific Ocean. J Fish Biol 92:105-130

Chih C-P (2009) Evaluation of the sampling efficiency of three otolith sampling methods for commercial king mackerel fisheries. Transactions of the American Fisheries Society 138:990-999

Coggins LG, Gwinn DC, Allen MS (2013) Evaluation of age–length key sample sizes required to estimate fish total mortality and growth. Transactions of the American Fisheries Society 142:832-840

Fitchett MD (2019) Estimating age and growth of Central North Pacific striped marlin using tagging data and direct observations of age. ISC/19/BILLWG-1

Goodyear CP (1995) Mean size at age: an evaluation of sampling strategies with simulated red grouper data. Transactions of the American Fisheries Society 124:746-755

Goodyear CP (2019) Modeling growth: consequences from selecting samples by size. Transactions of the American Fisheries Society 148:528-551

Humphreys R, Brodziak J (2019) Reproductive maturity of striped marlin, (*Kajikia audax*), in the central North Pacific off Hawaii. ISC/19/BILLWG-2/2

ISC (2019) Stock assessment report for striped marlin (*Kajikia audax*) in the Weatern and Central North Pacific Ocean through 2017. ISC/19/ANNEX/11

Ketchen K (1950) Stratified subsampling for determining age distributions. Transactions of the American Fisheries Society 79:205-212

Kritzer J, Davies C, Mapstone B (2001) Characterizing fish populations: effects of sample size and population structure on the precision of demographic parameter estimates. Can J Fish Aquat Sci 58:1557-1568

Lee H, Thomas L, Piner K, Maunder M (2017) Effects of age-based movement on the estimation of growth assuming random-at-age or random-at-length data. J Fish Biol 90:222-235

Mandado M, A.Vázquez (2011) On otoliths sampling. Northwest Atlantic Fisheries Organization, Scientific council meeting – June 2011, Serial No. N5906 NAFO SCR Doc. 11/023

Sun CL, Hsu WS, Chang YJ, Yeh SZ, Chiang WC, Su NJ (2011) Age and growth of striped marlin (*Kajikia audax*) in waters off Taiwan: A revision. ISC/11/BILLWG-2/07