

Stock Identification and Billfish Management

Robert A. Skillman

While economic and social evaluations of fisheries are today recognized as important elements in managing fisheries, determining the biological status of fish exposed to a fishery and to a management regime remains a basic and important element in management. For the status of a stock to be assessed, boundaries must be set. If the boundaries actually encompass more than one stock and management is carried out as if there were only one stock, the management scheme may perform satisfactorily on average for the two stocks. However, the more that population parameters, such as growth and mortality, differ among individual stocks, the more likely it is that the management regime will adversely impact one of the stocks. If the boundaries do not completely encompass a stock, then events external to the management area can significantly affect the stock.

This chapter reviews stock identification methods as they relate to fisheries management and, in particular, to billfish management. The stock concept, itself, will be discussed before reviewing the various methods used to study stock structure. Then, what is known about billfish stock structure will be reviewed, followed by recommendations regarding the most likely productive research strategies to follow for billfishes in the future.

The Stock Concept

Setting boundaries and identifying stocks is, in effect, determining what part of the total species population is going to be assessed and managed. Thus, the term stock or unit stock is used, "... to connote as well as circumscribe the basic grouping on which management needs to focus attention" (Kutkuhn 1981). This initial step in assessment has led to many reviews of

the unit stock concept, with many authors proposing new or modified definitions. Providing a historical perspective might be appropriate at this time.

Fishery biologists first defined a stock in terms of the various tools employed in conducting an assessment. For example, Cushing (1968) said, "... a stock may be defined as a population in which the vital parameters of recruitment, growth, and mortality are homogeneous." In practice, fishery biologists frequently identified stocks based on where the fish were found as larvae, as adults in the fisheries, or while spawning, as well as by how the fish looked (meristics and morphometrics). Then, the existence of these putative stocks was evaluated by using estimates of vital (or population) parameters. With the development of population genetics, the fishery biologists' definition of a stock was viewed as vague and not quantitatively rigorous compared with the geneticists' definition of a population or a subpopulation. Thus, fishery biologists began incorporating genetic concepts, and new definitions were proposed. For example, "... a unit fish stock is one consisting of randomly interbreeding members whose genetic integrity persists whether they remain spatially and temporally isolated as a group, or whether they alternately segregate for breeding and otherwise mix freely with members of other unit stocks of the same species" (Kutkuhn 1981). Along with this definition came numerous attempts to identify stocks by using various genetic techniques.

The debate on the utility of genetic techniques in fisheries stock assessment and fisheries management continues today. One problem is whether a population determined to be genetically homogeneous meets the needs of fishery biolo-

gists to conduct stock assessments; namely, the unit stock must be homogeneous with respect to recruitment, growth, and mortality. A second problem is whether genetic techniques can resolve the structure of a large population inhabiting an extensive area having vague and changing environmental boundaries when biological (fishery) information suggests some degree of stock structuring. While all the evidence is certainly not in, the genetic and fishery biological definitions apparently coincide reasonably well for demersal species and stocks with well-defined physical or environmental boundaries. On the other hand, they apparently do not coincide well for species inhabiting, as adults or larvae, the pelagic ecosystem with poorly defined physical and environmental boundaries.

Stock Identification Methods

As indicated above, the study of population structure in fisheries consists of two basic approaches. The traditional biological approach consists of a number of alternative techniques for identifying stocks. These stocks meet the fishery biologists' stock assessment needs but may not be the same as genetic subpopulations. The newer genetic approach consists of a few but growing number of techniques for identifying subpopulations that may or may not be helpful for stock assessment and management purposes.

Biological

Distribution. Probably the first method employed was to examine the geographical distribution of fishery catches, which often consist of adults. Thus, this method has direct applicability to defining the boundaries of a fishery, and possibly the boundaries of management action, but it may not be satisfactory for determining the boundaries of a stock unless the distribution of fishing effort is extensive. For example, if the fishing effort is directed at the species being examined, it is not likely to occur beyond the region where the species is commercially or recreationally important. In such cases, stocks may be distributed more extensively than indicated. Compiling the distribution of catches by size classes may help substantiate the existence of putative stocks when recruitment can be shown to vary.

Determining the distribution of spawning sites may result in more reliable identification of stocks. The existence of geographically or temporally separate spawning sites, with no

exchange of individuals among the sites, is necessary for genetic separation and could contribute to differences in vital parameters. The distribution of larvae and juveniles may also be used to identify stocks, particularly when the samples are collected independently from any fishery. Thus, using juveniles collected from the stomachs of commercially-landed predatory fishes should be done with care.

Population Parameters. Estimates of population parameters, such as growth, recruitment, and mortality, are used to separate stocks. In addition, they are commonly used to characterize putative stocks and evaluate whether their existence seems plausible; that is, whether the parameters are homogeneous over the range of the reputed stock. While demonstrating that parameter estimates are different among potentially separate stocks does not necessarily prove the existence of separate stocks, stock structuring is supported when geographical clumping or clinal variation of parameters occurs. Such results are consistent with a lack of genetic mixing (subpopulation formation) and a lack of exchange of fish among fishing grounds or mixing of individuals in nursery areas (stock formation) because separation, from either perspective, could lead to different population parameters. Given the poor ability to estimate mortality even for well-studied stocks, however, estimates of billfish mortality are not likely to provide as much information as growth estimates. On the technical side, comparison of the growth estimates is complicated because the commonly used von Bertalanffy growth parameters, maximum size (L_{inf}) and rate of approaching that maximum (k), are correlated. Simple cluster analysis conducted by plotting L_{inf} versus k for samples from different areas has proven productive in the identification of stocks. Other population parameters (e.g., the age at first maturity and gonadal index) are also used. Age at first maturity is strongly affected by stock size, which is, in turn, affected by the size of the fishery. Gonadal development is seasonal but may differ among stocks.

Parasites. Using the occurrence of fish parasites as a means of studying stock structure is based on the concept that parasites are naturally occurring "tags"; that is, the incidence of parasitic species varies geographically and these natural tags are not lost. The method is not applied frequently to large pelagic species for a number of reasons. Fishery biologists recognize

that parasitology is not a tool in the sense that morphometric and multivariate statistical methods are, but is an additional level of biological complexity requiring research itself. This complexity involves the identification of relatively bizarre animals; use of different sampling, preservation, and preparation techniques; and, most importantly, familiarity with a different set of life-history strategies involving host-parasite relationships. Parasitologists have tended to work more in freshwater and coastal marine habitats where fish stock sizes and parasite-to-host linkages are more amenable to research. Consequently, the life histories of parasites occurring on large pelagic species and the effect of environmental changes on infestation are not well known, and interpretation of results has been open to question. Research is needed on the possibility of tag loss (selective or differential loss of parasitic species or parasite size classes) with movement of fish into areas having different environments, and then reinfestation by other parasitic species. Also, application of the method to date has assumed that each natural tag (each parasitic species) is made up of one population, but I see no reason why they could not be divided into subpopulations as well. Nonetheless, such studies can provide a fishery-independent determination of stock structure, and additional long-term work on the basic biology of pelagic fish parasites is likely to improve the utility of the method as a stock identification tool.

Tagging. Tagging fish for the study of stock structure is very popular because it provides direct, if not irrefutable, evidence of fish movement and the lack of stock separation. Movement is the mechanism for exchange of individuals and the mixing of genetic products. However, the method has several problems, and care must be taken in analyzing the results (Hilborn and Sibert 1988). First, the method is expensive if large numbers of tagged fish are to be released, and this is certainly desirable if not a requirement with the large populations that exist for billfishes and other pelagic species. Also, a great deal of international promotion and cooperation are required to conduct such experiments successfully. Second, results are meaningful only if fisheries exist that have the potential of recapturing the tagged fish. Third, fishing effort statistics from these fisheries are required for quantitative evaluations of the recaptures. Fourth, without additional information about the biology of the fish and such specifics as the size and maturity of the fish

when released and retaken, recaptures may indicate movement but provide little information on stock structuring.

Morphometrics and Meristics

Fish exhibit greater observable (phenotypic) variation than other vertebrates, apparently because they are poikilothermic (cold-blooded) and have a capacity for indeterminate growth (e.g., Allendorf et al 1987). Thus, early workers were able to recognize stocks on the basis of appearance, and later workers built on this by analyzing measured characters (morphometrics) or analyzing counted characters (meristics). With the development of analytical tools in the fields of taxonomy and statistics, this approach flourished and provided a means for rigorously identifying stocks. However, morphometric and meristic characters were shown to be strongly influenced by the environment, and their use fell into disfavor with the development of electrophoresis for studying population genetics. Experience has shown that stocks identified by using morphometrics or meristics are in general agreement with subpopulations identified genetically (e.g., see Ihssen et al 1981). However, a greater degree of stock structuring is often found by using morphometric and meristic methods than by using genetic procedures, because of the superior power of the statistical tests associated with the former methods and the use of environmentally influenced characters.

Thus, among many biologists, morphometric and meristic methods are still viable means of investigating stock structuring. With the development of new techniques for studying shape, the statistical power of the methods has increased even more. Truss analysis (e.g., see Winans 1987) makes use of recently developed powerful multivariate analysis techniques. Showing great promise is the use of planar shape analysis, first used in the study of the evolution of ostracods (e.g., see Benson 1967) and recently making its way into fisheries (Bird et al 1986). This method is based on pattern recognition techniques using mathematical tools such as Fourier analysis and discriminant analysis. The collection of data for analysis using the truss and planar shape methods can be performed on microcomputer-based image processing systems, thus reducing the cost of collecting data in the field.

Genetics

The following historical perspective is drawn in part from Utter et al (1987). Although great strides in the inheritance of observable characters have been made from the time of the pioneering work of Mendel (1866) up to the 1930s, this work was not transferable to fish because of the magnitude of environmental influences on their observable characters. About this time, the inheritance of blood groups had been resolved, and attempts were made later to use the technique on tunas (Cushing 1956, Sprague et al 1963, Fujino 1970). This technique was unproductive because of the fragility of fish erythrocytes and problems in making and preserving the discriminating antisera. Lundstrom (1987) indicates that the use of monoclonal antibodies shows promise, but other genetic procedures probably show more potential for success with billfishes.

The determination of the structure of the DNA molecule by Watson and Crick (1953) led quickly to the determination of the relationship between genes and intracellular, enzymatic proteins, called isoenzymes or isozymes for short. By 1955, electrophoretic techniques were developed that allowed easy examination of the variation (polymorphism) of these proteins and, thereby, the genes that make them. Thus was born the most powerful and productive technique to date for studying population genetics, dominating since the mid-1960s. Examples even in the fisheries literature are too numerous to mention. A serious problem with the technique is that separation of stocks depends on statistically testing of what are called the Castle-Hardy-Weinberg gene proportions. This test is statistically weak and, with the typical genotypic ratios involved, requires large sample sizes to obtain meaningful results. After many years of work on skipjack tuna (*Katsuwonus pelamis*) in the Pacific Ocean (Fujino and Kang 1968, Argue et al 1986), some degree of population structuring is indicated, but distinct subpopulations have not been resolved. Grant et al (1987) state that marine fish, in general, exhibit little genetic population structuring because of the passive dispersal of larvae and active movement of adults (Ryman et al 1984; Shaklee 1984). Given the life history of most billfishes, electrophoretic study of isozyme variability is not likely to be very productive.

Recently, two additional DNA-based techniques have been developed. As the name

suggests, DNA sequence determination involves the resolution of genes directly on the DNA molecule, which is located in the cell nucleus. The method is sufficiently sensitive that relatedness of progeny and ancestors of a generation or two can be detected; beyond this, variability becomes so great that all individuals appear to be different (Wetton et al 1987). Thus, the name "DNA fingerprinting" has been used to describe this method. It is not likely to be of much benefit for the study of billfish stock structuring, although it may be the genetic "marker" so long sought for hatchery-reared fish released into the wild.

The second technique involves the analysis of DNA occurring in mitochondria located in the cell cytoplasm. Because mitochondrial DNA (mtDNA) is maternally inherited, each individual has an exact copy (except for rare mutations) of the mtDNA genotype from its mother. Therefore, the operational taxonomic unit is the individual rather than the population, as with nuclear gene analytical techniques such as electrophoresis. Thus, in practical terms, the statistical requirements are quite different, and sample sizes can be substantially less than with electrophoretic work (Ferris and Berg 1987). For example, reported sample lot sizes per species have varied from 1 to 12 (Avisé et al 1979, Berg and Ferris 1984, Graves et al 1984, Wilson et al 1985, 1987) with species totals in 2 studies reaching 36 (Avisé et al 1979) and 87 (Lansman et al 1981). This contrasts with sample lot sizes of 50 to 100 (Fujino and Kang 1968) or even 200 (IATTC 1978) and total sample sizes in the thousands for electrophoretic studies of fish. Although the technique apparently holds great promise for resolving stock structuring (Avisé et al 1979), little experience has been gained with pelagic species. Avisé (1987) could not find any evidence of stock structuring in the American eel (*Anguilla rostrata*) which spawns in the pelagic environment, whereas stock structuring was evident for several demersal or estuarine species. Graves et al (1984) did not find any difference between Atlantic and Pacific samples of skipjack tuna; however, the specimens were frozen, which considerably reduces the amount of mtDNA recovered for analysis (Lansman et al 1981; Ferris and Berg 1987).

Billfish Stock Structure

In the following sections, information on the stock structure of billfishes is summarized from a variety of sources. Papers presented at the first billfish symposium in 1972 (Shomura and

Williams 1974) discuss, for Atlantic, Indian, and Pacific oceans, the distribution of adults based on tuna longline catches, the distribution of larvae and ostensible spawning areas based on research data, and results from tagging. For the Atlantic Ocean, I am not aware of any single source summarizing information on billfish stock structure, so I have used the way billfish stocks are assessed and reported in the biennial reports of the International Commission for the Conservation of Atlantic Tunas (ICCAT) as an indication of the state of knowledge (e.g., see ICCAT 1987). For the Indian Ocean, participants at a 1979 tuna and billfish stock assessment workshop summarized the state of knowledge for billfish stock structure (FAO 1980). Likewise, for the Pacific Ocean, participants at the 1977 billfish stock assessment workshop (Shomura 1980) summarized what was known about the stock structure of billfishes as a prerequisite to assessing the status of the presumed stocks.

Atlantic Ocean

Among the several billfishes occurring in the Atlantic Ocean, the ICCAT biennial reports contain material on separate stocks only for sailfish (*Istiophorus platypterus*), namely eastern and western stocks. The basis for this separation seems to be the distribution of longline catches and tagging results (Mather, Tabb, Mason, and Clark 1974). While tagging results support the existence of separate northern and southern stocks of the Atlantic blue marlin (*Makaira nigricans*; Mather, Mason, and Clark 1974), the ICCAT reports contain discussions of stock assessment results for the entire Atlantic Ocean but present figures showing surplus production models for separate stocks. White marlin (*Tetrapturus albidus*) assessments are presented for one Atlantic-wide stock. For swordfish (*Xiphias gladius*), researchers (ICCAT 1987) now believe that separate eastern and western stocks exist, as well as a separate Mediterranean stock, based on longline catch distributions, tagging results, and the distribution of spawning activities and larvae.

Indian Ocean

Information on the stock structure of five billfishes is available for the Indian Ocean (FAO 1980). The distribution of longline catches and information on spawning suggest that there is a single stock of Indo-Pacific blue marlin (*M. mazara*) in the Indian Ocean. Similar kinds of data for striped marlin (*T. audax*), swordfish, sailfish,

and black marlin (*M. indica*) suggest multiple stocks. In addition, the workshop participants (FAO 1980) believed that movement of the latter species could occur between the Pacific and Indian Oceans although no tag recaptures had been made to support the contention.

Pacific Ocean

For the Pacific Ocean, stock structure information is available for six billfishes (Shomura and Williams 1974, Shomura 1980). Based on the distribution of tuna longline catches, tagging returns, and the distribution of spawning, the Indo-Pacific blue marlin is believed to consist of a single Pacific-wide stock (Shomura 1980), whereas the other billfishes exhibit some evidence of stock structuring. In an electrophoretic survey of blue marlin captured in Hawaii, sufficient polymorphism to conduct a population genetic study was found (Shaklee et al 1983). The only suggestion of population structuring (mixing of subpopulations) in this small sample collected at one site in 1 month, however, was a deficiency of heterozygotes for one of seven polymorphic gene systems surveyed. For black marlin, participants at the 1977 stock assessment workshop (Shomura 1980) indicated that separate eastern Pacific and two western Pacific stocks probably exist. Skillman (1989) assumed one Pacific-wide stock centered off Australia, based on the distribution of tuna longline catches. Nakamura (1983) indicates two spawning areas, one off Australia and a second in the north Pacific between the Caroline and Marshall Islands. Northern and southern stocks of striped marlin may exist, but the evidence is contradictory or inconclusive. For striped marlin, the area of high tuna longline catches in the eastern tropical Pacific appears to join or merge seasonally in many years with high catch areas in the middle latitudes of both the north and south Pacific. In contrast, the annual distribution of spawning stretches from comparable northern and southern central Pacific areas across the Equator in the western tropical Pacific (Nakamura 1983). Swordfish population is generally believed to consist of a single Pacific-wide stock, but may consist of separate stocks in the northwest, southwest, and eastern Pacific. Spawning grounds are located in warm, tropical waters in the western and central Pacific (Nakamura 1983). Sailfish are believed to be divided into eastern and western stocks based on tuna longline catch rates and distribution of spawning

sites. Distribution of tuna longline catches suggests separate northern and southern stocks of shortbill spearfish (*T. angustirostris*), and the distribution of spawning activity supports this conclusion.

Recommendations

The following research recommendations would, in my opinion, most likely contribute to our understanding of the stock structure of billfishes.

1. Tag-and-release programs, particularly for young fish, should be continued and extended to other tournaments and fisheries. Recaptures provide valuable information on movement and the relationship among fisheries, information not easily gotten by any other means. Although the number of billfish that could be released from most fisheries is small, and indeed probably smaller than desirable for estimating such parameters as fishing mortality, growth rate, and rate of exchange between fisheries, qualitative information on movement is still useful. Returning viable billfish to the sea without tagging them, or retaining all nontrophy or nonpoint-contributing billfish for tournaments, is, in effect, throwing away a valuable research opportunity. Support of tagging operations is particularly amenable to cooperative arrangements among national fishery agencies and recreational interests and, indeed, could provide the basis for further cooperation.
2. More effort should be expended on shape analysis, especially the newer truss and planar shape methods, but possibly on traditional morphometric and meristic methods as well. Although the newer methods require or would benefit from access to microcomputer-based image processing equipment and some specialized computer software (though not very sophisticated or costly), the traditional methods can be used by small fisheries offices with measuring devices, a microcomputer, and standard statistical software. Such studies would benefit from intergovernmental cooperation and, of course, collaboration with fishermen, tournament organizers, and fish processors.
3. Studies should be conducted to estimate

vital parameters, such as growth, age at first maturity, recruitment, and mortality, to ensure that valid stocks are identified and that models used to assess the status of stocks are applied correctly.

4. Billfish larval surveys should be designed and implemented. Results from ichthyoplankton tows, taken by different kinds of gear, at different depths, in different seasons, and, for the most part, without any experimental design (along with charts of the distribution of billfish catches by tuna longline gear), have been the most commonly used means of identifying stocks. Enough is now known, however, about the location of spawning grounds and seasonal occurrence of spawning for most billfishes, to formulate testable hypotheses about their stock structure. Because of the large areas involved, such experimentation would benefit from international collaboration among national fisheries agencies and universities.
5. Selected genetic studies using mtDNA or electrophoresis should be continued but not on a large scale. I suggest that selecting species such as sailfish, generally believed to consist of multiple stocks, would be more productive than choosing a species thought to consist of one panmictic stock. Also, regarding mtDNA analysis, the development of standard tissue collection and preservation procedures for situations where the samples cannot be immediately processed would benefit billfish research.

Summary

The identification of separate biological units or stocks is required for determining the status of the resources and for conserving them via fisheries management. A number of biologically based methods for separating stocks are available: using such methods on billfishes is likely to be more productive than using population genetic methods. The stock structures of billfishes are, in general, poorly known. The largest billfishes, blue and black marlins, appear to consist of single ocean-wide stocks, while there is some evidence for east and west or north and south stocks of the smaller striped marlin and swordfish. Evidence for multiple stocks for the smallest species (spearfish and sailfish) is stronger.

Literature Cited

- Allendorf, F.W., N. Ryman, and F.M. Utter. 1987. Genetics and fishery management. Past, present, and future. In N. Ryman, and F. Utter (eds.), Population genetics and fishery management, p. 1-19. Washington Sea Grant Prog., Univ. Washington Press, Seattle.
- Argue, A.W., P. Kleiber, R.E. Kearney, and J.R. Sibert. 1986. Evaluation of methods used by the South Pacific Commission for identification of skipjack population structure. In P.E.K. Symons, P.M. Miyake, and G.T. Sakagawa (eds.), Proceedings of the ICCAT Conference on the Skipjack Year Program, p. 242-251. International Commission for the Conservation of Atlantic Tunas, Madrid, Spain.
- Avise, J.C. 1987. Identification and interpretation of mitochondrial DNA stocks in marine species. In H.E. Kumpf, R.N. Vaught, C.B. Grimes, A.G. Johnson, E.L. Nakamura (eds.), Proceedings of the stock identification workshop: 105-136. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SEFC-199.
- Avise, J.C., R.A. Lansman, and R.O. Shade. 1979. The use of restriction endonucleases to measure mitochondrial DNA sequence relatedness in natural populations. I. Population structure and evolution in the genus *Peromyscus*. Genetics 92:279-295.
- Benson, R.H. 1967. Muscle-scar patterns in Pleistocene (Kansan) ostracods. In C. Teichert and E.L. Yochelson (eds.), Essays in paleontology and stratigraphy: 211-241. Univ. Kansas Press, Lawrence.
- Berg, W.J., and S.D. Ferris. 1984. Restriction endonuclease analysis of salmonid mitochondrial DNA. Can. J. Fish. Aquat. Sci. 41:1041-1047.
- Bird, J.L., D.T. Eppler, and D.M. Checkley, Jr. 1986. Comparisons of herring otoliths using Fourier series shape analysis. Can. J. Fish. Aquat. Sci. 43:1228-1234.
- Cushing, D.H. 1968. Fisheries biology. A study in population dynamics. Univ. Wisconsin Press, Madison, 200 p.
- Cushing, J.E. 1956. Observations on serology of tuna. Fish Wildl. Serv., Spec. Sci. Rep., Fish. 183. 14 p.
- FAO. 1980. State of selected stocks of tuna and billfish in the Pacific and Indian Oceans. Summary report of the Workshop on the Assessment of Selected Tunas and Billfish Stocks in the Pacific and Indian Oceans, Shimizu, Japan, 13-22 June 1979, 88 p.
- Ferris, S.D., and W.J. Berg. 1987. The utility of mitochondrial DNA in fish genetics and fishery management. In N. Ryman and F. Utter (eds.), Population genetics and fishery management: 277-299. Washington Sea Grant Prog., Univ. Washington Press, Seattle.
- Fujino, K. 1970. Immunological and biochemical genetics of tunas. Trans. Am. Fish. Soc. 99:152-178.
- Fujino, K., and T. Kang. 1968. Serum esterase groups of Pacific and Atlantic tunas. Copeia 1968:56-63.
- Grant, W.S., R.W. Leslie, and I.I. Becker. 1987. Genetic stock structure of the southern African hakes *Merluccius capensis* and *M. paradoxus*. Mar. Ecol. Prog. Ser. 41:9-20.
- Graves, J.E., S.D. Ferris, and A.E. Dizon. 1984. Close genetic similarity of Atlantic and Pacific skipjack tuna (*Katsuwonus pelamis*) demonstrated with restriction endonuclease analysis of mitochondrial DNA. Mar. Biol. (Berl.) 79:315-319.
- Hilborn, R., and J. Sibert. 1988. Is international management of tuna necessary? Mar. Policy 12(1):31-39.
- IATTC. 1978. Annual report of the Inter-American Tropical Tuna Commission, 1977. La Jolla, Calif., 155 p. [In Engl. and Span.]
- ICCAT. 1987. Report for biennial period, 1986-87. Pt. I (1986). Int. Comm. Conserv. Atl. Tunas, Madrid, Spain, 310 p.
- Ihssen, P.E., H.E. Booke, J.M. Casselman, J.M. McGlade, N.R. Payne, and F.M. Utter. 1981. Stocks identification: Materials and methods. Can. J. Fish. Aquat. Sci. 38:1838-1855.
- Kutkuhn, J.H. 1981. Stock definition as a necessary basis for cooperative management of Great Lakes fish resources. Can. J. Fish. Aquat. Sci. 38:1476-1478.
- Lansman, R.A., R.O. Shade, J.F. Shapira, and J.C. Avise. 1981. The use of restriction endonucleases to measure mitochondrial DNA sequence relatedness in natural populations. III. Techniques and potential applications. J. Mol. Evol. 17:214-226.
- Lundstrom, R.C. 1987. The potential use of monoclonal antibodies for identification of fish stocks. In H.E. Kumpf, R.N. Vaught, C.B. Grimes, A.G. Johnson, E.L. Nakamura (eds.), Proceedings of the stock identification workshop: 137-148. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SEFC-199.
- Mather, F.J., III., J.M. Mason, Jr., and H.L. Clark. 1974. Migrations of white marlin and blue marlin in the western North Atlantic Ocean — tagging results since May, 1970. In R.S. Shomura and F. Williams (eds.), Proceedings of the International Billfish Symposium, Kailua-Kona, Hawaii, 9-12 August 1972, Pt. 2. Review and contributed papers: 211-225. U.S. Dep. Commer., NOAA Tech. Rep. NMFS SSRF-675.
- Mather, F.J., III., D.C. Tabb, J.M. Mason, Jr., and H.L. Clark. 1974. Results of sailfish tagging in the western North Atlantic Ocean. In R.S. Shomura and F. Williams (eds.), Proceedings of the International Billfish Symposium, Kailua-Kona, Hawaii, 9-12 August 1972, Pt. 2. Review and contributed papers: 194-210. U.S. Dep. Commer., NOAA Tech. Rep. NMFS SSRF-675.
- Mendel, G. 1866. Experiments in plant hybridisation. [Transl. from German and republished in 1965 by the Royal Horticultural Society of London, Cambridge, Harvard Univ. Press. 41 p. (original paper published Versuche über Pflanzenhybriden. Verh. Naturforsch. Ver. Brünn. Abhandlungen IV, 1865, appeared in 1866.)]
- Nakamura, I. 1983. Systematics of the billfishes (*Xiphiidae* and *Istiophoridae*). Seto Mar. Biol. Lab. 28(5/6):255-396.
- Ryman, N., U. Lagercrantz, L. Anderson, R. Chakraborty, and R. Rosenberg. 1984. Lack of a correspondence between genetic and morphologic variability patterns in Atlantic herring (*Clupea harengus*). Heredity 53:687-704.
- Shaklee, J.B. 1984. Genetic variation and population structure in the damselfish, *Stegastes fasciolatus*, throughout the Hawaiian Archipelago. Copeia 1984:629-640.
- Shaklee, J.B., R.W. Brill, and R. Acerra. 1983. Biochemical genetics of Pacific blue marlin, *Makaira nigricans*, from Hawaiian waters. Fish. Bull., U.S. 81:85-90.
- Shomura, R.S. (ed.). 1980. Summary report of the billfish stock assessment workshop Pacific resources. U.S. Dep. Commer., NOAA Tech. Memo. NMFS, NOAA-TM-NMFS-SWFC-5, 58 p.
- Shomura, R.S., and F. Williams (eds.). 1974. Proceedings of the International Billfish Symposium, Kailua-Kona,

- Hawaii, 9-12 August 1972. Pt. 2. Review and contributed papers. U.S. Dep. Commer., NOAA Tech. Rep. NMFs SSRF-675. 335 p.
- Skillman, R.A. 1989. Status of Pacific billfish stocks. Current volume.
- Sprague, L.M., J.R. Hollaway, and L.I. Nakashima. 1963. Studies of the erythrocyte antigens of albacore, bigeye, skipjack, and yellowfin tunas and their use in subpopulation identification. In H. Rosa, Jr. (ed.), Proceedings of the World Scientific Meeting on the Biology of Tunas and Related Species: 1381-1393. La Jolla, Calif., 2-14 July 1962. FAO Fish Rep. 6(3).
- Utter, F., P. Aebersold, and G. Winans. 1987. Interpreting genetic variation detected by electrophoresis. In N. Ryman and F. Utter (eds.), Population genetics and fishery management: 21-45. Washington Sea Grant Prog., Univ. Washington Press, Seattle.
- Watson, J.D., and F.H.C. Crick. 1953. Genetical implications of the structure of deoxyribonucleic acid. Nature (Lond.) 171:964.
- Wetton, J.H., R.E. Carter, D.T. Parkin, and D. Walters. 1987. Demographic study of a wild house sparrow population by DNA fingerprinting. Nature (Lond.) 327:147-149.
- Wilson, G.M., W.K. Thomas, and A.T. Beckenbach. 1985. Intra- and inter-specific mitochondrial DNA sequence divergence in *Salmo*: rainbow, steelhead, and cutthroat trout. Can. J. Zool. 63:2088-2094.
- Wilson, G.M., W.K. Thomas, and A.T. Beckenbach. 1987. Mitochondrial DNA analysis of Pacific Northwest populations of *Oncorhynchus tshawytscha*. Can. J. Fish. Aquat. Sci. 4:1301-1305.
- Winans, G.A. 1987. Using morphometric and meristic characters for identifying stocks of fish. In H.E. Kumpf, R.N. Vaught, C.B. Grimes, A.G. Johnson, E.L. Nakamura (eds.), Proceedings of the stock identification workshop, Panama City Beach, Florida, November 5-7, 1985: 25-62. U.S. Dep. Commerce., NOAA Tech. Memo. NMFS-SEFC-199.