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REPORT TCCHINOOK (88)-1

SUMMARY OF A SEMINAR ON GENETIC STOCK IDENTIFICATION (GSI) OF CHINOOK SALMON: STATUS, NEEDS AND FUTURE

Editor: Rich Lincoln
Washington Department of Fisheries

August 1988

May 9, 1988

Mr. Ian Todd, Executive Secretary
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Dear Ian:

As Co-Chairs of the Joint Chinook Technical Committee, we are pleased to recommend Pacific Salmon Commission publication of the enclosed proceedings from the October 1986 Workshop on Genetic Stock Identification of Chinook Salmon: Status, Needs, and Future. We are grateful for the joint sponsorship of the Pacific Salmon Commission, the Washington Department of Fisheries, and the National Marine Fisheries Service. In particular, the PSC created the opportunity for this workshop by making meeting arrangements to coincide with regular Chinook Committee activities. These arrangements aided the coastwide exchange of information and ideas about the status, needs, and future of this emerging technology.

The presentations summarized in these proceedings present the viewpoints and personal conclusions of scientists active in chinook salmon genetic stock identification. While the results and conclusions presented here are those of the individual scientists, the Joint Chinook Technical Committee welcomes the PSC publication of these proceedings to encourage an open exchange of scientific information, perspectives, and ideas for the future.

Brian Riddell
Dr. Brian Riddell
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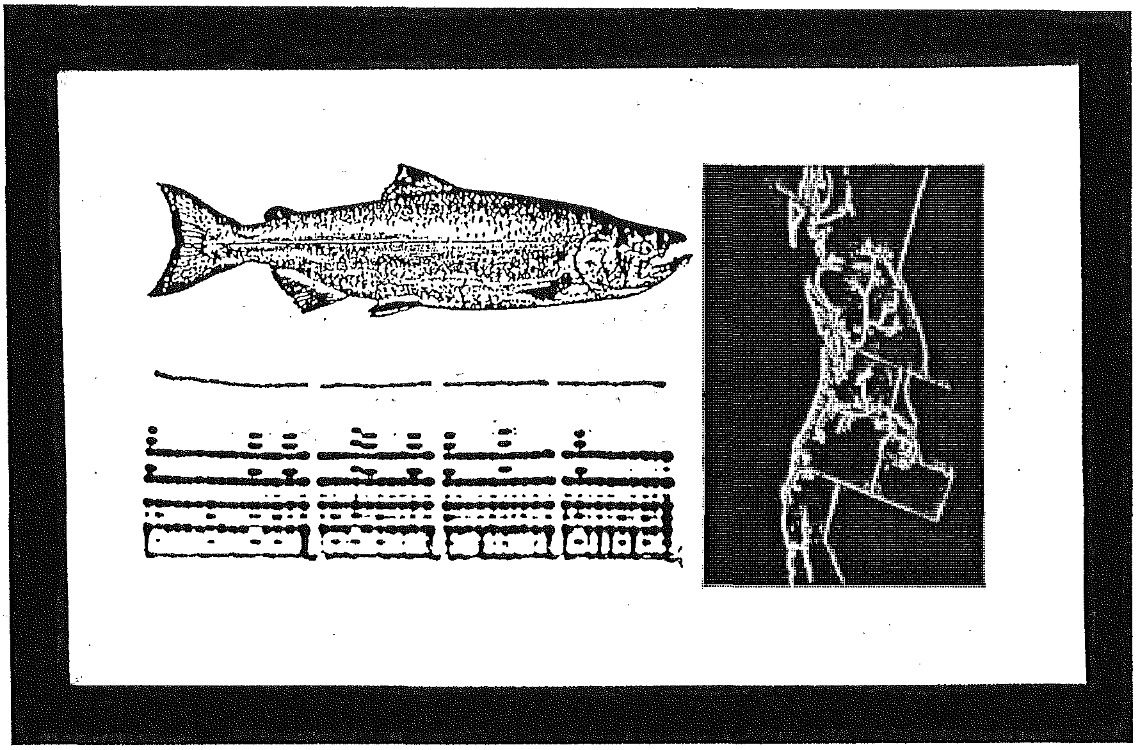
GENETIC STOCK IDENTIFICATION (GSI) OF CHINOOK SALMON:
STATUS, NEEDS AND FUTURE



Summary of a Seminar
On October 24, 1986

Sponsored by

Pacific Salmon Commission
Joint Chinook Technical Committee
Washington Department of Fisheries
National Marine Fisheries Service

August 1987

PERSPECTIVE

Rich Lincoln
Washington Department of Fisheries

In October 1986 several agencies sponsored a seminar on genetic stock identification (GSI) of chinook salmon. The questions we sought to answer included:

- What is GSI and why do we need it?
- What estimation methodologies are used and how good are they?
- What harvest management applications have occurred?
- What is the status of chinook GSI on the Pacific coast?
- What are the future opportunites and needs?

The individual presentations at the seminar, summarized in this report, were designed to provide information pertinent to these questions. Each presentation leads to an important conclusion, the sum of which I attempt to highlight in this executive summary, thereby providing my professional perspective of how GSI should fit into contemporary chinook salmon management on the Pacific coast.

The seminar contributors are leaders in development and application from the entire coast. Their written summaries reflect a blend between abstract and brief technical report. Much material is in press or planned for future publication, and readers are encouraged to contact authors for additional information. Addresses are provided in Appendix 2.

WHAT IS GSI AND WHY DO WE NEED IT?

Regulation of offshore salmon fisheries has evolved from virtually non-existent in the mid-1970's to active in the mid-1980's. Yet salmon managers coastwide have been handicapped in recent years with inadequate tools to achieve the level of regulatory refinement sought for mixed-stock fisheries. How can mixed-stock harvest be optimized, i.e. providing maximum harvest opportunities consistent with conservation needs of important, weak stocks? And how can stock-specific harvest be regulated to either equitably distribute the conservation burden or meet specific allocation mandates?

We have institutionalized coded-wire tagging programs and stretched them to their practical, theoretical and economical limits. The coded-wire tag (CWT) is a critical staple of our "stock identification diet" but the time has long past for managers and scientists to develop and implement new tools that can enhance management of mixed-stock fisheries. While genetic stock identification (GSI) is no more a panacea for meeting stock identification needs than the CWT, this exciting new tool can provide something heretofore unavailable - an accurate and precise picture of a fishery's stock-specific harvest impacts in any time/area stratum that can be practically sampled, in much the same way scale pattern analysis has been successfully used to manage Alaskan and Fraser River sockeye runs.

As described by Shaklee in this seminar, GSI is presently based on the ability to distinguish salmon stocks using starch gel electrophoresis - a biochemical lab procedure which has a very straightforward genetic basis. Genetic profiles are established for known-origin stocks, samples of unknown-origin are collected and electrophoretically characterized from a mixed-stock fishery, and finally the fishery samples are compared mathematically to the baseline stocks to estimate their origin and contribution. The genetic and biochemical techniques are sound and proven and they represent a powerful stock identification capability because harvested fish carry natural marks.

WHAT ESTIMATION METHODOLOGIES ARE USED AND HOW GOOD ARE THEY?

We learn from Millar that the mathematical technique used to analyze GSI data by U.S. and Canadian scientists computes the probability of each fish in a mixed-stock fishery sample belonging to the various stocks in the baseline. The application of this "maximum likelihood" approach to GSI estimation is a simple extension of existing, accepted statistical techniques, the properties of which are generally well-understood. Confidence limits for stock composition estimates can be directly computed to provide managers an indication of "how good" GSI results are. Steps are available to minimize estimate bias and areas for further sensitivity testing have been identified.

Similarly, Wood outlines results of evaluating bias and precision of stock composition estimates from the maximum likelihood technique. He suggests a very practical approach to optimizing the accuracy of estimates via groupings of stock similarity and provides a number of conclusions that confirm the statistical reliability of GSI results.

Continued development of GSI techniques and analytical procedures clearly will be a fixture for future refinements. The critical link for salmon management, however, is the step from lab results to real world management problems. A strong linkage already has been established.

WHAT HARVEST MANAGEMENT APPLICATIONS HAVE OCCURRED?

Part of the strength of using GSI is that simulation procedures can be used to evaluate the potential of a given application and to plan appropriate experimental design for sampling mixed-stock fisheries. Teel describes an actual example for the Fraser River test fishery which has resulted in a cooperative, joint agency assessment of chinook run timing and management periods using GSI.

The Columbia River spring chinook fishery application (Phelps) is an excellent example where GSI is being successfully used to monitor the effectiveness of regulations designed to maximize harvest of surplus hatchery stocks while protecting weak natural stocks. Comparisons of past GSI and CWT estimates for this fishery indicate close agreement in results. However in this case GSI provides a more direct approach to estimating stock composition and yields great precision for the sample sizes used.

Stock composition questions for ocean mixed-stock chinook fisheries also have been examined successfully with GSI. Teel's southwest Vancouver Island troll results show a decline in contribution of Columbia River tule stocks that was similarly observed in terminal run sizes. The examination of temporal changes in stock composition would seem to be an obvious extension of this application. When the question of possible time/area protection for depressed tules off Vancouver Island was discussed by the Joint Chinook Technical Team in the past, at least one member expressed the doubt that CWT data could provide the necessary basis to evaluate such potential. In fact the strata currently defined in the Team's key indicator stock model are broad annual, geographic time/areas based largely on a conclusion that this is the finest resolution for which confident results can be obtained from CWT-generated input data. In contrast, GSI techniques are ideally suited for evaluating refinements in chinook regulatory controls to optimize harvest and protection of various stocks.

Pattillo's discussion of chinook management by the Pacific Fishery Management Council (PFMC) represents perhaps the best operational example of GSI data being used as an integral part of the ocean fishery management process. GSI has been a key to recent refinements in evaluating and establishing annual chinook harvest quotas off the Washington coast. Pattillo's challenge to managers and scientists is an obvious one - why isn't this tool routinely being used to solve management problems under PFMC jurisdiction?

WHAT IS THE STATUS OF CHINOOK GSI ON THE PACIFIC COAST?

We learn from Winans that the genetic baseline for chinook salmon has evolved in quantum leaps during the past 10 years and is now extensive for stocks originating from California through southern British Columbia. The application of GSI to most mixed-stock fisheries in this geographic range is not limited by the technique but in most cases by the managers' lag time in recognizing its valuable potential for management planning. Winans also notes a priority need for collecting additional chinook baseline data for B.C. and Alaska stocks north of Vancouver Island.

Baracco's discussion of GSI activities in California provides an example where managers have recognized the potential of this new tool and have met the challenge framed by Pattillo. In this case the question is the relative importance of the various northern California chinook stocks to the adjacent ocean fishery. Since spawning escapement levels cannot be adequately monitored for some areas, GSI became an obvious choice for answering this question and evaluating the optimal configuration of fisheries impacting stocks of concern.

Finally, Shaklee outlines the extensive, cooperative work required to ensure integrity and validity of GSI applications. The GSI process is very sophisticated from a fisheries science standpoint and requires deliberate and extensive coordination and quality control. Shaklee's important message is that we already have made great strides in this area and have developed a framework for continued, future success.

WHAT ARE THE FUTURE OPPORTUNTIES AND NEEDS?

A clear opportunity exists for fishery managers to challenge their perceptions about impacts of mixed-stock fisheries. As Pattillo notes, this need is especially acute where we have new or expanding fisheries or where little is known about historical fisheries. We have learned much in the past 10 years about the exploitation of certain stocks through coded-wire tagging programs. This information remains essential for planning regulatory options and monitoring trends in annual harvest rates of indicator stocks with respect to expected results from implemented regulations. But if we are to optimize mixed-stock fishery harvest and conservation/allocation goals coincidentally, we need accurate and precise "pictures" of what the fishery impacts are on all component stocks. We need this capability for both hatchery and wild stocks. We need direct measurements that can be derived from a random sample of all fish in the catch. And we need tools that don't rely on an unrealistic capability to envision what stocks or fisheries may have management problems in 3 to 5 years that should now be the subject of comprehensive tagging programs.

GSI is not a panacea but this exciting and powerful new tool has many potential applications which were clearly demonstrated in this seminar. Its use may require managers and scientists to shed perceptions of what electrophoresis "can do" that are based on an obsolete 1970's state-of-the-art. Healthy skeptisism and professional scrutiny should be a component of developing credibility. The challenge exists, however, to collect and use the best available data for assuring long-term health of the resource and fisheries it supports. This latter challenge is clearly responsive to the charge from fishery administrators to be creative and innovative in developing mixed-stock fishery management options. This policy mandate carries the responsibility to assure stable funding support for the tools necessary to implement regulatory refinements.

The largest perception that GSI has dispelled for me is a previous belief that there were no new approaches or technological developments available to improve management of mixed-stock fisheries. We can measurably improve our management results, both for chinook and other species. Current progress in developing coastwide GSI capabilities has been built upon the successes and failures experienced in the CWT program. The level of coordination and cooperation that has marked implementation of operational GSI programs is extremely impressive for a new technology. The methodical approaches used to frame and answer statistical and quality control questions are commendable and provide a foundation for further improvements. GSI provides hope for the future of fisheries management. This new technology will complement and enhance our current capabilities, just as, in the future, other new technologies will be developed and utilized to do the same.

For the near future a high priority exists to expand the existing chinook baseline into northern B.C. and southeast Alaska. This effort will require considerable cooperation and coordination of the involved agencies to satisfy the needs of a truly coastwide program. Priority fishery management applications need to be identified and evaluated in response to current issues of Pacific Salmon Commission, MFCMA and regional importance. This process already has begun in many new areas such as California, the Strait of Juan de Fuca and Georgia Strait. New efforts must be successfully conducted and further development and planning must be continued.

ACKNOWLEDGMENTS

Many thanks go to the Pacific Salmon Commission staff and to the co-chairs of the Joint Chinook Technical Team for supporting and helping schedule this seminar. The presentors applied significant preparation time and care in making the seminar a meaningful communication mechanism and audience participation was insightful and productive.

Critical fiscal support for the work presented herein has included recent years' appropriations for the Pacific Salmon Treaty Act (P.L. 99-5), the Anadromous Fish Conservation Act (P.L. 89-304), and NOAA/NMFS programmatic areas. The Bonneville Power Administration supported important development work on the chinook baseline, as well as initiation of pilot and demonstration programs in offshore fisheries.

The evolution of genetic stock identification to its current status as a practical salmon management tool has resulted from the persistent dedication of various researchers who have had the vision and expertise to develop this capability. The open cooperation and coordination of current activities amongst respective agencies also warrants recognition.

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October 24, 1986

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INTRODUCTION

Rich Lincoln
Washington Department of Fisheries

Much work has been done in the past 15 years to develop biochemical/genetic tools to discriminate salmon stocks. More recently fisheries biologists and geneticists have made a concerted effort to develop these techniques into operational harvest management tools. The intent of this seminar is to share some of these developments and identify specific needs and opportunities for using genetic stock identification (GSI) techniques to improve chinook salmon management.

Our message is not that GSI is a panacea to solve all harvest management problems and replace other stock identification techniques. The message is: GSI is a powerful and viable new tool that can greatly enhance coastwide chinook management.

Contemporary salmon management must meet many ongoing and new challenges to implement effective and comprehensive conservation and allocation programs. These new challenges require new management tools, especially in the stock identification area. A strong key indicator identification program using coded-wire tags (CWTs) has been implemented as a primary chinook management tool by the Pacific Salmon Commission. Despite this commitment the CWT program cannot provide all the scientific information being requested by the panels and commission for joint international management of chinook stocks. These information needs can be met by bolstering the indicator stock program with: (1) new techniques to mass-mark hatchery fish and (2) new techniques to measure fishery stock composition directly.

An adaptive program to collect international scientific data will require a full array of stock identification tools which are complimentary and can be tailored to address a broad spectrum of new management questions.

The focus of this seminar is chinook GSI, an integral component of this developing array of management tools. The central question this seminar will address is, "How can GSI enhance coastwide chinook management?"

Present international mixed-stock fishery management efforts for chinook are designed to: (1) determine and implement harvest rate reductions necessary to achieve certain rebuilding goals and (2) monitor harvest rates (and escapements) to assure that regulatory measures are having the intended effect. Coded-wire tagging programs are an extremely effective tool for developing computer models to simulate answers to these questions for certain "indicator" stocks. However, this tool cannot answer questions such as: (1) what are the fishery impacts on all component hatchery and wild stocks being harvested? (2) how does the total stock composition "picture" change over time and area in a fishery? and (3) how can mixed-stock harvest be maximized while simultaneously protecting important weak stock components? Coded-wire tagging all hatchery and wild stocks contributing to a fishery to answer such questions is not feasible from a logistic, cost and/or timeliness standpoint. In contrast GSI is ideally suited to answer such questions directly.

GSI also can enhance terminal fishery management by providing accurate and precise stock composition data. Such data permits refinement of management periods for individual run components and can provide more accurate estimation of spawning escapements - the fundamental monitoring element to gauge success of chinook rebuilding efforts. These terminal area management improvements also complement offshore management measures by providing data to ensure pass through provisions of the Pacific Salmon Treaty.

REVIEW OF GSI TECHNIQUE

James B. Shaklee
Washington Department of Fisheries

Genetic stock identification (GSI) methodology relies on the combined use of biochemical and genetic procedures to provide estimates of proportional stock contributions to mixed-stock fisheries. The underlying basis for using GSI techniques to address this problem is inherent in the concept of stocks as self-sustaining breeding units within a species. Given that stocks are genetic units, one of the most direct tests of stock structure is to examine their genetic characteristics. At present, the technique of choice for this purpose is starch gel electrophoresis.

Electrophoresis is a process whereby charged molecules (such as enzymes and other proteins) can be separated in an electric field. Using electrophoesis, it is possible to document the genetic characteristics of individuals (and populations) because of the relationship between the genetic code (DNA) and the biochemical phenotype as expressed, after electrophoresis and enzyme staining, in the form of banding patterns on gels. Each enzyme (protein) subunit is encoded by a specific segment of DNA -- a gene locus -- which specifies its structure.

There are many steps in the application of GSI to analyzing mixed-stock fisheries. The initial step requires establishment of suitable electrophoretic protocols for detecting and characterizing the genetic variation present in the species under study. The next step is to collect tissue samples from fish in all potentially contributing stocks. These samples are then subjected to electrophoretic analysis to generate a baseline data set. The baseline data consist of a set of allele frequencies (for all variable gene loci) characterizing each stock in the baseline. Once these preliminary steps have been accomplished, one must collect representative samples from the fishery to be analyzed. The tissue samples from the mixed-stock fishery must be analyzed in the laboratory using electrophoresis. The genetic data are then entered into a computer for analysis. The actual statistical procedures involve use of both the baseline and fishery data sets using maximum likelihood estimation procedures employing the EM algorithm. The final product consists of estimated percentage contributions of each stock to the fishery together with standard errors of these estimates.

Numerous salmonid mixed-stock fisheries have been analyzed using GSI techniques within the last five years. These fishery analyses have been accomplished in at least three different laboratories. Examples include:

CHINOOK
- Columbia River spring gillnet
- Columbia river fall gillnet
- Skagit River gillnet
- WA Indian treaty troll
- WA May troll
- WA July troll
- WA coastal sport
- west coast Vancouver Island troll

CHUM
- upper Johnstone Strait net
- northern Puget Sound net

PINK
- Thompson Sound test fishery

A more detailed description of the GSI technique is contained in:

Milner, G.B., D.J. Teel, F.M. Utter, and G.A. Winans. 1985. A genetic method of stock identification in mixed populations of Pacific salmon, *Oncorhynchus* spp. Mar. Fish. Rev. 47(1):1-8.

MAXIMUM LIKELIHOOD ESTIMATION OF MIXED STOCK FISHERY COMPOSITION[1]

Russell Millar
University of Washington, Department of Statistics

We estimate mixed stock fishery composition using the method of maximum likelihood. Assuming that the baseline data gives the true allelic frequencies, the maximum likelihood composition estimates are those that maximize the probability (likelihood) of observing the mixed fishery sample data. The maximum is over all possible compositions.

In "standard" applications of the maximum likelihood method the properties of the estimates are well known. For example, the estimates are approximately distributed according to the Normal distribution (bell shaped). An estimate of their variance can be calculated explicitly. They can be slightly biased but the bias disappears very quickly relative to the size of the variance.

The application of maximum likelihood to the stock composition estimation problem is not quite "standard" because we are estimating proportions and they must all be non-negative and sum to 1.0. These constraints prevent us from taking for granted the properties mentioned above, nonetheless the estimates obtained are valid and we have made considerable progress at assessing their behavior. Enough is already known about the method, both in theory and practice, to say that it is "guaranteed" to produce composition estimates. That is, for any practical analysis there will be no statistical problems concerning the existence and uniqueness of the estimates and it will always be possible to calculate them. The question of importance is how well they estimate the true composition.

<u>Other Features:</u>

The composition estimates cannot be calculated explicitly and are found using a maximizing algorithm. I have been using the EM (expectation maximization) algorithm. The amount of CPU time required by a typical analysis is in the order of seconds on the University of Washington's Cyber. The "bookkeeping" (input/output, setting up arrays, data checking, etc.) takes up considerable time. The program is written in Fortran 77 and is totally self-contained and portable.

When all stocks in the mixture contribute a reasonable amount then the constraints on the estimates do not matter and the estimates will behave according to the standard results. It is when small contributors and non-contributors are present that the estimates' behavior may depart from "standard" maximum likelihood properties.

An alternative explicit formula to calculate estimate variance has been established and is working extremely well. This formula works as well as the standard formula under all situations and is far superior to it when non-contributing stocks are included in the analysis.

The maximum likelihood method can use continuous data also. Often some kind of discriminant/classification type approach is used with continuous data. It can be shown that these approaches are also based on maximum likelihood, but in a way that will result in inferior estimates.

The mixed-stock fishery sample can have missing data, i.e. it may not have been possible to score some loci. This will not upset the maximum likelihood method.

The composition estimates can be biased. This is something that we need to find out more about. We known when bias is most likely to be a problem when similar stocks differ greatly in their contribution to the mixture, and so can take some preventative steps. The current approach is to eliminate the potential for bias by aggregating "similar" stocks.

Estimate reliability is dependent on the baseline data allele frequencies being close to the true frequencies. More needs to be known about how sensitive the estimates are to departures from this assumption.

1/ A presentation of:

Millar, R.B. 1987.
Maximum likelihood estimation of mixed stock fishery compostion. Can. J. Fish. Aquat. Sci. 44:583-590.

SIMULATION ANALYSIS TO EVALUATE THE MAXIMUM LIKELIHOOD MIXTURE MODEL FOR ESTIMATING STOCK COMPOSITION[1]

Chris Wood
Canada Department of Fisheries and Oceans

Simulations were performed to evaluate the bias and precision of stock composition estimates from the maximum-likelihood mixture model (e.g., Fournier et al. 1984) using hypothetical multi-locus characters. It is shown that the maximum-likelihood mixture model utilizes more information available from the mixture sample than the classification-with-correction approach (e.g., Pella and Robertson 1979). Bias and precision were examined in relation to the number of stocks being resolved, the number of loci available and the difference in allelic frequency among stocks at each locus, using Monte Carlo simulations with different levels of sampling error in the mixture and learning samples. Model performance improved with increasing stock separation and number of loci available. Bias was not affected by the number of stocks resolved in simulations where mixture contributions from individual stocks remained constant. Learning sample size had little effect on bias for realistic sample sizes (> 50). These results provide guidelines for reducing the complexity of genetic stock-identification problems by summing estimated mixing proportions for individual stocks within groupings based on stock similarity. The tradeoff between improved accuracy and level of grouping can be examined graphically to determine the most useful level of grouping for the problem at hand. We illustrate this procedure with a real example from mixed-stock fisheries on sockeye salmon (*Oncorhynchus nerka*) along the British Columbia-Alaska coast.

Literature Cited

Fournier, D.A., T.D. Beacham, B.E. Riddell, and C.A. Busack. 1984. Estimating stock composition in mixed-stock fisheries using morphometric, meristic and electrophoretic characertistics. Can. J. Fish. Aquat. Sci. 41: 400-408.

Pella, J.J. and T.L. Robertson. 1979. Assessment of composition of stock mixtures. Fish. Bull. 77: 387-398.

1/ A presentation of:

Wood, C.C., S. McKinnell, T.J. Mulligan, and D.A. Fournier. 1987. Stock identification with the maximum-likelihood mixture model: sensitivity analysis and application to complex problems. Can. J. Fish. Aquat. Sci. 44:866-881.

FISHERY SIMULATION: FRASER RIVER CHINOOK SAMPLE

David Teel
National Marine Fisheries Service

Computer simulations of potential GSI applications are useful for project planning. This process entails two steps. First, a large number of hypothetical stock mixtures with known compositions are created from baseline data. Second, maximum likelihood analysis is used to estimate the actual stock proportions in each hypothetical mixture. Variables which can be studied include relative proportion of stocks in the mixture, gene loci used in the analysis (reflecting tissue availability), and sample size. Simulations allow evaluation of expected accuracy and precision of composition estimates for a specific fishery. With this information fishery managers can determine the usefulness of a GSI application and plan appropriate experimental design for sampling the mixed-stock fishery.

We simulated a lower Fraser River CDFO test fishery to plan such a GSI application. Each year returning adult chinook are captured near Mission, B.C. from April through September. Stock contribution/timing data are needed for 3 groups -- Thompson, mid Fraser, and upper Fraser stocks. Frequencies for 14 gene loci (available in eye and muscle tissues) from 10 baseline stocks were used to create 100 hypothetical mixtures of 250, 500, and 750 fish each (i.e., 300 mixtures total). The stock proportions of the mixtures were established to reflect a composition likely to be encountered. Average estimates ($\pm$ 1 SD) for 10 individual stocks were computed and estimates for the 3 aggregate management groups were very good and, as expected, their precision increased with increased sample size (Figures 1 and 2). These results will be used to plan GSI field sampling of the test fishery by CDFO in 1987 (CDFO contact: Neil Schubert - see Attendee List).

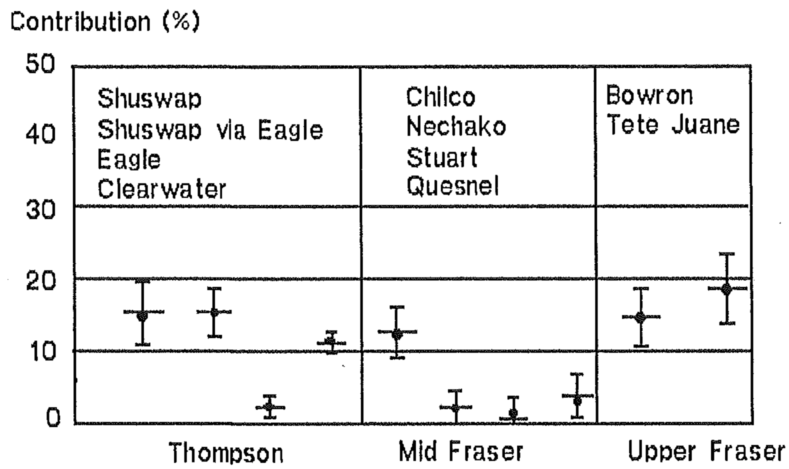


FIGURE 1. Maximum likelihood estimates and standard deviations (N=500) for the contribution of ten stocks of chinook salmon to a simulated Fraser River fishery. 1/

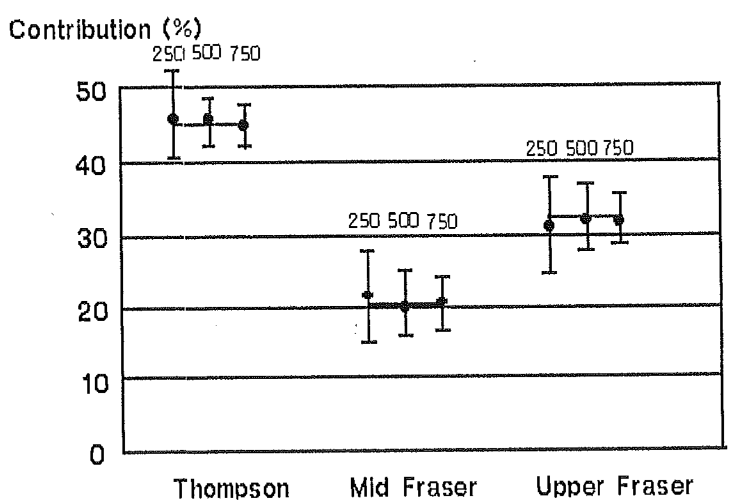


FIGURE 2. Effect of sample size on maximum likelihood estimates and standard deviations for the contribution of three chinook stock groups to a simulated Fraser River fishery. 1/

1/ Legend: Horizontal bars = actual percentages; circles = mean percentages from 100 iterations; "I bars" = ± 1 standard deviation

COLUMBIA RIVER COMMERCIAL SPRING CHINOOK FISHERY

Steve Phelps
Washington Department of Fisheries

The lower Columbia River commercial spring chinook fishery is a drift gillnet fishery targeted on lower Columbia River hatchery stocks. The fishery typically occurs at the end of February - beginning of March; prior to the entrance into the river of large numbers of the upriver component of spring chinook, a collection of stocks needing conservation protection. WDF estimated the stock composition of this fishery in 1986 using GSI because low numbers of coded-wire tag (CWT) returns were expected, especially from stocks spawning above Bonneville Dam.

Heart and liver tissue were excised from 924 spring chinook sampled in the 1986 commercial fishery from landings at Astoria, Oregon and at Chinook and Ilwaco, Washington on 24-26 February and on 3,4 March. Almost all of the samples were from the later time period. We used standard starch gel electrophoretic methods to assay 17 genetically variable loci which previously had been determined to be the most useful for differentiating Columbia River spring chinook stocks. The total mixed-stock fishery sample was analyzed for individual stock contributions using the maximum likelihood estimation procedures and EM algorithm of Milner et al. (1983) as refined and discussed by Millar in this seminar. The baseline data used in the analysis were a subset of 13 stocks of the July, 1986 baseline (provided by David Teel, NMFS Manchester Laboratory).

We estimated the following contribution (± 1 sd) of individual stocks to the fishery: Eagle Cr./McKenzie (57% ± 2), Rapid R./Red R. (11% ± 2), Cowlitz/Kalama (10% ± 2), Carson/Leavenworth (9% ± 2), Naches (Yakima) (4% ± 2). Estimated contributions for the remaining eight baseline stocks used in the analysis were all less than 3% each, and none were significantly different from zero (Table 1). The contributions of major stock groups were: Willamette (57% ± 2), the Cowlitz-Kalama-Lewis group (12% ± 3), and the above Bonneville Dam group (31% ± 3).

From this GSI analysis we concluded that the timing of the fishery was successful at targeting the catch on the harvestable surplus of lower river hatchery spring chinook and avoiding weaker upriver stocks. By using the 1986 run size estimates we calculated that only 2.6% of the spring chinook destined for above Bonneville Dam were harvested, while 9.5% of the Willamette and 8% of the Cowlitz-Kalama-Lewis spring chinook stock groups were caught (Figure 1).

A comparison of the 1986 stock composition estimates with CWT and GSI estimates from previous years indicates a larger component of above Bonneville Dam stocks in 1986 than in the past four years (Table 2). CWT estimates from 1982-1985 ranged from 10%-5% for above Bonneville Dam stocks and 69%-85% for Willamette spring chinook. GSI estimates from 1982 agreed closely with 1982 CWT estimates. The change in the 1986 fishery stock composition estimate may have been due to many factors, but the larger upriver run size and river conditions which resulted in most of the fish being caught the last few days of the fishery likely contributed to the increased percentage of upriver fish caught in the fishery.

GSI proved to be a powerful technique for determining stock composition in the lower Columbia River spring chinook gillnet fishery. This is a terminal fishery with a well-defined management goal: to maximize harvest of surplus lower river hatchery stocks while limiting the harvest of naturally spawning stocks above Bonneville Dam. Large genetic differences occur among the three major stock groups. Genetic variation within the above Bonneville Dam component is sufficient to obtain good estimates of individual wild and hatchery stocks from this area. The modest number of stocks potentially contributing to the fishery and a relatively high level of genetic differentiation among stocks produce stock contribution estimates with high precision.

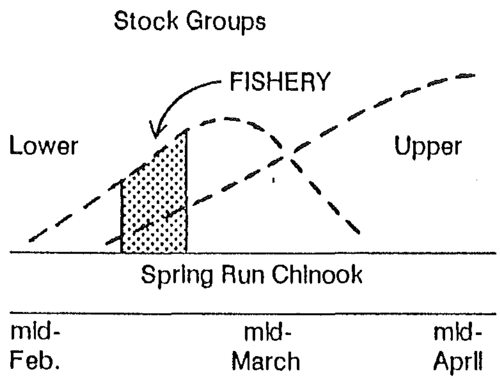
TABLE 1. GSI estimated contribution of stocks to the 1986 Columbia River commercial spring chinook gillnet fishery.

Baseline Stock	Major Mgt. Group *	Est. % Contribution (± 1sd)
Eagle Cr. NFH/McKenzie R. NFH (Oregon)	L	57 ±2
Rapid R., Idaho Hat./Red R., Idaho wild	S	11 ±2
Cowlitz Sal. Hat./Kalama Falls Sal. Hat., WDF	L	10 ±2
Carson NFH/Leavenworth NFH (Wash.)	U	9 ±2
Naches R., (Yakima, WA) wild	U	4 ±2
Winthrop NFH (1979 brood from Carson NFH)(Wash.)	U	3 ±3
Lewis R. Sal. Hat., WDF	L	3 ±2
Klickitat Sal. Hat., WDF	U	1 ±2
Valley Cr. (upper Salmon R., Idaho) wild	S	1 ±1
Warm Springs NFH/Round Butte Hat. ODWF	U	1 ±1
John Day R. (Oregon) wild	U	<1 ±<1
Sawtooth R. (progeny of wild broodstock collection reared at McCall Hat.) IDFG	S	<1 ±<1
Tucannon R., (progeny of wild broodstock collection reared at Lyons Ferry Sal. Hat.) WDF	S	<1 ±<1

Note: Estimated contribution of stocks below the dashed line are not significantly different than zero.

* L = Lower Columbia River, S = Snake River, U = Upper Columbia River (above Bonneville Dam).

FIGURE 1. 1986 Columbia River spring chinook salmon run size and stock composition estimates, and schematic of entry timing characteristics.



1986 Run Size

Willamette	-	60,000	(30%)
lower River	-	15,000	(8%)
upper River	-	120,000	(62%)

1986 Fishery Composition*

Willamette	-	5,700	(57%)
lower River	-	1,200	(12%)
upper River	-	3,100	(31%)

* estimated by GSI

TABLE 2. Estimated % stock composition of Columbia River spring chinook below Bonneville Dam 1982-1986 by GSI and CWT.

		Stock (Management Group)					
		Willamette		below Bonneville*		above Bonneville	
Year	Harvest	CWT	GSI	CWT	GSI	CWT	GSI
1982	5,100	70%	72 (±0.1)	20%	17 (±0.6)	10%	11 (±1.4)
1983	7,700	69%	--	23%	--	8%	--
1983**	279	15%	20 (±4.0)	64%	62 (±1.4)	20%	18 (±7.0)
1984	9,600	85%	--	10%	--	5%	--
1985	12,800	80%	--	11%	--	9%	--
1986	10,000	?	57 (±2.2)	?	12 (±2.6)	?	31 (±2.7)

* Cowlitz, Kalama, and Lewis (CWT includes Sandy)
** test fishery: Carrol's Channel at mouth of Cowlitz R.

Literature Cited

Milner, G.B., D.J. Teel, and F.M. Utter, 1983.
Genetic stock identification study. NOAA/NMFS, Northwest and Alaska Fish. Center, Seattle, WA 98112.

VANCOUVER ISLAND TROLL FISHERY PILOT

David Teel
National Marine Fisheries Service

CDFO, WDF, and NMFS collaborated on a pilot application of GSI to a chinook troll fishery conducted off southwest Vancouver Island in mid July of 1984 and again in mid July of 1985. Fish caught off southwest Vancouver Island were sampled at fish buyers at the nearby port of Ucleulet. Eye fluid was extracted from fish with a syringe and skeletal muscle was taken at the anterior end of the spine from a lobe which remains after the fish is dressed. Fish were dressed at sea precluding the sampling of any visceral tissues. Samples were put in test tubes and immediately placed on dry ice where they were held until transfer to a cryogenic freezer (-85°C). Sample sizes were 731 and 877 fish in 1984 and 1985 respectively. Electrophoresis was conducted for 19 gene loci. Maximum likelihood analysis was completed using a baseline data set consisting of 87 stocks ranging from the Sacramento River in California to the Skeena River in central British Columbia.

Study results for the two years successfully detected an observed change in stock composition between years and significant changes in contribution for two major regions -- Columbia River and Canadian (Figures 1-3). The estimated decrease in Columbia River contribution between 1984 and 1985 is coincident with the collapse in abundance of "Tule" stocks while the concomitant increase in Canadian contribution during the same years is reflected in the Fraser River components (Figures 3 and 4).

Specific stock composition data have not been directly available for this fishery prior to these analyses. The results mirror abundance changes of major stock components and demonstrate the potential for examining temporal changes in stock composition necessary to optimize harvest regimes.

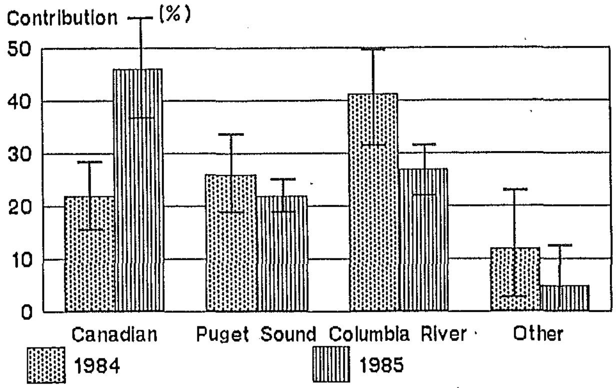


FIGURE 1. Estimated contribution of four major chinook stock groups to the 1984 and 1985 southwest Vancouver Island troll fishery.[1]

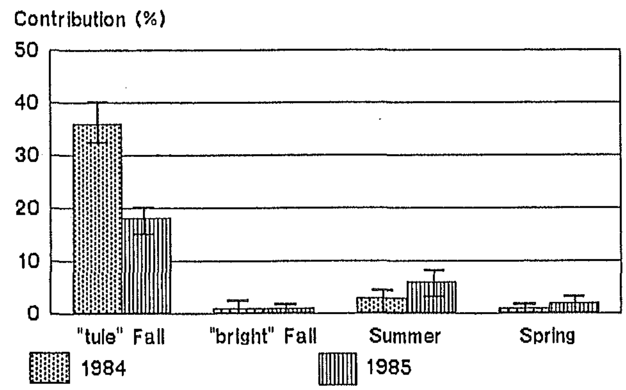


FIGURE 2. Estimated contribution of four Columbia River-origin stock groups to the 1984 and 1985 southwest Vancouver Island troll fishery.[1]

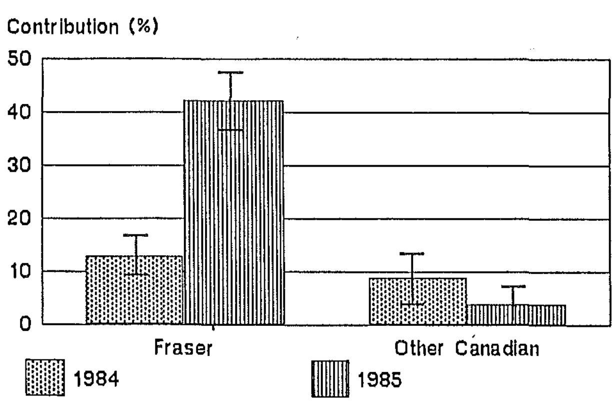


FIGURE 3. Estimated contribution of two Canadian-origin chinook stock groups to the 1984 and 1985 southwest Vancouver Island troll fishery.[1]

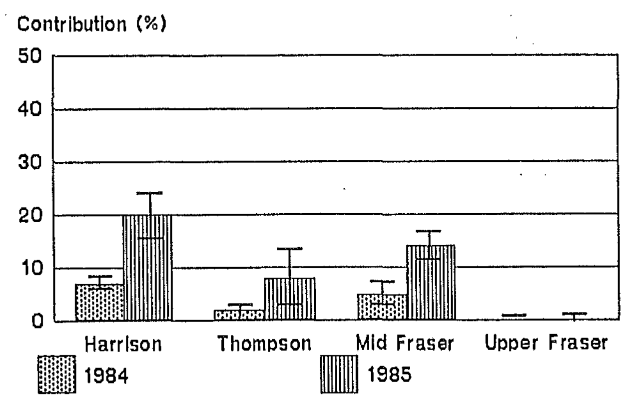


FIGURE 4. Estimated contribution of four Fraser River-origin chinook stock groups to the 1984 and 1985 southwest Vancouver Island troll fishery.[1]

[1] Vertical "I bars" indicate ± one standard deviation about the estimate

PACIFIC FISHERY MANAGEMENT COUNCIL (PFMC) CHINOOK MANAGEMENT

Pat Pattillo
Washington Department of Fisheries

Recreational and commercial salmon fisheries operating in ocean waters off the coasts of Washington, Oregon and California have been actively managed to control impacts on chinook salmon since the mid-1970's. Management has addressed chinook salmon concerns based on the status or needs of individual stocks. Generally, these stock concerns can be categorized into four major management units or areas defined by their relative abundance and migrational characteristics: (1) the Columbia River stock management area (from the mouth of the Columbia River north to the Canada-U.S. border); (2) the Oregon Coastal management area (south of the Columbia River to Cape Blanco, Oregon); (3) the Klamath/Rogue Rivers management area (southern Oregon and northern California), and; (4) the Sacramento River management area (south of approximately Fort Bragg, California).

Management goals for individual stocks within these four management areas have been pursued via three major active approaches - fishery restriction by time period, restriction by area, and restriction by direct harvest control, e.g., catch quotas. A given condition for successful, contemporary chinook management is a willingness to act in the face of information deficiencies. Management effectiveness, however, can be improved with the availability of a sound information base. Recognizing the stock orientation of management in the PFMC area, genetic stock identification techniques have been applied in several fishery circumstances, resulting in improved and useful chinook stock information.

In the Columbia River management area, GSI sampling of chinook catches in fisheries since 1982 has been used for post-season assessment of fishery stock impacts and identification of relative impact on critical stocks by time, area and gear type. The array of stock composition information has been combined with pre-season stock abundance estimates to develop an effective pre-season impact assessment and planning capability thereby improving annual determination of catch quotas.

Numerous needs and opportunties exist for new application of GSI techniques in the PFMC area. Some fishery management situations require expansion of existing information bases e.g. Klamath Rogue management area. In addition, several examples of newly developing or unplanned fisheries exist where little or no stock specific information is currently available, e.g., treaty Indian troll operating in Strait of Juan de Fuca.

The primary objective of harvest management should be to maximize harvest opportunities consistent with conservation of the salmon resource. Optimization of this responsibility demands relentless pursuit of the "best available" information. This is, in fact, a statutory requirement of the MFCMA. Aside from this requirement new, stock specific information sources, such as GSI, challenge managers and scientists to review existing perceptions about stock contribution and fishery impacts in the interest of improved and more effective salmon resource management. While GSI is being increasingly applied within PFMC's purview, we have yet to fully meet the management obligation of collecting and using the best available information to regulate offshore fisheries.

STATUS OF CHINOOK BASELINE DATA

Gary Winans
National Marine Fisheries Service

Electrophoretic data for chinook salmon have been collected for over two decades. Samples have been taken from California to central British Columbia. Sampling on a coast-wide basis continues as we expand the geographic extent of the database and attempt to understand some of the underlying genetics of the stocks, both within and between river systems.

Our first concerted effort to collect baseline data was in the Columbia River basin from 1976 to 1979. Over 40 spawning and/or rearing locations were sampled, including fall, spring, and summer run fish. With this Columbia River baseline, we completed a preliminary stock separation analysis of adult fall chinook passing Bonneville Dam in 1980. For the next several years we collected baseline data from river systems in California, Oregon, Washington, and British Columbia. As the database in the Columbia River basin expanded, we applied it to various in-river fisheries (e.g., "Columbia River Commercial Spring Chinook Fishery", described by Phelps in this seminar). As the coastwide database expanded, we applied the GSI technique to an increasing number of mixed-stock fisheries (e.g., "Vancouver Island Troll Fishery Pilot", Teel and "PFMC Chinook Management", Pattillo). In 1986, through cooperation with CDFO, we added 30 new stocks, primarily from the Fraser River and Vancouver Island streams, to the database, bringing the coastwide baseline to a total of 96 stocks (Figure 1). Fraser River data will be applied to studies of run timing in the lower Fraser (e.g., "Fishery Simulation: Fraser River Example", Teel). The expanding electrophoretic study of Canadian samples has involved three separate management agencies and this degree of cooperation is now typical for GSI studies. Importance of such cooperation between agencies is discussed in "Coordination, Standardization, Documentation, and Validation", Shaklee.

In summary, the GSI database for approximately 20 polymorphic loci has expanded from a start in the Columbia River to include over 160 sampling locales/stock units ranging from California to British Columbia. Baseline expansion has provided increased capability to analyze harvest impacts of a growing number of new mixed-stock fisheries. We currently can evaluate simple fisheries - e.g., in the Columbia River -- as well as complex ocean fisheries -- Washington troll fishery. In each, the reliability of the GSI estimates is dependent on the extent of the baseline data.

The greatest current deficiency in baseline coverage is for stocks originating north of Vancouver Island. There are important fisheries on chinook salmon north of Vancouver Island which are within the management purview of the Pacific Salmon Commission. To expand the application of the GSI technique to these northern fisheries, baseline data from stocks in British Columbia (primarily north of Vancouver Island) and Southeast Alaska are needed. This is now the highest priority for new data acquisition.

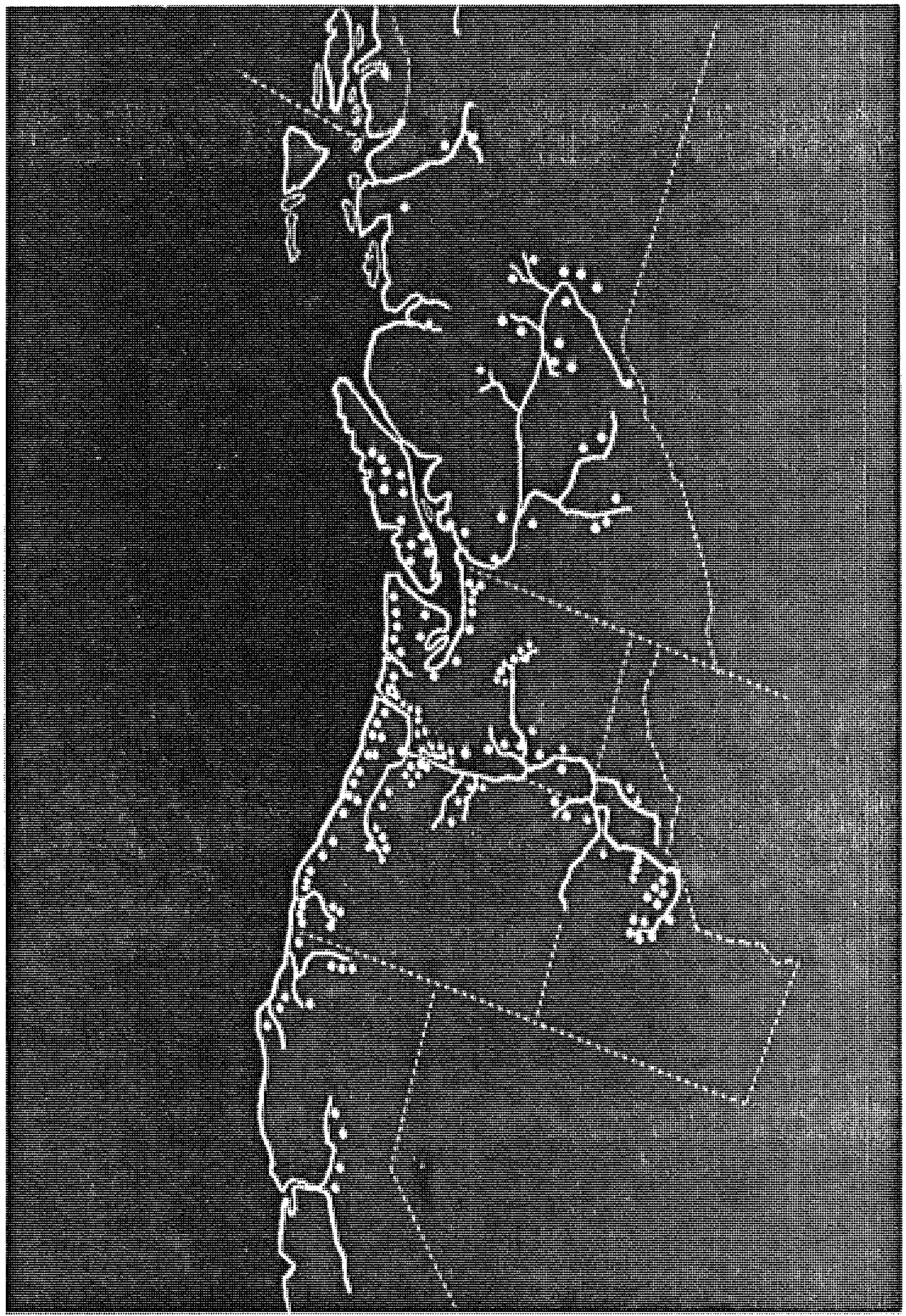


FIGURE 1. Geographic distribution of chinook GSI baseline collections, circa October 1986.

STATUS OF GSI ACTIVITIES IN CALIFORNIA

Alan Baracco
California Department of Fish and Game

California has been involved in GSI for several years. Department of Fish and Game (CDFG) personnel have cooperated in baseline sample collection and have offered advise to NMFS and U.C. Davis workers on evaluating stock origins and relationships. Both coho and chinook salmon baseline data have been collected, but in the past several years efforts have been concentrated on chinook. Some baseline data has been collected on virtually all California drainages that contain significant chinook populations. Additional sampling is needed both to screen the wider range of loci being analyzed today and to increase baseline sample size.

CDFG has participated in GSI activities involving standardization of laboratory techniques and nomenclature, financially assisting U.C. Davis' efforts to coordinate with NMFS' and the Washington Department of Fisheries' labs. We consider this effort essential if GSI is to fulfill our management needs in the future, and we will continue to insist that the efforts of all agencies be compatible.

The California legislature passed a bill in 1985 (A.B. 1727) requiring CDFG to make chinook spawning escapement estimates on the Smith, Klamath and Eel Rivers in northern California. In-river estimates were felt to be an inadequate way of accomplishing the intent of the legislation on the Eel River due to high flows during the chinook run. Therefore, efforts on this aspect of the law will center on a GSI analysis of the ocean mixed stock fishery. Dr. Graham Gall, U.C. Davis, has been named the principal investigator for this GSI analysis, which will be conducted over a three-year period (July 1986 through June 1989). Dr. Gall's effort will include:

1. Additional baseline sampling.
2. A GSI/CWT simulation.
3. Ocean mixed stock sampling and processing.
4. An analysis of mathematical procedures used for analyzing GSI data.

The first two tasks listed above will be completed by the summer of 1987, with ocean sampling scheduled for 1987 and 1988. An advisory committee, comprised of CDFG biologists, fishery interests (both sport and commercial) and legislative personnel, as well as U.C. Davis participants, has been formed to guide the project to a successful conclusion. We are looking forward to the results of the next three years in the hope that management of chinook fisheries can be enhanced through the application of GSI.

GSI COORDINATION, STANDARDIZATION, DOCUMENTATION, AND VALIDATION

James B. Shaklee
Washington Department of Fisheries

In the early 1970s only one laboratory (NMFS-Seattle) was actively involved in investigating the use of genetic stock identification (GSI) techniques to study the problem of mixed-stock fisheries analysis of Pacific salmonids. Since then, at least 13 laboratories world-wide have used this approach to study genetic aspects of stock structure in the five species of anadromous salmonids covered under the Pacific Salmon Treaty and in steelhead. At least eight different laboratories in North America have explored the use of GSI in studies of chinook salmon populations. Laboratories currently involved in GSI studies of chinook salmon include: NMFS (Seattle and Manchester laboratories), WDF, Univ. California at Davis, NMFS (Auk Bay), and the Univ. of Washington (Table 1).

The number and diversity of laboratories now involved in GSI studies, the complexity of the species and fisheries under investigation, and the increasing number of management applications of GSI data have necessitated major efforts regarding: 1) validation of the statistical procedures used in GSI analysis; 2) coordination of baseline and fishery sampling activities; 3) standardization of laboratory techniques, methodologies, and nomenclature and; 4) documentation and publication of results (including formats of shared databases). Each of the above major topics has been addressed to some degree over the past few years. In some cases this has involved individual effort on the part of a single researcher or agency while in other instances it has been the result of inter-agency meetings involving personnel from two to as many as six different agencies. Quarterly meetings involving personnel from the various GSI laboratories together with semi-annual, coast-wide coordination meetings involving both GSI staff and management biologists from numerous state and federal agencies are the primary vehicles for coordinating GSI research activities at present (Table 2).

Major accomplishments of these groups to date include:

1. Standardization of electrophoretic techniques among laboratories.

2. Establishment of a uniform system of nomenclature for: enzymes, loci, and alleles.

3. Documentation and exchange of recipes for electrophoresis buffers and enzyme staining.

4. Development of a scheme for exchanging electrophoretic mobility standards among laboratories.

5. Investigation of the genetic basis for electrophoretic variation in salmonids.

6. Development of procedures for field sampling, transport, and frozen storage of tissue samples.

7. Mathematical verification of the statistical procedures currently used in GSI analysis of mixed-stock fisheries.

8. Establishment of a coast-wide GSI database for chinook salmon stocks.

9. Distribution of minutes from the quarterly GSI meetings to other GSI laboratories in the U.S. and Canada.

10. Establishment of a dialogue between GSI personnel and management biologists regarding concerns, objectives, and long-term goals.

TABLE 1. Laboratory involvement in chinook salmon GSI in recent years.

1970	NMFS-Seattle							
1975	NMFS							
						(OSU Coop)		
1980	NMFS							
1983	NMFS							
1985	NMFS	WDF	UCD	UA-Juneau	(CDFO)	(OSU Coop)	(USF&WS)	
1986	NMFS	WDF	UCD	UA-Juneau		(OSU Coop)		(UW)
1987*	NMFS	WDF	UCD	NMFS-A.B.L.	CDFO		USF&WS	

TABLE 2. GSI coordination meetings convened in recent years.

Laboratories Only

Sept. 85	NMFS	CDFO		
Sept. 85	NMFS	OSU Coop		
Oct. 85	NMFS	WDF		
Feb. 86	NMFS	WDF		
April 86	NMFS	WDF		
Sept. 86	NMFS	WDF	UC Davis	UW

Laboratories + Managers

May 84	NMFS	WDF	ODFW	CDFG			
Sept. 84	NMFS	WDF	ODFW	CDFG	UC Davis		
June 85	NMFS	WDF	ODFW	CDFG	UC Davis	CDFO	
Sept. 85	NMFS	WDF				CDFO	Wishard Nooksack Tribe (chum)
May 86	NMFS	WDF	ODFW	CDFG	UC Davis		
June 86	NMFS	WDF				CDFO	
Sept. 86		WDF					Nooksack Tribe NWIFC (chum)

OPEN DISCUSSION

A very real need exists to review baseline data over time to insure representativeness and validate temporaral stability. This is a key component of the comprehensive quality control program for GSI.

A reasonable next step for chinook GSI would be to choose a specific management problem where the Pacific Salmon Treaty process could be enhanced and apply the technique. Georgia Strait hook and line fisheries were discussed as a reasonable, potential candidate.

APPENDIX 1 - PRESENTATION QUESTIONS AND ANSWERS
GSI SEMINAR

October 24, 1986
Vancouver, British Columbia

Review of GSI Techniques - James B. Shaklee

Question: Are there differences in baselines resulting from juvenile and adult collections from the same stocks?

Answer: Both juveniles and adults from selected stocks have been examined, and no consistent statistical differences in allele frequencies have been found between these two life history stages.

Question: Can old baselines be expanded with new baseline (contemporary) data to allow reanalysis of historical mixed-fishery data?

Answer: This is generally not possible because the analysis would be constrained by the number of loci originally examined from the mixed-stock fishery samples.

Question: How many of the presently known polymorphic loci have been cross-checked by laboratory experiments for inheritance?

Answer: Approximately one-half have been verified as exhibiting Mendelian inheritance.

[POSTSCRIPT: WDF will be conducting further inheritance studies during 1987 and 1988 for such verification.]

Question: Is baseline information collected by age class within a sample and has it been tested for stability?

Answer: Yes, it has been examined and is generally stable across ages. However, rigorous testing is often not possible given the small sample sizes which result from stratifying collections by age.

Question: Ultimately, how many stocks do you want in the baseline?

Answer: Enough to cover all stock components which significantly contribute to mixed-stock fisheries of concern.

Maximum Likelihood Estimation of Mixed Stock Fishery Composition - Russell Millar

Question: Is the problem of stock similarity one of allele similarities?

Answer: Yes.

Question: Can lack of independence of loci present a problem?

Answer: No problem exists if you can quantify dependence relationship. Present analyses are based upon presumed independence.

Question: Are there rules we can follow to avoid bias thereby enhancing application of the technique to harvest management?

Answer: You can look for stock similarities (i.e., using covariance results) and qualify results appropriately.

Question: How do you deal with catches that include contributions from stocks that are not in the baseline?

Answer: Since we know nothing about the characteristics of fish from "missing" stocks there is nothing we can do other than strive for comprehensive baseline so that the proportion of such fish will be insignificant.

Question: Explain further why the classification measure is inferior to maximum likelihood.

Answer: The classification measure fails to take advantage of all information available in allele frequencies and requires an intermediate step which is equivalent to maximum likelihood estimate.

Question: Is it possible to adjust for bias as in classification method?

Answer: Maximum likelihood tries to do it by using all available information.

Question: Have you compared the classification method to the E.M. algorithm; how do they compare?

Answer: We haven't compared them yet.

[POSTSCRIPT: A comparison between classification and maximum likelihood is currently underway using scale pattern data (Feb. 1987, Millar, UW)]

Simulation Analysis to Evaluate the Maximum Likelihood Model for Estimating Stock Composition - Chris Wood

Question: What is the effect of changing the learning ("baseline") sample size?

Answer: A bigger sample can improve estimate but its usually more efficient to increase sample size of mixed-fishery.

Question: Can our present knowledge be used to recommend optimum sampling schemes?

Answer: Yes, if you have some learning samples and can articulate desired levels of stock resolution and error, given available funding.

Question: When doing bootstrapping to analyze sample size, what sub-sample size did you choose?

Answer: We resampled with replacement to generate a new sample of the same size as the original.

Columbia River Commercial Spring Chinook Fishery - Steve Phelps

Question: How large was your sample size, and what did the analysis cost?

Answer: The sample size was approximately 1,000 fish, with 15 person-days of sampling plus 45 person-days of laboratory analysis.

Question: What Columbia River baseline was used for the analysis?

Answer: All baseline data were from 1981 or subsequent years' collections.

Vancouver Island Troll Fishery Pilot - David Teel

Question: Given current capabilities, can you electrophoretically separate tules into their management unit components above and below Bonneville Dam?

Answer: Not with any degree of reliability. The transfer of hatchery stocks from Bonneville Pool to many lower river hatchery facilities has resulted in a practical inability to distinguish them electrophoretically.

PFMC Chinook Management - Pat Pattillo

Question: What are relative merits of sampling landed catch vs. the population residing in the area where catches occur?

Answer: Trade-offs between cost and how information is applied have to be evaluated. Port sampling is cost-efficient and adequate for catch analysis when sampling and catch reporting accurately segregate catch area. On-board vessel sampling is expensive and presents potential experimental design problems (question of representativeness of sample in relation to fishery). Assuming that we are interested in measuring impacts of existing fisheries, sampling landed catch would seem preferable.

Question: What level of information is sufficient for making new management decisions?

Answer: There is no clear-cut answer to that question, but it is very important. We need to answer it on a case-by-case basis given the questions being asked and the level of stock-specific information otherwise available.

Status of Chinook Baseline Data - Gary Winans

Question: How many genetic comparisons of wild vs adjacent hatchery stocks can be made with existing database?

Answer: I don't know the number but there are quite a few in Oregon.

Question: How do straying rates affect baseline construction and maintenance?

Answer: In theory, perhaps significantly; in practice that's why it is important to periodically resample baseline stocks, to monitor whether any gene transfer is occurring.

Comment from audience: Babine sockeye now produced in a spawning channel are now GSI unique from adjacent wild stock even though both share common parentage.

Question: Would you recommend archiving mixed-stock samples for re-analysis with new baseline data?

Anwser: Archiving would be an ideal but practical storage constraints impose severe limitations on this capability.

Question: Can you give us a cost perspective?

Answer: A rough approximation for sockeye screening 5 loci, would be 2.5 people for 2 weeks to process and run samples from 800 fish. We could estimate cost for any particular application and experimental design.

Coordination, Standardization, Documentation, and Validation - James B. Shaklee

Question: Are questions regarding appropriate statistical methods resolved?

Answer: The U.S. and Canadian procedures yield similar results. Both approaches are valid.

[POSTSCRIPT: Millar (this seminar) demonstrated that current U.S. and Canadian approaches use the same likelihood function. The maximization procedures used (E.M. algorithm and nonlinear optimization algorithm respectively) have been tested on the same data sets with comparable results. Currently planned work between U.S. and Canadian scientists will document such comparisons including estimates of variance. Classification models are not routinely used for salmon GSI although comparisons of classification and maximum likelihood are planned in the near future.]

APPENDIX 2 - ATTENDEE LIST

CHINOOK GSI SEMINAR

October 24, 1986
Vancouver, B.C.

NAME	AGENCY	ADDRESS
Alan Baracco	California Department of Fish & Game	1701 Nimbus Road, Suite B Rancho Cordova, CA 95670
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