Review of Stock Identification Studies on the Yukon River

THE UNITED STATES/CANADA
YUKON RIVER JOINT TECHNICAL COMMITTEE

by the

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1. INTRODUCTION

Managing salmonid populations requires not only information on absolute or relative abundances, but also an understanding of the population structure as well as information on timing and migratory pathways. This second type of information, gathered from a variety of techniques, has been collectively termed stock identification, and data for stock identification of salmonid populations from the Yukon River has been gathered for over 30 years. Further, recent studies in the Pacific Northwest have heightened concerns about conserving diversity inherent within and among salmonid populations. It is now recognized that the long-term survival of salmonid populations depends on genetic diversity within and between local populations (NRC 1996), and that stock identification information is a critical first step in this process. For this paper, stock and population are used interchangeably and are defined as fish spawning in a particular river or lake (or portion of) at a particular season, which fish to a substantial degree do not interbreed with any group spawning in a different place, or in the same place at a different season (Ricker 1972).

Stock identification techniques fall into at least three categories: physical, environmental, and genetic. Each category has unique advantages and limitations as well as a unique set of accompanying assumptions (Table 1).

Physical tagging requires the direct manipulation of the individuals and includes visible tags, coded-wire tags, fin clips, and radio tags. These techniques provide a direct positive identification of the individual, and coded-wire tags have been particularly useful on the Yukon River with hatchery evaluation programs for chinook salmon. Physical tagging of adults, using both visible and radio tagging, has also been used extensively to assess migratory pathways and runtiming.

Environmental stock identification techniques rely on differing characteristics among populations as a result of varying environmental factors and are useful across many life history stages in wild populations. Techniques in this category include scale pattern analyses (SPA) and parasite infestation rates. Otolith marking, in which distinctive otolith bands are laid down as a result of fluctuating temperatures or other environments factors, can be considered both an environmental and physical tag as the mark can be induced in hatcheries by varying water temperatures. Of these techniques, SPA has been applied most intensively with an ongoing program for chinook salmon on the Yukon River.

In general, both physical and environmental stock identification requires continual tagging or updating of the baseline information. In contrast, genetic techniques rely on information coded in the DNA which is inherited across generations. This means that information gathered in one year can be directly applied to subsequent generations, and the genetic information can be assayed from any life history stage. Naturally occurring genetic differences have been used extensively among Pacific salmonids for stock identification. In addition, genetic information has been used extensively in the description and conservation of biological diversity.

No comprehensive review of stock identification programs on the Yukon River has been conducted in recent years. As a result, the Yukon River Joint Technical Committee (JTC) tasked the subcommittee on stock identification to undertake a comprehensive review (JTC 1996). The

objectives of this report include not only a review of pertinent stock identification research and programs, but also evaluation of the potential of each method and recommendations for future research.

2. SUMMARY AND RECOMMENDATIONS

- The analyses commonly referred to as scale pattern analysis (SPA) consist of 1) linear discriminant function (LDF) analysis of scale pattern data, 2) analysis of observed differences in age composition between escapements, and 3) analysis of geographic occurrence of catches.
- Contribution rates for major age classes of chinook salmon in the Yukon River District 1 and 2 catches have been estimated for each fishing period on a postseason basis using SPA. The estimates are reported by three general categories termed Lower (U.S.), Middle (U.S.), and Upper (Canada) Yukon. Average classification accuracies achieved have been normally between 65 and 80%. Major sources of variability are accounted for in the LDF analysis; however, smaller sources of variability associated with age composition and geographic segregation are not. Results indicate that SPA is not a very powerful tool, but it does differentiate between U.S. and Canadian chinook salmon stocks in a cost-effective manner. Finer-level differentiation will require alternative techniques such as genetic stock identification, particularly if inseason estimates are desired.
- SPA has been investigated as a stock identification tool for chum salmon in the 1970's and 1980's, but accuracies were unacceptably low. Those studies concluded that SPA does not provide a feasible method of estimating stock composition for Yukon River chum salmon. No further development of SPA for chum salmon is recommended.
- The use of genetic data (e.g. alleles at allozyme or nuclear (n)DNA loci or mitochondrial (mt)DNA haplotypes) as a stock identification tool has been investigated since 1984. Genetic data, particularly allozymes, can be obtained in a cost efficient manner from a larger number of individuals and can be applied on an in-season basis. A very comprehensive allozyme database exists for chum salmon on the Yukon River; a less comprehensive and older allozyme dataset exists for chinook salmon from the Yukon River. Results can be used for stock identification as well as documentation of genetic diversity and population structure.
- Results indicate that chum salmon can be reliably identified into the following groups using allozymes: 1) Lower Summer, 2) Middle Summer, 3) Fall Tanana, 4) Border (Chandalar/Sheenjek/Fishing Branch/Mainstem), 5) White, and 6) Teslin. Either in-season or post-season analyses could be applied immediately throughout the Yukon River drainage to address questions such as relative contribution to fisheries, relative abundance, and timing and migratory patterns. Finer differentiation is possible within regions or drainages. For example, allozyme data could potentially be used to differentiate among Tanana River stocks, particularly Toklat versus non-Toklat components.
- Results indicate that chinook salmon can be reliably identified using allozymes into the following groups: 1) Lower, 2) Lower Middle (Gisasa, SF Koyukuk, Henshaw/Jim), 3) Upper Middle (Chena and Salcha), and 4) Upper (Canadian). Finer discrimination is likely possible. However, the allozyme database has not been updated since 1992, as researchers decided to rely solely on SPA analyses for stock identification of chinook salmon. Further allozyme analyses on chinook salmon are recommended, and comprehensive stock identification analyses would be possible in the relatively near future.
- DNA methods (particularly nuclear markers such as microsatellites) will likely differentiate both chum and chinook salmon at a level equal to or greater than allozymes. Advantages

include non-lethal sampling, potential to sample from archived body parts such as scales, a nearly unlimited number of potential loci, and simplified sample collection without the need for cryopreservation. Analyses are more expensive than allozymes, but costs are declining with improved technology. In-season analyses are a possibility. Comprehensive baselines for both species, however, must be developed before large-scale stock identification programs could be implemented. DNA techniques could potentially provide additional discrimination among Middle Summer chum salmon, a group intermediate to upper and lower stock groupings.

- Coding wire tagging (CWT) can provide information on migration routes and timing, and survival and rates of contribution to fisheries through mark-recapture estimates. Advantages of CWT include: 1) sufficient resolution to identify small groups or even individuals; 2) ease of recognition of tagged fish through adipose fin clips; and 3) CWT does not require expensive technology. Disadvantages include: 1) CWT it is not a natural mark; 2) individual fish must be handled; and 3) marking sufficient wild fish can be difficult—most large scale programs involve hatchery fish.
- Groups of upper Yukon River chinook salmon have been tagged using CWT annually by CDFO since 1985. Approximately 80% of all tagged fish have been from the Whitehorse Rapids Fish Hatchery. Tags have been recovered from the Bering Sea Pollock "A" fishery, from commercial sampling in Districts 1, 2, and 4, from fishwheels upstream of the Canada/US border, and from fishers through reward programs. If sufficient numbers of individuals are released, CWT has the potential to provide an accurate estimate of the contribution of specific upper Yukon stocks to U.S. and Canadian fisheries.
- The only CWT project for chum salmon in the Yukon River was initiated in 1992 with the Toklat fall chum salmon, a Middle Yukon River stock. Analysis of adult returns is now underway. Objectives include evaluation of the hatchery program in the Toklat River and estimation of timing and contributions in proximal fisheries.
- For both chum and chinook salmon, it is recommended that standardized sampling procedures be established in as many fishery strata as possible in order to gain from current CWT release programs. Sampling rates for chinook salmon should be established with a view to using the data for stock identification of Upper Yukon stocks. It is also recommended that CWT sampling results be included in annual JTC reports.
- Radio telemetry studies have been used concurrent with mark-recapture programs to determine distribution, migratory patterns, and behavior and spawning locations of specific upper Yukon chinook and chum salmon stocks. Reporting units and power are limited by the number of tags applied/recovered that can be attributed to a specific stock. A Rampart fall chum salmon tagging project is currently in place, and has the potential for locating undocumented spawning populations and identifying stock-specific movement patterns such as timing through fisheries, holding patterns, and bank orientation.

3. SCALE PATTERN ANALYSIS

3.1 Chinook salmon

Schneiderhan (1997) provides a detailed history of SPA as applied to the stock identification of Yukon River salmon. The analytic methodology employed in the Yukon River chinook salmon SPA studies consists of linear discriminant function analysis (Seber 1984) of scale pattern data, analysis of observed differences in age composition between escapements, and analysis of geographic occurrence of catches.

Generally, escapement samples from Alaska and salmon tagging study samples from Canada have provided scales of known origin that are used to build a three-way run of origin classification model for Yukon River chinook salmon based on linear discriminant function analysis (LDF) of scale variables. Scales representing major age classes that are common to all stocks from sampled tributaries are selected for building run-of-origin models. Scales are obtained from Lower Yukon Run stocks, i.e. the Andreafsky and Anvik Rivers; the Middle Yukon Run stocks, i.e. Chena and Salcha Rivers; and the Upper Yukon Run stocks which are represented by samples collected from fish captured in test fish wheels operated by the Canada Department of Fisheries and Oceans (CDFO) at the White Rock and Sheep Rock sites about 10-20 km upstream from the U.S.-Canada border.

Only scales with one freshwater annulus (age 1.) are considered for inclusion in the scale pattern analysis. Salmon scales from the dominant age classes, normally ages 1.3 and 1.4, that are sampled from the District 1 and 2 (Figure 1b) commercial gillnet fishery are classified to run-of-origin using the discriminant functions.

Contribution rates for major age classes of fish in the District 1 and 2 catches are estimated for each fishing period. Results of SPA by fishing period are summed to estimate total contribution by run of origin for major age classes of chinook salmon to the District 1 and 2 commercial catches.

Age classes in the District 1 and 2 commercial catches which are not classified by SPA are apportioned to run of origin based on escapement age composition ratios. Escapement age composition data, either unweighted or weighted by acceptable escapement estimates, are used to compute ratios of proportional abundance for each run. In previous years the proportion of age-1.1, -0.3, -1.2 and -0.4 fish in escapement samples have tended to decrease as the distance upriver increased; therefore, proportions for the age class are divided by the proportion of age-1.3 fish, which analogously have displayed a similar tendency and are also from a recent brood year. Proportions of age-2.2, -2.3, -1.5, -2.4, -1.6, and -2.5 fish are similarly treated as analogs of age-1.4 fish because these ages have historically increased with distance upriver and are the oldest group of fish in the return. Age-0. fish are treated the same as age-1. fish from the same brood year.

Estimates of run composition from SPA and age composition ratio analysis are used to classify District 1 and 2 commercial catches by fishing period. Classifications of Districts 1 and 2 subsistence catches are based on estimates of run composition from SPA and age composition ratio analysis of catches taken in the first commercial period in each district. The proportions by age class and run obtained through analysis of total District 2 commercial and subsistence catches are then used to classify commercial and subsistence catches in Districts 3 and 4.

Subsistence harvests in the upper Koyukuk River in District 4 and commercial and subsistence harvests in District 5, District 6, and Yukon Territory are classified to run of origin based on geographic segregation of stocks. The entire District 5 harvest is assumed to be from the Upper Yukon Run. This assumption is known to be violated because a small but unknown

proportion of the District 5 subsistence harvest is normally taken on the south bank below the Tanana River confluence. Those fish are believed to be of Tanana River, i.e. District 6, origin; however, the relatively small numbers of fish in the harvest create only a slight bias. The bias introduced in that manner affects the results of this study by providing a small overestimate of the Upper Yukon Run and a corresponding underestimate of the Middle Yukon Run. Also, small numbers, i.e. typically 100 fish, of subsistence catches of salmon taken in the Chandalar River by residents of Venetie are clearly not of Canadian origin. Those fish are assigned to the Middle Yukon Run.

The entire District 6 harvest is considered to be from the Middle Yukon Run because neither Lower nor Upper Yukon Runs are considered to be present in the Tanana River. The Yukon Territory harvest is assigned to the upper run because neither lower nor middle runs are considered to be present in Yukon Territory.

Reference to the Yukon River chinook salmon stock identification analysis as SPA may be misleading. Although the analysis is based on stock composition estimates derived using SPA methodology as the first step, the entire analysis actually consists of three separate analytic procedures as described above: 1) scale pattern analysis of major age classes, 2) age composition ratio analysis, and 3) catch composition based on geographic segregation. Each succeeding step in the analysis amplifies and builds on the preceding step. Of the three components of the analysis, the major sources of variability are accounted for in the SPA analysis; however, smaller sources of variability associated with the age composition ratio and the geographic segregation analyses are not accounted for. This makes it difficult to compare the precision of the results of the analytic process with other more compact methods. Questions concerning precision may only be answered definitively by referring to the classification accuracy (Table 2) of SPA by itself.

SPA is only capable of defining the general stocks or runs that are termed Lower, Middle, and Upper Yukon. Classification accuracies achieved for models based on those regions of origin are normally between 65 and 80 percent. Conversely, misclassifications of stocks typically range between 20 and 35 percent overall; however, in a properly selected model, misclassifications are more or less balanced among the aggregate of the various misclassified categories and tend to cancel each other out.

SPA and the associated analyses classify all Yukon River catches to run of origin by age class. This enables reconstruction of the Upper Yukon Run which comprises all of the stocks of Canadian origin. The brood year table which results is potentially very useful in understanding production and harvest dynamics operating on Canadian chinook salmon.

Although SPA is not a very powerful tool, it does provide some very important information for Yukon River chinook salmon: it differentiates among three stock groupings or runs, and has the advantage of doing so with relative efficiency in terms of project resources.

3.2 Chum salmon

Alaska Department of Fish and Game (ADF&G) has investigated SPA as a possible method for obtaining estimates of Yukon River fall chum salmon stock contributions. Investigators observed low classification accuracies of pooled age models and large differences in scale feature measurements between age groups. Results from these studies lead to the conclusion that the utility of SPA could not be determined for Yukon River fall chum salmon unless: 1) more accurate methods of aging could be developed; and 2) scale sampling programs

are designed to meet SPA requirements for sample sizes and numbers of stocks sampled. For a complete review see Schneiderhan (1997).

4. GENETIC STOCK IDENTIFICATION

4.1 History of research

Genetic variants (e.g., alleles at allozyme or nuclear (n)DNA loci or mitochondrial (mt)DNA haplotypes) possess many attributes that make them invaluable for various applications in fisheries biology. They are directly heritable in a Mendelian fashion for nDNA or matrilineally transmitted from mother to offspring for mtDNA, and as such are not subject to environmentally-induced variation. Variants are expressed throughout the life cycle, and thus adults and juveniles are equally identifiable. The frequencies of genetic variants are generally fairly constant over time, which reduces the need to continually restandardize characterizations of individual stocks. Finally, genetic data can be obtained fairly easily from a large number of individuals at reasonable cost and effort.

Stocks can be characterized by allele or genotype frequencies, and a variety of statistical techniques have been derived to estimate the proportional contributions of stocks to mixed-stock fisheries. The homing of salmon to their natal streams produces a series of local reproductively isolated stocks. Over time, this reproductive isolation will lead to genetic differentiation. If the same allele occurs at different frequencies in different stocks, it is possible to estimate the proportion of individuals from each stock when they occur in a mixture.

The use of genetic data to delineate stocks and/or stock groupings, termed genetic stock identification (GSI), of chum and chinook salmon has been an ongoing area of research in the Yukon River since 1984. To date, genetic variation has been assayed primarily using protein electrophoresis. A pilot study using allozyme data to describe the population genetic structure of fall chum salmon was conducted by CDFO from 1984 to 1986 (Beacham et al. 1988). They used data from seven polymorphic loci and found that the Tanana drainage was genetically distinct from the Porcupine River and the Canadian portion of the Yukon River Drainage. Beacham et al. (1989) also examined genetic variability in chinook salmon and found substantial differences among stocks.

In 1987, ADF&G, the U.S. Fish and Wildlife Service (USFWS), and CDFO began a new GSI study for both chum and chinook salmon, expanding on the initial work of Beacham et al. (1988, 1989). The intent of this project was to extend sampling coverage and to increase the number of variable loci in the analysis. Genetic baselines for both species were presented, assessed for their ability to estimate stock of origin, and used to analyze actual mixture samples (Wilmot et al. 1992). Since 1992, no new data have been added to the chinook baseline because genetic stock composition estimates for chinook salmon were generally similar to estimates using SPA (Wilmot et al. 1992). However, since SPA is not a reliable stock discrimination technique for chum salmon, improvement of the genetic baseline for chum salmon has been ongoing.

4.2 Description of methods

Maximum likelihood (expectation maximization (EM) algorithm; Dempster et al. [1977]; Milner et al. [1981]; Pella and Milner [1987]; Smouse et al. [1990]) estimates the relative contribution for each of the potential contributing stocks by comparing the distribution of genotype frequencies of each stock with that of the mixture. In the case of bi-parentally inherited loci, genotypic distributions from the baseline populations are estimated from allele frequencies (or counts of alleles) under the assumption of random contributions of alleles, i.e. Hardy

Weinberg equilibrium, and loci, i.e., gametic phase equilibrium. The EM approach finds the stock composition of a mixture for which the observed genotypic frequencies would be most probable. The EM algorithm is constrained in the sense that it produces a sequence of positive estimates of the baseline contributions to the mixture, summing to one, such that the likelihood function during the search of the likelihood surface is non-decreasing (Dempster et al. 1977). Iteratively reweighted least squares analysis (IRLS, Pella [1986]; Pella and Milner [1987]; Xu et al. [1994]) minimizes the sum of squared distances between observed and expected genotypic frequencies for both the baseline stocks and mixed harvest. Other statistical analyses such as the use of gametic disequilibrium (Waples and Smouse 1990) have also been used to detect mixtures of different contributing stocks.

Both EM and IRLS approaches assume: 1) that all stocks contributing to the mixture are represented in the baseline (but see approach described by Smouse et al. [1990] whereby incomplete baseline data may be used); 2) characters are independent; 3) each of the baseline stocks is in Hardy-Weinberg equilibrium (or in the case of mtDNA, a type of analysis for continuous or meristic data can be used [Fournier et al. 1984]); 4) variation in the characters among stocks is larger than the variation among individuals within a stock; 5) sample sizes are large enough to represent the baseline stocks and the mixture so that sampling error about the estimates of stock allele (and genotypic) frequencies are minimal; and 6) the frequencies of the characteristics are constant over time such that baselines need not be collected from each spawning cycle (unlike SPA which requires annual sampling).

Factors affecting the accuracy and precision of stock allocations to mixed-stock fisheries are discussed in Pella and Milner (1987). In brief, accuracy depends on the number of contributing stocks, the degree of genetic differentiation among stocks, and whether all stocks are included in the baseline. Estimates of precision are dependent on the actual composition of the mixture, the precision and reliability of estimates of genotypic composition of the baseline and the mixture. Bias will be largest when stocks that are genetically similar differ in abundance. For example, if a stock that makes a contribution of near zero to a mixed-stock fishery is genetically similar to a stock with a major contribution, then the stock contributing zero will, on average be overestimated at the expense of the major contributor being underestimated. The performance of the analyses for fall chum on the Yukon River may be affected similarly due to the similarity of border stocks from the U. S. and Canada.

4.3 Allozymes

4.3.1 Chinook salmon

We performed a series of analyses to assess the performance of the allozyme baseline for chinook salmon in the Yukon River for stock identification including mixed-stock fishery applications. Our objective was to identify the finest level of stock grouping required to achieve acceptable accuracy and precision.

The loci used for these analyses were reported by Wilmot et al. (1992) and included *sAAT-3*, ADA-1*, ALAT*, PEPA*, GPIB-1*, IDDH-1*, MEP-2*, MPI*, sSOD-1*, TPI-4*, sAAT-4*, sMDHB-1,2*, TPI-2*, sAH*, LDHB-2*, MEP-1*, PGM-1*, mSOD*, PEPB*, sIDHP-1**, and *sIDHP-2**. *MEP-2** was treated as a nonMendelian-segregating character, and *sMDHB-1,2** was treated as an isolocus.

We used the stocks reported by Wilmot et al. (1992) for these analyses. Their baseline comprised 31 collections that were pooled by geographic proximity and year to form 16 stocks, eight of Alaskan origin and eight of Canadian origin (Table 3; Figure 1a).

Initially, we evaluated the ability of the GSI model to identify the individual stocks. We used the computer program SIMSQURT (M. Masuda, NMFS, Auke Bay Lab., Juneau, personal communication) to perform 100% simulations with each of the 16 stocks. All 16 stocks were included in the baseline for all of the simulations. For each 100% simulation, an artificial stock mixture was created that represented a 100% contribution of an individual stock. Stock contributions were then estimated for each of the stock mixtures. The results showed the degree of misallocation from the 100% stock to other stocks in the baseline. A stock with a unique genetic profile would be readily detectable with an allocation of nearly 100%. A stock that was genetically similar to other stocks in the baseline would receive an allocation of much less than 100% due to misallocation to those similar stocks. The resulting patterns of allocation and misallocation determined how the individual stocks were pooled to form stock groups.

We then performed additional simulations to assess and describe the performance of the stock groups. Sequential simulations were performed for each stock group with group contributions ranging from 0% to 100% at intervals of 20%. The Relative Root Mean Squared Error (RRMSE) was the summary statistic used to assess baseline performance and was calculated for each of the 100% estimates of the stock groups. Performance was compared to the level where the RRMSE = 0.2 [see Section 8.1].

Of the U.S. origin stocks, all of the individual stock estimates from the 100% simulations were less than 90% (Table 4; Figure 2). This was due to misallocations among genetically similar stocks. Misallocations occurred primarily within two stock groups: the Andreafsky, Anvik, Nulato, and Gisasa stocks; and the SF Koyukuk, Henshaw/Jim, Chena, and Salcha stocks. Negligible misallocation occurred between those two groups.

Both Andreafsky and Anvik were misallocated to Nulato at 11% and 15% respectively. Nulato misallocated to Andreafsky and Anvik at 13% to 12%. Up to 7% of Anvik was misallocated to Gisasa in the Lower Middle reach. Gisasa misallocated 6% to Andreafsky and 2% each to Anvik and Nulato.

The SF Koyukuk and Henshaw/Jim stocks misallocated to each other and to the Chena and Salcha stocks. The Chena and Salcha stocks misallocated primarily to each other, with negligible misallocation to the SF Koyukuk and Henshaw/Jim stocks.

Among the Canadian origin stocks, individual stock estimates were greater than 90% for each of the N. Klondike, McQuesten, Pelly, Takhini, and Nisutlin stocks. Misallocations occurred primarily among the Tatchun, Little Salmon, and Big Salmon stocks. Misallocations between U.S. origin and Canadian origin stocks were negligible. Of the U.S. origin stocks, only two had acceptable RRMSEs and of the Canadian origin stocks, only two had unacceptable RRMSEs (Table 5).

A second set of simulations were performed on enlarged stock groupings (Table 5). The 100% simulations for each of the stock groups resulted in estimates equal to or greater than 90% (Figure 3) and RRMSEs that were less than 0.2 (Table 5). The U.S. origin stocks clustered into two stock groups, Lower and Middle, whose contributions were estimated at about 96% each. A third U.S. origin stock group, the Upper Middle, was a subgroup of the Middle stock group and was estimated at 97%. Of the Canadian origin stocks, five separate stocks returned estimates greater than 90%. The Canadian origin group comprising Tatchun, Little Salmon, and Big

Salmon returned an estimate of 90%. The grouping of those three stocks accounted for most of the misallocations associated with those stocks (Table 5), considerably improving the pooled estimate over the individual estimates. The addition of Nisutlin improved that group's estimate to 94%.

Accuracy graphs show the baseline performance for incremental proportions based on the stock groups in Table 5 (Figure 4). All estimates were within 10% of the true value and standard deviations were less that 10%, with most estimates being within a few percentage points of the true proportion (Figure 4). Assessment of RRMSEs showed acceptable performance for all groupings (Table 5).

Tests using reduced baselines where downstream stocks were dropped out of the baseline to represent a mid-river sample showed a negligible change in performance over the full baseline. The exception was when we split a stock group, e.g., dropping Andreafsky, Anvik, and Nulato but leaving Gisasa representing a sample above the Nulato River and below the Koyukuk River. We found that the stock groups in a reduced baseline retained their performance properties observed in the full baseline.

Population substructuring of Yukon River chinook salmon generally reflects a subpopulation model nested within an isolation by distance model where stocks that are near each other are more genetically similar than they are with distant stocks. The stock groupings in Table 5 reflect the presence of genetic boundaries in the system that is currently detectable with a reasonable degree of confidence.

Positive identification of each individual stock would provide managers with the best tool for meeting harvest and conservation goals. The results of this baseline assessment suggest that individual stock identification may be achievable for some stocks. Other stocks had to be pooled to counter the misallocations that arose from genetic similarities among those stocks. The strategic pooling of those stocks on a limited geographic scale resulted in improved accuracy and precision of the estimates. The level of baseline performance that was achieved in these tests should permit managers to assess patterns of harvest and run composition, run timing, and bank orientation for specific stocks or small stock groups.

The stock groups in Table 5 should provide useful resolution for harvest allocation assessment and for evaluating patterns of stock composition, run timing, and bank orientation of returning adults. The level of accuracy and precision of estimates based on the stock groupings in Table 3 would be relatively stable throughout the drainage. Abundance estimates coupled with stock composition estimates could be used to assess stock strength. There may also be opportunities to use the baseline in early life history studies to assess stock interactions in rearing areas.

Genetic monitoring of stocks or stock groups over time could possibly be used to detect genetic changes associated with reduced population size, hatchery supplementation, or introgression of genomes of cultured salmon in the future. The baseline could also be useful in developing rehabilitation or restoration strategies.

4.3.2 Chum salmon

Over the last decade, baseline genetic data for chum salmon in the Yukon River have been collected for 79 collections and standardized for 20 polymorphic loci. Over 8,000 individuals have been analyzed. Crane et al. (in prep.) assembled these data into a genetic

baseline of 23 pooled stock groupings for mixture analyses using the general guidelines of Shaklee and Phelps (1990) and White (1996). Genetic analysis of the chum salmon baseline suggested eight reporting groups that could potentially be identified in mixtures: 1) Lower Summer (Andreafsky, Chulinak, Anvik, Rodo, Kaltag, Nulato, Lower Koyukuk-early, and Melozitna); 2) Middle Summer (Upper Koyukuk-late, South Fork Koyukuk-early, Tozitna, Chena and Salcha); 3) Toklat River; 4) Upper Fall Tanana (Delta, Bluff Cabin, Tanana Mainstem); 5) Chandalar/Sheenjek ; 6)Fishing Branch/Canadian Mainstem (Fishing Branch, Pelly, Big, Tatchun, and Minto); 7)White River (Kluane and Donjek); and 8)Teslin River.

These reporting groups were evaluated using 100% simulations (Crane et al. in prep.). In each simulation, the mixture was composed 100% from a single reporting group. Therefore, the mean estimate for 100 simulations should equal 100% for the reporting group under study; in addition, it can easily be seen where misallocation occurs. We considered a reporting group to be identifiable when the mean estimate was ≥ 90%.

Lower Summer, Upper Fall Tanana, White River, and Teslin River had mean estimates greater than 90% (Table 6). Middle Summer and Toklat River had correct allocations of 85% and 88%, respectively (Table 6). Chandalar/Sheenjek had a correct mean allocation of 81% and Fishing Branch/Mainstem had a correct allocation of 83%; the majority of the misallocation occurred between these two reporting groups. We enlarged Toklat and Upper Fall Tanana into a Fall Tanana reporting group and Chandalar/Sheenjek and Fishing Branch/Canadian Mainstem into a Border reporting group. The enlarged reporting regions of Fall Tanana and Border had correct allocations exceeding 90%.

A second simulation study was performed on five realistic stock mixtures (Table 7) to assess the power of the genetic model. Individual population estimates for the mixtures were summed into three hierarchical levels. The first level presents estimates for all eight reporting groups, the second into six reporting groups (Lower Summer, Middle Summer, Fall Tanana, Border, White, and Teslin), and the third into summer and fall reporting groups. Two measures were used to evaluate model performance: coefficient of variation (CV) and RRMSE. A reporting group estimate with a CV of less than 50% can be shown to have contributed to the mixture using a 95% confidence interval (Marlowe and Busack 1995) and may be a useful measure when managers are interested in the presence or absence of a stock, for instance, when monitoring run-timing of summer and fall stocks. A RRMSE of 0.10 or 0.20 is desired for estimates of stocks that compose 20% or more of the mixture when relative abundance is being determined (see Section 8.1).

In general, if a reporting group contributed greater than 10% to the mixture, the CV was less than 50% (Table 7). Not surprisingly, expanding the reporting regions resulted in smaller CVs. Using the RRMSE criterion, the eight reporting groups will need to be condensed. Chandalar/Sheenjek and Fishing Branch/Mainstem will need to be combined into the single Border reporting group; when separated, even if these individual groups composed greater than 20% of the mixture, the RRMSE exceeded 0.20 (Mixture 2, 3, 4, and 5; Table 8). Similarly, the Toklat River and Upper Tanana Fall will need to be combined for drainage-wide studies (Mixture 4, 5; Table 7); further simulation studies will need to be done to determine if these two stocks can adequately be separated when only these two groups are expected to contribute to the mixture for Tanana River studies. The Middle Summer reporting group composed 34% of (Mixture 3); the RRMSE for this estimate was 0.34, indicating this reporting group should be enlarged as well. However, because this group has an intermediate relationship with both the

Lower Summer and fall reporting groups (Crane et al. in prep), it may be wise to leave it as its own reporting group until further baseline populations are obtained or additional genetic marks are examined.

4.3.3 Status of coastwide baselines

An international effort has been conducted to develop comprehensive databases of gene frequencies for chinook salmon and chum salmon inhabiting the North Pacific Ocean since the mid-1980's. Cooperative databases for both species have been created and are shared by Pacific Rim researchers for use in the analysis of complex fisheries. To date, the baseline for chinook salmon is composed of 196 populations ranging from the Sacramento River in California to the Stikine River in Alaska and British Columbia. The database is managed by Northwest Fisheries Science Center, National Marine Fisheries Service (NMFS), Seattle. Data were collected by NMFS, Washington Department of Fish and Wildlife (WDFW), and University of California, Davis; a large portion of the data can be found in Utter et al. (1989); Bartley et al. (1992); and Waples et al. (1993). This baseline has been used extensively to estimate the stock contribution to Columbia River, coastal Washington, and Strait of Juan de Fuca fisheries of six major groupings: 1) California-Oregon; 2) Columbia River; 3) Washington Coast; 4) Puget Sound; 5) British Columbia: Fraser River; and 6) British Columbia: non-Fraser River (e.g. Marshall et al. 1991; Miller et al. 1993). During 1997, it is anticipated researchers from ADF&G, USFWS, and NMFS-Auke Bay Laboratory will be contributing data for the Alaska portion of the range of chinook salmon.

The database for chum salmon is more comprehensive and has been used in high-seas fishery analyses. It includes allozyme data from over 250 collections ranging throughout the North Pacific Rim. Original data can be found in Kondzela et al. (1994); Phelps et al. (1994); Wilmot et al. (1994); Winans et al. (1994); Seeb and Crane, submitted; the database is currently managed by ADF&G.

This database has been used to identify the stock of origin of chum salmon caught in the South Unimak Island fishery during June 1993 and June 1994 (Seeb and Crane, submitted). The baseline and eight additional Asian populations were used to identify stock of origin of chum salmon caught in Bering Sea trawl fisheries (Wilmot et al. 1995, 1996). Stock estimates for all three studies were given for eight reporting regions: 1)Japan; 2)Russia; 3)Northwest Alaska Summer; 4)Fall Yukon; 5)Alaska Peninsula/Kodiak; 6)Southeast Alaska (including Prince William Sound); 7)British Columbia; and 8) Washington.

4.4 DNA analysis

Increasing attention is being focused on the applications of molecular genetic markers for use in applied fisheries management. Interest has been stimulated in part by the proliferation and increased accessibility of molecular technologies to fisheries biologists. While various molecular genetic markers (see Park and Moran [1994] for a review of available techniques and research applications) have been employed in a number of studies for both chinook (e.g., mtDNA--Cronin et al. [1993]; Adams et al. [1994]; minisatellites--Beacham et al. [1996]; microsatellites--Banks et al. [1996]; introns and exons of coding genes-- Park et al. [1995]) and chum (e.g., mtDNA--Cronin et al. [1993]; Park et al. [1993]; minisatellites--Beacham [1996]) salmon in several

locations in the United States and Canada, few molecular data exist for chinook or chum salmon from the Yukon River drainage.

The following sections describe the molecular genetics studies which have been undertaken on the Yukon River for chum and chinook salmon. Sampling locations are defined. The extent of inter-population variation is described for each of the various genetic markers employed, and where appropriate, a review of the merits and current capabilities of these markers to GSI is discussed. Issues related to statistical power, i.e. accuracy and precision, are also presented.

4.4.1 Chinook salmon

Molecular genetic data for Yukon River chinook salmon are limited to three studies, each relatively small in scale. Estimates of the degree of population differentiation in allele frequency are provided in two of the three studies (Beacham et al. 1996; Scribner et al. 1996). Results of the third study which was recently initiated by the ADF&G Fisheries Genetics Laboratory have not been published (see Crane et al. 1996 for description of the scope of the project).

Scribner et al. (1996) surveyed three populations of chinook salmon from the upper Yukon River drainage in the Yukon Territory (Klondike River, McQuesten River, and Stony Creek of the Takhini River). Sixteen microsatellite loci were assayed for 89 individuals. Twelve of 16 loci were polymorphic and seven loci exhibited significant differences in allele frequency among populations. While no attempt was made to perform mixed-stock assessments for these populations, the magnitude of allele frequency variation at this spatial scale was comparable to, or exceeded that described for protein allozymes (Wilmot et al. 1992), suggesting that microsatellite loci would be able to discriminate the contributions of these stocks to mixed-stock fisheries with considerable accuracy and precision.

Beacham et al. (1996) used three minisatellite loci to document the extent of genetic differentiation among 28 chinook stocks from British Columbia and three stocks from the Yukon Territory. These authors estimated stock composition of simulated mixed-stock fisheries, using specific drainage groups from British Columbia. Stocks from the Yukon River drainage included the Teslin River, Whitehorse hatchery, and Yukon River mainstem. Data consisted of allele frequencies at one locus, and for two additional probes, counts of the number of bands in each of several fragment size categories were used. Analyses suggest that the stocks from the Yukon drainage differed in minisatellite allele and band frequencies, though explicit statistical tests were not conducted for these populations alone.

Crane et al. (1996) conducted an extensive allozyme analysis of 51 samples from 39 populations of chinook salmon from spawning grounds throughout Alaska and the Yukon Territory. Appended to the Crane et al. (1996) report, the authors outline aspects of ongoing microsatellite analyses of many of the same populations including Stony Creek from the Yukon drainage. Data have not been compiled.

4.4.2 Chum salmon

Three studies have utilized molecular genetic markers to examine chum salmon spatial population structuring in the Yukon River Drainage. Two studies (Taylor et al. [1994] and Beacham [1996]) used several Yukon drainage stocks to address the extent of population

structuring within and among regions from across the Pacific Rim. Scribner et al. (submitted) focused analyses solely on stocks of fall chum salmon within the Yukon River drainage.

Scribner et al. (submitted) obtained samples from eight spawning aggregations of fall chum salmon from the Yukon River drainage in the United States and Canada. Stocks used in the analyses included Delta from the Tanana River, Chandalar River, Sheenjek River and Fishing Branch from the Porcupine River, Big Creek, Minto, and Tatchum from the Yukon River mainstem in the Yukon Territory, and the Kluane River. Individuals were assayed for seven loci from two classes of genetic markers: mtDNA and nuclear DNA. Analyses were conducted to compare the marker classes in terms of the relative accuracy and precision of stock allocations to simulated mixed-stock fisheries and to examine different analytical strategies related to the use of escapement data and assignment of reporting groups.

Significant differences in nuclear and mitochondrial allele frequencies were observed among populations. Significant allelic heterogeneity was observed when populations were grouped into five drainages (Tanana, Chandalar, Porcupine, Yukon mainstem, Kluane), though little evidence for differentiation among populations within a drainage was found. Stocks from the U.S.-Canada border region (Chandalar, Sheenjek, Fishing Branch, and Canadian Mainstem) were not clearly distinguishable based on multilocus allele frequencies. Estimates of the extent of population differentiation and partitioning of variance within and among populations, i.e. F-statistics, were highly concordant between marker classes. Simulations of mixed-stock fisheries composed of varying contributions of U.S. and Canadian stocks revealed a consistent bias for over-allocation of Canadian stocks when expected Canadian contributions varied from 0-40% (Tables 8 and 9 for nDNA and mtDNA, respectively), due primarily to misallocations of border stocks. Estimates of accuracy and precision from the simulations suggest that desired statistical standards may be achieved for all possible stock mixtures except 100% U.S. and 0% U.S. contributions. Estimates of the relative contribution of U.S. stocks to the fall run are approximately 60% (Wilmot et al. 1992). Results were entirely consistent regardless of the assumptions used to establish specific stock contributions to U.S. and Canadian reporting groups in the simulated mixture analysis, i.e., when stocks were assumed to contribute equally or when stocks were weighted in proportion to escapement estimates.

Taylor et al. (1994) surveyed 42 stocks of chum salmon from across the Pacific Rim, including populations from Japan, Russia, the Yukon River, SE Alaska, and British Columbia. Stocks from the Yukon River included Andreafsky (summer), and four fall stocks (Kluane River, Tatchun Creek, Sheenjek River, and Fishing Branch of the Porcupine River). Each population was surveyed using one minisatellite probe (*Ssa1*) which hybridizes to two presumed linked loci. Variation was quantified for each population based on the counts of DNA fragments of various sizes across 31 size bins. The authors use neural networks and discriminant function analysis to assess the utility of this minisatellite probe in simulated mixed-stock analyses.

Taylor et al. (1994) found that populations could be broadly separated into three major geographic regions (Japan, Russia and the Yukon River, and SE Alaska and British Columbia). Neural networks and discriminant function analysis could allocate individual fish to Northern Pacific (Japan, Russia, Yukon) and southern (SE Alaska and British Columbia) with a high degree of precision. High levels of precision were documented for simulations using Japan vs Russia and the Yukon River as reporting groups. The precision of simulations using Russia and the Yukon River as reporting groups was much lower. No comparisons among Yukon River stocks were reported.

Beacham (1996) surveyed 42 stocks of chum salmon from across the Pacific Rim including Japan, Russia, the Yukon River, SE Alaska and British Columbia. Stocks were the same as described in Taylor et al. (1994), including one summer stock, Andreafsky River, and four fall stocks, Kluane River, Tatchun Creek, Sheenjek River, and Fishing Branch, from the Yukon drainage. Three minisatellite probes were used for the analysis including two probes which each resolved a single locus (*pSsa-A33* and *pSsa-34*) and the multi-locus probe *Ssa-1* used by Taylor et al. (1994). Significant differences in allele frequency were found among stocks from broadly separated geographic regions, and among stocks within each major region. Several analyses focused on samples from the Yukon drainage. Beacham found that the single summer population (Andreafsky) was more genetically similar to Russian stocks than to Yukon River fall stocks.

Simulations were conducted to examine the accuracy and precision of estimated stock contributions to mixed fisheries. Simulations were also preformed to examine the feasibility of assigning individuals to their proper stocks. Simulations of Yukon River chum salmon mixtures suggested that all five stocks were distinct from each other and that accurate and precise estimates of stock composition may be possible based on minisatellite DNA variation. Further, results indicate that the U.S. border stock Sheenjek was distinguishable from Canadian stocks. Results of simulations allocating individual fish to a specific stock indicated that 75% of the samples from the Yukon Drainage were correctly assigned to that region. However, accuracy for assignment of individual stocks was considerably lower (range 10.7 to 39.5% for the five Yukon River stocks).

5. CODED-WIRE TAGGING

5.1 History of research

The application of marks to salmonids has been used for many years to evaluate various aspects of salmon life histories and fisheries. Marking can provide information on migration routes and timing, survival, and rates of contribution to fisheries. External fin clip marking experiments have been used in hatchery evaluation programs as early as the 1960's. Although fin clips are still in limited use (particularly with pink and chum salmon), the small number of unique combinations possible forced researchers to develop a new marking technique.

The coded-wire tag (CWT) was introduced in 1971 as a method for marking large numbers of juvenile salmonids. A CWT is a segment of a spool of stainless steel wire etched with a binary code. The standard length of a CWT is 1.1mm; tags double or half of this length are also used. CWTs are applied by insertion into the nose cartilage of anaesthetized fish. Tag retention is checked over a period of time which could vary from 24 hours to a year (Kuhn et al 1988).

Coastwide usage of the CWT quickly followed its introduction and led to the establishment of ocean sampling and recovery programs by several agencies. A Regional Mark committee was formed and a Regional Mark Processing Centre established for coastwide CWT release and recovery data and the associated catch and sample data. CDFO maintains an equivalent database on the Pacific Biological Station's Vax computer.

The explosive growth seen in the use of the CWT made it imperative that a single fin mark be reserved as the external flag for CWT marked salmonids. The policy of removing the adipose fin as the external mark to indicate the fish had received a CWT was agreed to coastwide in the early 1970's for chinook salmon. The coastwide restriction was later expanded to include chum, sockeye, steelhead and pink salmon, with some exceptions made for the use of multiple fin clips. Steelhead salmon were later exempted from the restriction so that the adipose fin clip could be used to indicate hatchery fish for selective fisheries. This latter usage did not pose a problem for agencies with ocean recovery programs since there was no coastwide sampling program for chum salmon.

The CWT program has continued to expand steadily over the past two decades. Currently there are over 55 federal, provincial, state, tribal and private entities now releasing tagged salmonids for research and assessment. An estimated 47 million salmon are now tagged annually. Chinook salmon are tagged the most frequently at an annual rate of approximately 32 million juveniles (Johnson 1995).

Recovery of CWTs is possible wherever the tag group is fished, as well as at escapement enumeration or enhancement facilities and on spawning grounds. Examination of a fixed portion of a harvest and escapement by designated personnel is the predominant method of "sampling" for CWTs. Alternately, rewards are sometimes offered to fishers for returning tags. The method used is determined, in part, by the type of information sought. However, it should be noted that solicitation of CWTs from fishers has the potential to improve recovery rates, but it can seriously reduce the potential for acquistion of contribution rate data.

5.2 Description of method

A CWT program involves three distinct processes: releasing, sampling, and recovering tagged fish. Information resulting from these three processes are stored separately in relational databases including the CDFO Mark-Recapture Program (MRP) database. The release process involves marking and releasing the fish; the sampling process consists of sampling of harvests either by examining a portion of the catch, or solicitation from fishers; and the recovery involves the retrieval of the actual tagged fish (for size, sex etc) and the associated CWT (which is subsequently decoded).

Although there are many different types of CWT studies, they can be divided into three major categories. These are experimental studies, hatchery stock assessment studies, and stock contribution studies (Johnson 1990). The stock contribution study is the most relevant to stock identification studies. It involves estimation of the number of fish of the marked stock caught in a given fishery stratum. In order to do this, the sampling process must include information of the number of fish examined for missing fins.

Some assumptions must be made in CWT studies. For example, it must be assumed that the tagged fish are representative of the group from which they were drawn, i.e. the marking has no effect on migration patterns (for example, straying), catchability, or survival.

In order to measure, with some degree of confidence, the contribution rate to a fishery of a group of fish which has been tagged, a sufficient number of marks must be applied and a sufficient sample be examined for marks. The level of precision and the confidence that can be placed in the data are both directly affected by this. Relaxing the standards from the 95% CI and 10% error rate typically used for research dramatically reduces the number that has to be marked or sampled. Increasing the marking rate will reduce the number of fish which have to be sampled. Coastwide sampling standards have been established by the regional mark committee. These are: 20% for harvests, 30-100% for hatchery escapements. These sampling rates are often adjusted to suit the goals of specific studies.

The advantages of the coded-wire tag as a stock assessment tool are as follows. It can have sufficient resolution to identify small groups of fish or even an individual fish (providing sequential tags are used). The adipose fin clip is easily recognizable as an external mark. Unlike GSI, SPA or age composition analysis, identification is postive. Coded-wire tag recovery or reading does not require sophisticated or expensive technology.

Disadvantages include the fact that the CWT is not a natural mark. It requires that individual fish be handled. For this reason, marking sufficient wild fish to provide meaningful results can be difficult (consequently most large scale marking programs involve hatchery fish). In order to recover tags, sacrificial sampling is required - however, this is not a problem in determination of contribution rates to fisheries.

5.3 Chinook salmon

To date, chinook salmon stocks from the Lower or Middle Yukon River drainage have not been coded-wire tagged except for four years in the 1980's when chinook salmon juveniles were tagged at Clear Hatchery. However, groups of upper Yukon River chinook salmon have been tagged annually in the Yukon Territory since 1985 (principally by CDFO). Approximately

80% of all tagged fish were hatched and incubated at the WRFH. This facility was constructed in 1984 concurrent with the construction of a fourth turbine at the Whitehorse, Yukon Territory hydroelectric dam. The WRFH was constructed in order to offset the impact of the hydropower generating on juvenile chinook salmon migrating downstream from the upper lakes area of the Yukon River in Canada. Over the 1985 to 1996 period the hatchery has released a total of more than three million chinook salmon fry. Of these, 1.8 million have been marked with CWTs. Marked release groups have, on average, numbered 150,000 fry and have comprised from 34% to 100% of the hatchery release annually. The tags are applied to young of the year (also known as age "sub 1" or "0 check") fry in late May or early June, after a period of rearing subsequent to ponding, i.e. transfer from egg incubation trays to rearing troughs, in February. The majority of the fry have subsequently been released into the Yukon River upstream of the hydroelectric facility. However, each year from 1989 to 1994, approximately 50,000 marked fry were released immediately downstream of the hydroelectric dam, in the fishway constructed to allow adult passage past the dam. This was done with the objective of gaining information on the effect of the dam by comparing return rates of "above dam" releases to "below dam" releases.

In addition to the WRFH, small scale incubation systems at three different locations in the upper Yukon River drainage have produced fry. Two of the three incubation systems were established in 1989; the other one was established in 1991. The first release of chinook salmon fry marked with CWTs from these incubation boxes occurred in 1991. Over the period 1991 to 1996, approximately 490,000 fry were released from all three incubation systems combined. Of these, 445,000 fry were marked with CWTs. Annually, marked release groups have, on average, numbered 78,000 fry and have comprised from 80% to 100% of the releases. As with the WRFH, releases have involved young of the year fry. Low water temperatures have prevented rearing of some fry to a size suitable for full tags; consequently, half tags have been used frequently.

At the time of writing, only four upper Yukon chinook salmon tag recoveries have been reported from offshore fisheries. Three recoveries were in the Pollock "A" fishery in the Bering Sea; one in 1992 and two in 1994. The fourth fish was caught in the "A" fishery in the Gulf of Alaska in 1995.

Commercial sampling in Districts 1, 2 and 4 (Figure 1b) has included a CWT component. In District 1, the number of fish examined for CWTs has averaged approximately 3,200 annually over the period 1992-1994. The number of tags recovered in each of these years has averaged 10. Based on this data, CWT fish comprised from 0.08% to 0.4% of the sample for these years.

Two fishwheels located just upstream of the Canada/US border used to live capture chinook and chum salmon for a mark/recapture program also act as a test fishery to some degree. Numbers of marked fish captured in the fishwheels have been recorded since 1994. CWTs are not recovered in this location, i.e. fish are not sacrificed. Hence, only the "mark rate" is determined (determination of "mark composition" is not possible without retrieving CWTs). Of the fishwheel catch, marked fish have comprised 1.2% in 1994 (N=1290), 1.3% in 1995 (N=2216) and 0.6% in 1996 (N=1749).

In 1994 and 1995, CWTs were solicited from fishers (primarily commercial) by offering a reward of $10 for each recovery. This was done in an attempt to maximize the recoveries of tags in the absence of a directed sampling program. Without information on the exact number of fish examined for CWTs, determination of contribution rates, i.e. mark rate, of the Whitehorse hatchery and incubation boxes to the fisheries was not possible. The focus was on determination

of mark composition. The number of CWTs recovered in 1994 from the commercial fishery was 20 (0.2% of the commercial chinook harvest of 12,028); no CWTs were recovered from the domestic, Aboriginal and sport fisheries combined. In 1995, commercial fishers supplied 57 heads that contained CWTs (0.5% of the commercial chinook harvest of 11,146). In addition, a sampler examined 2,100 commercially harvested chinook for missing adipose fins prior to removal of tagged fish by fishers; 0.75% of these fish were marked. However, it is not known what proportion of these marked fish contained CWTs. These marked fish were not distinguished from heads voluntarily submitted by fishers and are included in the above total of 57.

In 1996, the reward system was not used. Determination of mark rate, as well as mark composition, was an objective. Fishers were asked to ignore adipose-clips. Instead, a fixed number of chinook salmon were examined for CWTs by a designated sampler. The designated sampler was a fisherman contracted to provide matched age, length and sex and CWT samples from the harvest in the vicinity of the confluence of the Fortymile River with the Yukon River, where a significant proportion of the total commercial harvest is taken. Out of a sample of 1600 chinook, six (0.4%) marked fish were recovered. CWT processing has not yet been completed.

Sampling for mark rate in escapement has been conducted at the Whitehorse Rapids Fishway since the hatchery program commenced. However, apart from some broodstock sampling, sampling for mark composition did not begin at the fishway until 1995. The sampling involved the sacrifice of a number of marked fish which ascended the fishway. Due to sensitivities associated with the sacrifice of chinook salmon at a tourist facility, sampling rates to date have been low. In 1995, 53 (7%) of the 757 marked fish were removed for CWT samples. Survival to escapement of the age-5 component of the cohort spawned in 1990 averaged 0.4% (range 0.1 to 0.6%) for the different release groups. In 1996, 48 (11%) of the 423 marked fish were removed for CWT analysis. Processing of 1996 data is incomplete at time of writing.

Coded-wire tagging has the potential to provide very discrete reporting units - resolution is possible not only to the level of a specific group but also, if sequential tags are used, to the level of the individual. Provided sufficient marked fry are released and the level of sampling is sufficient, coded-wire tagging has the potential to provide an accurate estimate of the contribution of a specific upper Yukon stock to U.S. and Canadian fisheries. Contribution rate information specific to this stock could be used to estimate the contribution rate of the Upper Yukon stock aggregate.

The marking rate of upper Yukon River juvenile chinook salmon at the Whitehorse Rapids Fish Hatchery more than doubled in 1996. All 325,000 chinook salmon fry released into the Yukon River system were marked. Arrangements have been made to tag 310,000 fry scheduled for release in June 1997. It is possible, for the near future at least, that all fry released from the hatchery into the Yukon River will be marked. It is also possible that the current instream incubation box program will be expanded, resulting in the release of more CWT chinook salmon fry.

5.4 Fall chum salmon

In contrast to the chinook salmon situation, the only coded-wire tagging conducted for chum salmon in the Yukon River drainage has been in Alaska. At the time of writing, no upper Yukon River chum salmon have received CWTs. In Alaska, coded-wire tagging has involved only the Toklat fall chum salmon, a Middle Yukon River drainage stock. Spawning escapements to the Toklat River were not meeting the escapement goal in years prior to 1991, despite

conservative fishery management actions. As a result of growing public interest in investigating restoration options for the stock, an artificial incubation and coded-wire tagging feasibility study involving Clear Hatchery was initiated in 1992. In 1993, all 92,000 Toklat fry on hand at the hatchery were coded-wire tagged and released back into the Toklat River. In 1994, out of 195,000 fry released into the Toklat River, 163,000 were tagged. In 1995, all 324,000 Toklat River hatchery fry were tagged (JTC November 1995). A total of 186,000 tagged fry were released in 1996 for the fourth and final outplant of the feasibility study.

In 1996, a four component recovery program was initiated for tagged Toklat fall chum salmon. The first component was to evaluate the proportion of the Toklat fall chum return consisting of hatchery reared fish. Components two and three were to evaluate the contribution to, and timing of, Toklat fall chum salmon in the proximal fisheries. The fourth component was to evaluate the homing to the release sites in the Toklat River springs spawning ground area (JTC October 1996).

Reporting units and power are the same as those of chinook salmon. The Toklat coded-wire tag project has now entered the tag recovery phase. Other stocks have not been selected for large scale coded-wire projects.

6. MARK-RECAPTURE AND RADIO TELEMETRY STUDIES

6.1 History of research

The mark-recapture method was first applied to fish populations more than a century ago. To date, it has probably been the most popular method used to estimate abundance of small freshwater fish populations. In western Canada and Alaska, numerous tagging studies have been conducted successfully on salmon returns in large rivers.

Radio telemetry has been used since the 1960's to study a variety of free-ranging animals including fish. Until recently, most telemetry studies have been limited to small numbers of individuals (usually less than 40) and to small study areas. However, technical advances have increased the scope of the tool and increasingly telemetry is being used to obtain quantitative information on large aggregates of fish including Pacific salmon (Eiler 1995).

On the Yukon River, mark-recapture studies have been conducted to estimate the abundance of chinook and fall chum salmon in the Canadian section of the Yukon River since 1982 (excluding 1984). Chena and Salcha River chinook salmon stocks have also been the focus of intermittent mark-recapture studies. A mark-recapture feasibility study for fall chum is currently underway on the Tanana River and a fall chum tagging program was initiated in 1996 on the Yukon River mainstem near the village of Ramparts, Alaska.

Radio telemetry studies involving chinook and fall chum salmon were conducted in the Canadian section of the mainstem Yukon River in 1982 and 1983 (Milligan et al. 1985; Milligan et al. 1986), concurrent with the mark-recapture program. The purpose of the studies was to determine the distribution, migratory patterns, behavior and spawning locations of specific upper Yukon chinook and chum salmon stocks. The Ramparts fall chum mark-recapture project also incorporates a radio telemetry component. In 1996, 50 chum salmon were radio tagged to determine tagging response and general movement patterns. Radio telemetry studies were also conducted for fall chum salmon in the upper Tanana River in 1989 (Barton 1992), and in the Toklat River in 1997. A large scale project involving the deployment of up to 1000 radio tags in the Rampart area is currently in the planning stage.

6.2 Description of method

Riverine mark-recapture studies provide estimates of abundance upstream of marking sites. The existence of different studies throughout the drainage basin provides an opportunity for comparisons of abundance of specific stocks or stock groupings. Information on migration rates, bank orientation and timing can also be obtained where fish are recovered at weirs or in fisheries.

Radio telemetry has been an effective technique for studying fish in large river systems where access and visibility are limited. It can provide detailed information on distribution, movement patterns, timing, and location of spawning areas. Radio telemetry can facilitate collection of genetic baseline data.

Combined mark-recapture and telemetry studies would provide information beyond that which could be obtained if each method was used independently. In this case, most of the fish would be marked with inexpensive external markers such as spaghetti tags, while a lesser number would receive radio transmitters. This integrated approach would make it possible to

apportion the run to identified spawning areas, thereby estimating total and stratified stock-specific abundance.

Mark-recapture techniques for estimating the abundance of fish populations are established tools of fishery management and are routinely used with acceptable accuracy and precision. Fish are captured, marked, and released. In studies involving returning adult salmon, fish are subsequently captured further upriver in fisheries, at weirs and during spawning ground surveys, and the proportions of marked and unmarked fish are used to estimate abundance. A successful mark-recapture study must include two interrelated components: 1) sampling, both the tagging and subsequent recovery, must meet certain statistical assumptions as closely as possible, and 2) the statistical methods used for data analysis must be consistent with the sampling design.

Several factors related to sampling in a mark-recapture study are essential. Adequate numbers of fish must be captured and tagged proportionately throughout the run and subsequently recaptured. Capture and tagging methods must not alter the behavior or physical abilities of the fish. Tagged fish must be marked in a way that is clearly visible and recognizable if recovered. Insufficient numbers of fish tagged, disproportional mortality between marked and unmarked fish, physical loss of tags, dysfunctional behavior of tagged fish, and other factors can introduce unacceptable bias. The significance of these factors is difficult to evaluate, but can sometimes be measured in properly designed studies.

The statistical method used to estimate abundance from mark-recapture information depends on the sampling method, and the assumed behavioral and movement characteristics of the fish. Numerous mark-recapture models exist for a variety of populations and sampling designs, however, their application to salmon returns in large rivers requires special considerations. Simple methods such as the Chapman estimator are often used in these situations, with results which are assumed acceptable for management purposes. However, assumptions used in traditional models may be violated when used for riverine applications. More advanced and perhaps more appropriate estimation techniques are currently appearing in the scientific literature, although many of these newly developed approaches are fairly specialized and can be somewhat limited in their application. As with any statistical procedure, one must use the best available technique with a full realization of its flaws and design studies to evaluate the assumptions or be willing to accept the uncertainty of the technique and not attempt the procedure (JTC 1996).

Radio telemetry has direct application to stock identification in large river systems where access and visibility are limited. Distributional information combined with stratified abundance estimates can provide information on stock composition. Genetic samples taken at the time of tagging from radio-tagged fish tracked to their spawning areas would also provide genetic baseline data and verification of the stock identification results. Spawning ground surveys for radio-tagged fish can also facilitate expanded baseline sampling for GSI.

In order to obtain stock-specific information from spaghetti tagging there must be recovery of tagged fish in areas proximal to respective spawning areas. This is expensive if a terminal fishery or escapement sampling program does not exist, particularly if the area is remote. Radio telemetry requires only tracking, not recovery, of tags to areas proximal to spawning grounds. This is generally more successful and less expensive in remote drainages than actual ground surveys for tag recovery. If stock-specific abundance estimates or expanded GSI sampling are required, then ground surveys are essential.

Tag recovery from within a fishery will not generally provide information for stock-specific identification unless the fishery is situated in a location such that there is no ambiguity as to which stock the harvest targets (as would be the case in a terminal fishery). However, information on stock aggregates would be available from fisheries that target more than one stock. Reporting units and power are limited by the number of tags applied/recovered that can be attributed to a specific stock.

The Rampart fall chum salmon tagging project, currently in progress, has the potential for locating undocumented spawning populations. Updating of existing GSI and SPA baselines could be facilitated. New baselines could be established as spawning populations are identified. Stock-specific movement patterns such as timing of fisheries migration rates, holding patterns and bank orientation could be identified. Information obtained from the Ramparts fall chum tagging project could provide a framework for directing smaller sub-basin or tributary-specific studies which would be less expensive and could provide more detailed stock-specific information. The infrastructure established for the Ramparts project could be used for studies directed on chinook salmon upstream of the Tanana River.

7. DATABASE COMPARISONS

7.1 GSI and SPA estimates of the run composition of Yukon River chinook salmon harvests

The ADF&G annually conducts a stock identification study of chinook salmon harvested in Yukon River fisheries using SPA. Scale samples are taken from harvests, as well as various representative escapements. The region of origin of abundant age classes, termed major age classes, is estimated using linear discminant function (LDF) analysis (Seber 1984) of scale measurement data. The region of origin of less abundant age classes, termed minor age classes, is estimated from information obtained during the LDF analysis, as well as differences in the age composition observed in the escapement scale samples (e.g., Schneiderhan 1997). Three aggregate chinook salmon runs have been identified based on broad geographic location (e.g., Schneiderhan 1996; Section 2.1, this document). The Lower Run is composed of chinook spawning in tributary streams in Alaska that drain the Andreafsky Hills and Kaltag Mountains, the Middle Run is composed of chinook spawning in the upper Koyukuk River and Tanana River drainages, and the Upper Run is composed of chinook spawning in Canada.

From 1987-1991 the USFWS conducted a GSI study in District 1 (Figure 1b) of the Yukon River using allozyme data. The results of that study are summarized in Spearman and Wilmot (1995). Spearman and Wilmot (1995) present a table of annual estimates of the run composition of District 1 harvests based upon both GSI and SPA. The estimates are fairly similar. Based on that similarity, the JTC decided to focus additional efforts to refine the GSI technique within the Yukon River on chum salmon, for which other stock identification tools are unavailable.

The Spearman and Wilmot (1995) comparison of the annual GSI and SPA estimates of run composition is informative, but can be further refined. In some cases, not all harvests were sampled, or samples from different fisheries or fishing periods were pooled differently in the analyses. In addition, a comparison of the estimates of the basis of a single period would perhaps be informative, and would allow a more accurate comparison of the methods to be made. This report attempts to compare the estimates on the finest possible level, using samples that are directly comparable.

The focus of the comparison was limited to estimates of the run composition of District 1 commercial harvests. The stratification systems used in the GSI analysis (Spearman and Wilmot 1995) and the SPA analyses (Merritt 1988; Wilcock 1990; Schneiderhan and Wilcock 1992; Schneiderhan 1993; 1994) were compared. The GSI and SPA strata for which samples were taken from a single, common commercial period were identified and included in the analysis. SPA strata that could be pooled consistent with the GSI stratification were also identified and included in the analysis. In all other cases, SPA and GSI estimates would not be directly comparable, and those data were excluded from further consideration.

GSI estimates of run composition and estimated standard errors were taken directly from Spearman and Wilmot (1995). SPA provides estimates of run composition and standard errors for each major age class. The run composition of minor age groups was estimated using a slight modification of the method described by Schneiderhan (1996), pooling all age classes into combined major and minor groups. The estimates of run composition for each age group were summed to estimate the run composition of all age classes combined. The standard errors of the combined run composition estimates were estimated by assuming the relative precision of the

estimates of major age classes was equal to the relative precision of the combined estimates. Note that this method of estimating standard errors does not incorporate variability associated with estimating the age composition of the harvest and only indirectly incorporates variability attributed to the minor age classes. For strata consisting of multiple commercial periods, period-specific SPA estimates were combined, weighting by harvest size, to provide estimates directly comparable to GSI estimates.

For each year, the run composition estimates were combined, weighting by harvest size in each stratum, to estimate the run composition of the combined harvest. This is similar to the Spearman and Wilmot (1995) comparison of GSI and SPA estimates, but is restricted to the subset of the data for which strictly comparable estimates are available.

Comparable estimates were available for a total of 29 strata; 5 strata in 1987, 8 strata in 1988, 7 strata in 1989, 5 strata in 1990, and 4 strata in 1991. The estimates of run composition, estimated standard errors (SE), and estimates of relative precision (CVs) are presented in Table 10. The combined estimates of run composition of all strata in each year are presented in Table 11. In all tables, strata in which the estimates are significantly different are indicated by shading in the table. Estimates were defined to be significantly different in asymptotic normal 80% confidence intervals about the estimates did not overlap. Figure 7 contains scatterplot graphs of GSI versus SPA estimates for each of the three runs.

In many instances, the GSI and SPA estimates of run composition for individual strata are quite similar. In many other instances, the estimates appear somewhat divergent, but are not statistically different. Only in a few cases (13) are the estimates significantly different. Obtaining significantly different estimates of the same quantity from two methods is somewhat disturbing. However, differences will occur occasionally just due to chance, particularly as the number of comparisons increases, and this number of significant differences is not particularly alarming.

Figure 7 indicates that the two methods tend to, on average, produce similar estimates for the Lower and Upper runs, although the relationships are fairly variable. There appears to be no relationship between the two methods with respect to the Middle Run.

An absolute comparison of the precision of the estimates produced by the two methods must be made with caution. The GSI estimates of precision were obtained using bootstrap techniques and should provide a fairly accurate representation of estimator variability. The SPA estimates of precision do not incorporate all sources of variability, although the major sources are accounted for, and may tend to underestimate the true variability of the estimator. Given that caution, the precision achieved by the two methods appear to be fairly similar. A comparison of the coefficients of variation in Table 10 reveals that SPA estimates for the Lower Run tend to be somewhat more precise than the GSI estimates. That comparison is generally reversed for the Upper Run, where GSI estimates tend to be more precise. Neither method seems to produce consistently superior estimates for the Middle Run.

In summary, the two methods seem to produce comparable estimates of run composition for the stock groups defined as Lower, Middle, and Upper runs. At this level of resolution, a choice between the methods would be best made based on cost, and a qualitative evaluation of the assumptions inherent in each method. However, GSI is the only method capable of providing estimates at a finer level of resolution.

7.2 Comparisons of allozymes and DNA loci

Assessing the relative merits of the various genetic marker classes is complicated by the lack of consistency across studies with regard to the geographic extent of sampling. In addition, the preponderance of existing data for both chinook and chum in the Yukon drainage are based on protein allozymes. Studies of DNA variation have examined fewer populations, generally at fewer loci.

Comparative analyses of the utility of the various marker classes for mixed-stock fisheries analysis are further complicated due to differences in the statistical methods employed in the various studies in the quantification of population differences in genetic characteristics and in the procedures used to estimate stock composition. Application of DNA markers will to a certain extent depend on standardization of allelic nomenclature. Researchers from ADF&G, USFWS, and USGS have utilized similar analytical methodologies and to some extent have used the same samples. The minisatellite results (Taylor et al. 1994; Beacham 1996; Beacham et al. 1996) are difficult to compare to results for the other genetic studies do to the nature of the analyses performed.

Despite substantial differences between allozymes, nDNA, and mtDNA in terms of the rate and mode of evolution, and on the extent of allelic variation, for those studies which analyzed populations within the same geographic area, results were very similar. In chinook salmon, inter-population relationships based on differences in allele frequency assayed using microsatellites and protein allozymes were highly concordant for the three populations surveyed (Scribner et al. 1996), suggesting broad application in further, more extensive analysis of chinook in the drainage. DNA analyses of chum salmon have not been conducted for summer stocks or from many of the fall chum populations. For eight populations of fall chum which have been surveyed intensively with several different genetic markers, results suggest no single marker class is superior in discriminating among populations or is more accurate and precise in allocating stocks within a mixed-stock fishery. Allozymes and nDNA microsatellite and intron loci were similarly precise and estimates of precision were highly concordant (Table 1; Scribner et al. submitted). Mitochondrial DNA alone was both imprecise and inaccurate (Table 2; Scribner et al. submitted). Greater precision was realized when all loci were combined in the simulated mixed-stock analysis. Results from minisatellite analysis of chum (Taylor et al. 1994; Beacham 1996) were compelling. These authors report a higher accuracy than was found for the allozyme (Wilmot et al. 1992; Scribner submitted) or other nDNA markers (Scribner et al. submitted). It is not intuitively clear whether the high accuracy and precision is a function of intrinsically different features of the minisatellite loci relative to other class of genetic markers (allozymes, mtDNA, microsatellites), or due to differences in the way the data were quantified and analyzed. All studies show that populations of chinook and chum salmon are genetically different and readily distinguishable on relatively fine geographic scales. Concordance of results across marker classes suggests that these loci appear to capture the same signature of microevolutionary events which have given rise to the present spatial allelic diversity.

If no single class of genetic markers proves superior for stock discrimination and assessments of stock allocation, other factors must be considered in order to forward recommendations to managers. Factors include cost and ease of collection and analysis,

versatility, and time and cost necessary to complete baselines necessary for the analyses of fisheries samples of relevance to managers.

All techniques are fairly expensive and involve laboratory protocols of moderate complexity. Further, processing time for laboratory analyses can be a factor in applying these techniques to large-scale mixed-stock fisheries questions. Processing time for the techniques can be ordered from most to least rapid as (allozymes > mtDNA and RFLP analysis of gene products (introns) > microsatellites > minisatellites).

Sample collection and storage requirements differ greatly among the genetic marker classes. Collections of samples for allozyme analyses necessitates the immediate freezing of samples in the field. DNA samples can be preserved in the field at ambient temperatures using a variety of high salt buffers or alcohol. Protein coding loci are frequently expressed in different tissues. Thus, collections for multi-locus surveys invariably require that individuals be sacrificed and that multiple tissue sources, i.e., eye, muscle, liver, heart, be taken. DNA is ubiquitously distributed in the cells of all tissues and as such can be collected non-destructively from fin clips, scale samples, and blood. Sampling for genetic markers which are assayed using polymerase chain reaction (PCR)-based technology can be accomplished using extremely small samples (e.g., scales or 10^{-3} g of tissue). Samples can also be highly degraded which allows analysis of old samples (e.g., museum specimens, scales saved for many years). Minisatellite analysis requires the use of larger quantities of DNA and thus somewhat larger tissue sources.

Perhaps the biggest concern involves the time and expense required to accumulate existing baseline information to the point where the necessary sampling of background data, i.e., putative spawning aggregations, is complete and statistical methodologies have been rigorously tested. Each marker class appears to provide the accuracy and precision necessary for analysis at nearly all spatial scales within the drainage. However, extensive baseline data is available only for allozyme loci. Genetic stock identification analyses for chinook and chum salmon could move forward immediately based on existing allozyme data. A minimum of several additional years of laboratory analyses would be necessary to bring DNA baselines to the point where mixed-stock analyses could be conducted over the spatial scales identified by managers.

8. MANAGEMENT QUESTIONS RELATED TO YUKON RIVER STOCKS AND STOCK GROUPS

8.1 Chinook Salmon

Conservation and management of Yukon River chinook stocks have been addressed in an Alaska Board of Fisheries approved management plan and the U. S. / Canada Interim Yukon River Salmon Agreement. In order to achieve the management objectives set out in these plans, biologists in Alaska and the Yukon Territory must assess the performance of management actions taken to deliver chinook stocks to various portions of the drainage for harvest and escapement.

A critical management question is "What is the origin of chinook salmon harvested in the lower Yukon River commercial fisheries?" Harvest strategies within the drainage are presently predicated upon assumptions about the general migration timing and distribution of three major stock groups which can be differentiated with available stock identification techniques. At this level of resolution, minimum reporting units are major stock groups (upper, middle and lower Yukon River stocks) for specified Yukon River districts by fishing period and include Districts Y-1, Y-2, and Y-4 (Figure 1b) below the mouth of the Tanana River. Temporal data requirements can be achieved presently by postseason analysis of data through the peak of the chinook run which is generally compressed into a ten day period in early to mid-June.

In general, the coefficient of variation,

$$CV = \frac{\sqrt{\text{var}\,iance}}{estimate},$$

is suggested as a summary statistic of the statistical performance of stock composition estimators. If estimator performance is to be assessed under controlled conditions using simulation techniques, the Relative Root Mean Squared Error,

$$RRMSE = \frac{\sqrt{\text{var}\,iance + (bias)^2}}{estimate},$$

is recommended as the preferred summary statistic. The desired standard for either of these statistics is for them to be less than 0.20 for all stock groups estimated to compose at least 20% of the total.

In the future, management questions about the contribution of specific spawning stocks to harvests are needed to evaluate productivity by stock of origin or to provide specific management consideration for a discrete stock of concern. The limited resolution of SPA requires that other techniques be pursued. The recent genetic analyses suggest that at least three U.S. and five Canadian regions can be identified with acceptable performance as measured by RRMSE. Further evaluation and development of these techniques is recommended.

Future concerns within Canada regarding conservation, harvest allocations (e.g. obligations to manage for basic needs of First Nations) and management of specific Canadian-origin chinook stocks will increase pressure to develop stock identification capability in the Canadian section of the drainage. Development of restoration and enhancement programs may also require the development of evaluation protocols that could very likely include stock identification considerations. Besides increasing manageability on a stock specific basis, greater

stock identification capability would allow further quantification of escapement indices, provide the rationale for potential revisions to the current escapement monitoring program and provide alternate methods to assess returns into Canada on both a broad (border escapement) and more specific scale (individual stocks or groups of stocks). Due to limitations previously described for SPA, genetic stock identification approaches are recommended should implementation be required.

8.2 Fall Chum Salmon

Conservation and management of Yukon River fall chum stocks are addressed in the Alaska Board of Fisheries approved management plans and the U. S. / Canada Interim Yukon River Salmon Agreement. In order to achieve the management objectives set out in these plans, biologists in Alaska must determine inseason the abundance of fall chum salmon available for harvest by recreational, commercial, and subsistence fisheries in Alaska in excess of drainage wide escapement needs and border delivery agreements with Canada. A management plan adopted by the Alaska Board of Fisheries sets drainage-wide passage targets or management action targets which provide for upriver biological escapement goals (BEGs), Alaskan subsistence harvests and Canadian border passage agreements. Effective implementation of the plan requires that Alaskan biologists accurately estimate the fall chum salmon passage into the upper portion of the drainage.

The overlap in run timing of the more abundant summer chum salmon with fall chum during July potentially could contribute a significant source of error in estimating the early abundance of fall chum salmon. A critical management question is "What are the proportions of chum salmon stocks or stock groups migrating through the lower Yukon River commercial fishing districts?" Weekly inseason estimates of the contribution of summer and fall chum stock groups would allow Alaskan managers to more accurately estimate fall chum salmon run passage. At this level of resolution, minimum reporting units are major stock groups (lower, middle and upper Yukon stocks) for specified Yukon districts by fishing period and include Districts Y-1, Y-2, and Y-4 below the mouth of the Tanana River.

During transition between the summer and fall runs of Yukon chum salmon in mid-July, abundance of chum salmon generally declines by an order of magnitude from the peak passage of the summer chum run observed in late June or early July. Chum salmon stocks which may be different or intermediate between the summer chum and fall chum stock groups defined in the GSI model have been suggested, i.e. Chena and Salcha River "summer" chum or stocks not included in the baseline. Given the reduced abundance and the possible presence of genetically intermediate stocks of chum salmon which have not been included in the model, ADF&G management staff have raised concerns about accuracy of the present model to discriminate between the two major stock groups during the time period of interest. It may be necessary to expand the baseline to include stocks that, although in relatively small abundance over the entire run, may be significantly represented during the transition period. Use of radio telemetry or conventional tagging to track and locate the spawning destination of chum salmon entering the river during the transition period may be warranted, if feasible. Also, additional simulations employing stock mixtures which include a higher representation of stocks which classify as more intermediate forms might be informative. Stocks in the Koyukuk, mid to late August spawning stocks in the upper Tanana mainstem, Goodpasture and Nenana Rivers may be candidates for evaluating possible intermediate stock contributions.

Future application of stock identification procedures should concentrate on discrimination of specific fall chum stock groups. Stock identification to river or tributary of origin would be needed to address more specific stock management concerns. For example, to assess management options in the Lower Yukon River commercial fishery which would lower exploitation on a target stock, e.g. Toklat River, would require apportioning run passage estimates obtained at the Lower Yukon River sonar project at Pilot Station. Yukon River chum salmon stocks are harvested by commercial and subsistence fisheries in Alaska operating in the mainstem from the mouth to the Canadian border and in the Tanana River. An important long term goal for Yukon River management is to develop the capability to assess the productivity of various stock components. Assessments of this type have been very difficult due to the lack of data on the yields of specific Yukon River stocks and/or stock groups. Post season analysis and run reconstruction for the purpose of forecasting future returns will require knowledge of the stocks of origin for salmon harvested .

Stock identification data collected to address the question: "What are the origins of chum salmon harvested in the lower and upper Yukon River commercial and subsistence fishing districts in Alaska?" would require minimum reporting units including major spawning stock groups for combined districts by week. At a minimum, mixed-stock fisheries sampling would need to be collected in the lower Yukon fishing districts and upper Yukon fishing districts Y-5 and Y-6. Analysis could be accomplished postseason with a desired statistical standard of a summary statistic (CV or RRMSE ≤ 0.10) for all stock groups estimated to compose at least 20% of the total.

The question: "What are the origins of chum salmon harvested in the commercial and subsistence fishing subdistricts of the Tanana River?" is an ongoing challenge to Yukon River fisheries managers. Chum salmon stocks harvested in the lower Tanana River and in the mainstem Yukon River near the mouth of the Tanana River originate in spawning areas in both the lower and upper Tanana River drainage. Post season assessment of stock contributions would allow an evaluation of the timing and abundance of Toklat (Kantishna) and upper Tanana River (non-Kantishna) stock groups in commercial and subsistence harvests. This information would assist in planning harvest strategies that may allow more specific targeting of stock groups when appropriate, for greater exploitation or conservation in the Tanana River fisheries.

Minimum reporting units for stock identification for mixed-stock fisheries in the Tanana River would include the two major stock groups (Kantishna and non-Kantishna River) for combined commercial harvest subdistricts Y-5A and Y-6A by week. A postseason analysis could be accomplished with a summary statistic (CV or RRMSE $\leq$ 0.20) for any stock group comprising at least 20% of the total.

As discussed in the previous section, future concerns within Canada regarding conservation, harvest allocations (e.g. obligations to manage for basic needs of First Nations) and management of specific Canadian-origin chinook stocks will increase pressure to develop stock identification capability in the Canadian section of the drainage. Development of restoration and enhancement programs may also require the development of evaluation protocols that could very likely include stock identification considerations. Besides increasing manageability on a stock specific basis, greater stock identification capability would allow further quantification of escapement indices, provide the rationale for potential revisions to the current escapement monitoring program and provide alternate methods to assess returns into Canada on both a broad (border escapement) and more specific scale (individual stocks or groups of stocks). For upper Yukon, Canadian-origin chum stocks, there is currently a sufficient GSI database to initiate

annual stock identification sampling programs now. Implementation to this point has been limited by other higher priority programs and funding constraints.

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Table 1. Comparison of various stock identification techniques utilized on Yukon River salmonids.

Technique	Advantages	Limitations	Pertinent citations
Physical			
Physical tagging	Positive individual ID Lethal sampling not required	High cost Low mark percentage Yearly marking required	McFarlane et al. (1990)
Coded wire tags	Positive individual ID	High cost Difficult to tag wild populations Yearly marking required Lethal sampling	Shaul and Clark (1990)
Radio telemetry	Positive individual ID Migratory data Lethal sampling not required	High cost Low mark percentage	Eiler (1990)
Environmental			
Scale Pattern Analysis	Low cost Lethal sampling not required	Yearly update of baseline	Schneiderhan (1996, 1997) Wilcock (1987)
Otoliths marks	Positive individual ID Low cost	Limited utility for wild populations Yearly marking and/or update of baseline required Lethal sampling	Brothers (1990)
Parasites	Multiple generations possible	Limited by distribution of parasites Lethal sampling	Moles et al. (1990)
Genetic			
Protein Electrophoresis	Baseline stable across generations Provides information of gene diversity Extensive baseline for chum and chinook salmon	No positive ID Lethal sampling	Beacham et al. (1988) Beacham et al. (1989) Wilmot et al. (1992) Gharrett et al. (1987) Crane et al. (1996) Crane et al. (In prep.) Seeb and Crane (Submitted)
DNA	Baseline stable across generations Provides information of gene diversity Lethal sampling not required	No positive ID Potentially high cost Development of baseline required	Park et al. (1993) Cronin et al. (1993) Scribner et al. (1996) Scribner et al. (Submitted) Beacham et al. (1996)

Table 2. Accuracy of three-way classification of age 1.4 chinook salmon in Yukon River catches, 1982-1995.

Year	Lower	Middle	Upper	Average
1982	0.857	0.805	0.675	0.779
1983	0.756	0.635	0.692	0.694
1984	0.751	0.660	0.576	0.662
1985	0.771	0.646	0.716	0.711
1986	0.864	0.626	0.598	0.696
1987	0.925	0.735	0.683	0.781
1988	0.750	0.729	0.492	0.657
1989	0.959	0.805	0.821	0.862
1990	0.913	0.755	0.667	0.778
1991	0.813	0.703	0.713	0.743
1992	0.790	0.667	0.805	0.754
1993	0.843	0.714	0.699	0.752
1994	0.837	0.691	0.698	0.729
1995	0.644	0.704	0.813	0.720

Table 3. Baseline stocks for chinook salmon showing sample composition. SF=South Fork; NF=North Fork

Stock	Sample	Year Collected
	United States	
Andreafsky	Andreafsky	1988
Anvik	Anvik	1987
	Anvik	1988
Nulato	Nulato, SF	1988
	Nulato, NF	1988
Gisasa	Gisasa	1987
	Gisasa	1988
Henshaw/Jim	Henshaw	1987
	Jim	1987
SF Koyukuk	Koyukuk, SF	1987
Chena	Chena	1988
	Chena	1988
Salcha	Salcha	1988
	Canada	
Klondike	Klondike, NF	1990
	Klondike, NF	1989
McQuesten	McQuesten	1989
	McQuesten	1990
Pelly	Ross	1988
	Ross	1989
	Blind	1989
Tatchun	Tatchun	1988
	Tatchun	1989
Big Salmon	Big Salmon	1988
	Big Salmon	1989
Little Salmon	Little Salmon	1988
	Little Salmon	1989
	Bear Feed	1989
Nisutlin	Nisutlin	1989
Takhini	Takhini	1988
	Takhini	1990
	Stony	1990

Table 4. Results of 100% simulations by individual stock for chinook salmon showing allocations (bold values) and patterns of misallocation (the three largest misallocations per mixture are underlined). Standard errors are italicized.

	Allocation															
	United States								Canada							
	Lower			Lower Middle			Upper Middle		Upper							
Mixture	AND	ANV	NUL	GIS	SFK	HEN	CHE	SAL	NKL	MCQ	PEL	TAT	LIT	BIG	NIS	TAK
Andreafsky	**0.782**	0.034	0.114	0.025	0.000	0.005	0.001	0.002	0.019	0.001	0.000	0.007	0.004	0.002	0.001	0.004
	0.1230	*0.0630*	*0.1099*	*0.0528*	*0.0018*	*0.0125*	*0.0032*	*0.0096*	*0.0288*	*0.0077*	*0.0023*	*0.0145*	*0.0105*	*0.0093*	*0.0036*	*0.0094*
Anvik	0.059	**0.660**	0.153	0.071	0.000	0.012	0.001	0.001	0.020	0.002	0.000	0.006	0.010	0.001	0.003	0.002
	0.0696	*0.1281*	*0.1123*	*0.0778*	*0.0017*	*0.0255*	*0.0031*	*0.0048*	*0.0306*	*0.0075*	*0.0029*	*0.0136*	*0.0173*	*0.0068*	*0.0082*	*0.0051*
Nulato	0.133	0.120	**0.660**	0.061	0.000	0.015	0.001	0.000	0.003	0.000	0.001	0.002	0.002	0.001	0.001	0.002
	0.1051	*0.1120*	*0.1283*	*0.0709*	*0.0018*	*0.0263*	*0.0039*	*0.0021*	*0.0085*	*0.0021*	*0.0051*	*0.0060*	*0.0065*	*0.0037*	*0.0049*	*0.0048*
Gisasa	0.059	0.017	0.022	**0.867**	0.000	0.008	0.000	0.001	0.009	0.002	0.000	0.004	0.002	0.002	0.005	0.001
	0.0715	*0.0411*	*0.0457*	*0.0876*	*0.0008*	*0.0160*	*0.0019*	*0.0050*	*0.0154*	*0.0074*	*0.0028*	*0.0103*	*0.0073*	*0.0063*	*0.0092*	*0.0028*
SF Koyukuk	0.005	0.003	0.006	0.002	**0.803**	0.072	0.083	0.019	0.004	0.000	0.000	0.002	0.000	0.000	0.001	0.001
	0.0117	*0.0093*	*0.0135*	*0.0071*	*0.0925*	*0.0676*	*0.0834*	*0.0392*	*0.0100*	*0.0023*	*0.0011*	*0.0067*	*0.0016*	*0.0017*	*0.0025*	*0.0018*
Henshaw	0.009	0.008	0.011	0.007	0.033	**0.810**	0.067	0.037	0.011	0.001	0.000	0.001	0.001	0.001	0.003	0.000
	0.0170	*0.0195*	*0.0235*	*0.0150*	*0.0446*	*0.0949*	*0.0691*	*0.0538*	*0.0196*	*0.0042*	*0.0026*	*0.0048*	*0.0025*	*0.0027*	*0.0060*	*0.0013*
Chena	0.000	0.000	0.000	0.000	0.014	0.002	**0.885**	0.094	0.003	0.000	0.001	0.001	0.000	0.000	0.000	0.000
	0.0023	*0.0000*	*0.0021*	*0.0005*	*0.0328*	*0.0087*	*0.0918*	*0.0869*	*0.0076*	*0.0015*	*0.0046*	*0.0037*	*0.0005*	*0.0001*	*0.0005*	*0.0013*
Salcha	0.000	0.000	0.000	0.000	0.010	0.002	0.218	**0.739**	0.023	0.000	0.000	0.004	0.000	0.003	0.000	0.000
	0.0020	*0.0005*	*0.0018*	*0.0005*	*0.0270*	*0.0085*	*0.1201*	*0.1291*	*0.0317*	*0.0002*	*0.0018*	*0.0087*	*0.0009*	*0.0070*	*0.0007*	*0.0000*
NF Klondike	0.003	0.001	0.001	0.001	0.000	0.000	0.000	0.000	**0.960**	0.022	0.003	0.001	0.002	0.004	0.001	0.000
	0.0076	*0.0049*	*0.0043*	*0.0044*	*0.0007*	*0.0014*	*0.0016*	*0.0018*	*0.0309*	*0.0269*	*0.0080*	*0.0036*	*0.0058*	*0.0105*	*0.0053*	*0.0022*
McQuesten	0.000	0.002	0.001	0.000	0.000	0.001	0.000	0.000	0.039	**0.928**	0.009	0.001	0.006	0.011	0.002	0.001
	0.0001	*0.0077*	*0.0042*	*0.0020*	*0.0020*	*0.0028*	*0.0013*	*0.0018*	*0.0437*	*0.0533*	*0.0155*	*0.0051*	*0.0170*	*0.0215*	*0.0067*	*0.0039*
Pelly	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.000	0.002	0.003	**0.940**	0.013	0.006	0.021	0.004	0.006
	0.0029	*0.0034*	*0.0035*	*0.0034*	*0.0006*	*0.0028*	*0.0033*	*0.0018*	*0.0061*	*0.0080*	*0.0435*	*0.0250*	*0.0161*	*0.0332*	*0.0106*	*0.0117*
Tatchun	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.012	**0.877**	0.025	0.047	0.021	0.018
	0.0002	*0.0004*	*0.0000*	*0.0006*	*0.0000*	*0.0004*	*0.0000*	*0.0048*	*0.0000*	*0.0000*	*0.0233*	*0.0817*	*0.0459*	*0.0636*	*0.0384*	*0.0292*
Little Salmon	0.000	0.001	0.000	0.001	0.000	0.000	0.000	0.000	0.002	0.014	0.014	0.028	**0.835**	0.064	0.017	0.024
	0.0017	*0.0036*	*0.0010*	*0.0041*	*0.0004*	*0.0014*	*0.0000*	*0.0002*	*0.0054*	*0.0202*	*0.0223*	*0.0415*	*0.0931*	*0.0837*	*0.0269*	*0.0363*
Big Salmon	0.002	0.001	0.001	0.002	0.000	0.001	0.000	0.001	0.011	0.016	0.037	0.059	0.100	**0.691**	0.036	0.044
	0.0067	*0.0067*	*0.0038*	*0.0065*	*0.0009*	*0.0026*	*0.0010*	*0.0048*	*0.0165*	*0.0263*	*0.0444*	*0.0619*	*0.1000*	*0.1341*	*0.0429*	*0.0507*
Nisutlin	0.000	0.000	0.000	0.001	0.000	0.002	0.000	0.000	0.002	0.001	0.001	0.028	0.012	0.014	**0.922**	0.018
	0.0009	*0.0021*	*0.0004*	*0.0046*	*0.0004*	*0.0066*	*0.0011*	*0.0007*	*0.0067*	*0.0049*	*0.0050*	*0.0414*	*0.0304*	*0.0389*	*0.0689*	*0.0308*
Takhini	0.003	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.017	0.014	0.004	0.001	**0.956**
	0.0072	*0.0028*	*0.0028*	*0.0012*	*0.0003*	*0.0000*	*0.0016*	*0.0001*	*0.0006*	*0.0001*	*0.0100*	*0.0288*	*0.0278*	*0.0131*	*0.0049*	*0.0410*

Table 5. Assessments based on the RRMSE for 100% simulation results for individual stocks and stock groups of chinook salmon. The baseline included all of the stocks for each set of simulations. RRMSEs less than 0.2 were considered acceptable (ϰ) and those greater were considered unacceptable (⊗).

Group	Mean	SE	RRMSE	
Individual Stocks				
Andreafsky	0.782	0.1230	0.3204	⊗
Anvik	0.696	0.1281	0.5512	⊗
Nulato	0.660	0.1283	0.5515	⊗
Gisasa	0.867	0.0876	0.1840	ϰ
S.F. Koyukuk	0.803	0.0925	0.2718	⊗
Henshaw\Jim	0.810	0.0949	0.2628	⊗
Chena	0.885	0.0918	0.1663	ϰ
Salcha	0.739	0.1291	0.3938	⊗
McQuesten	0.928	0.0533	0.0963	ϰ
N. Klondike	0.960	0.0309	0.0524	ϰ
Pelly	0.940	0.0435	0.0793	ϰ
Tatchun	0.877	0.0817	0.1684	ϰ
Little Salmon	0.835	0.0931	0.2270	⊗
Big Salmon	0.691	0.1341	0.4883	⊗
Nisutlin	0.922	0.0689	0.1126	ϰ
Takhini	0.956	0.0410	0.0632	ϰ
Stock Groups				
Andreafsky, Anvik, Nulato, Gisasa	0.962	0.0329	0.0522	ϰ
S.F. Koyukuk, Henshaw/Jim, Chena, Salcha	0.973	0.0243	0.0375	ϰ
Chena, Salcha	0.972	0.0348	0.0457	ϰ
N. Klondike	0.959	0.0343	0.0560	ϰ
McQuesten	0.929	0.0536	0.0960	ϰ
Pelly	0.939	0.0449	0.0805	ϰ
Tatchun, Little Salmon, Big Salmon	0.902	0.0627	0.1289	ϰ
Tatchun, Little Salmon, Big Salmon, Nisutlin	0.940	0.0469	0.0811	ϰ
Nisutlin	0.917	0.0725	0.1204	ϰ
Takhini	0.955	0.0404	0.0630	ϰ

Table 6. Mean estimates of 100 simulations where each mixture (N=400) is composed of chum salmon from each reporting group. Bold values should equal 100%, italicized values are SEs for the estimates.

	Allocation									
Mixture	Lower Summer	Middle Summer	Toklat	Upper Fall Tanana	Fall Tanana	Sheenjek/ Chandalar	Fish. Branch/ Mainstem	Border	White	Teslin
Lower Summer	**0.954**	0.027	0.003	0.001		0.003	0.004		0.002	0.005
	0.0313	*0.0330*	*0.0070*	*0.0055*		*0.0089*	*0.0077*		*0.0044*	*0.0115*
Middle Summer	0.055	**0.851**	0.028	0.014		0.017	0.023		0.005	0.008
	0.0384	*0.0551*	*0.0380*	*0.0218*		*0.0277*	*0.0292*		*0.0106*	*0.0137*
Toklat	0.011	0.040	**0.881**	0.033	**0.914**	0.016	0.011		0.005	0.004
	0.0171	*0.0510*	*0.0782*	*0.0450*	*0.0593*	*0.0280*	*0.0198*		*0.0086*	*0.0078*
Upper Fall Tanana	0.005	0.012	0.022	**0.907**	**0.928**	0.013	0.021		0.018	0.004
	0.0087	*0.0191*	*0.0373*	*0.0546*	*0.0481*	*0.0211*	*0.0329*		*0.0239*	*0.0094*
Sheenjek/ Chandalar	0.012	0.026	0.018	0.017		**0.807**	0.109	**0.916**	0.009	0.003
	0.0149	*0.0306*	*0.0290*	*0.0329*		*0.1004*	*0.0902*	*0.0051*	*0.0152*	*0.0075*
Fish. Branch/Mainstem	0.013	0.009	0.002	0.011		0.094	**0.835**	**0.929**	0.015	0.021
	0.0203	*0.0143*	*0.0085*	*0.0229*		*0.0902*	*0.0952*	*0.0045*	*0.0216*	*0.0222*
White	0.001	0.005	0.000	0.006		0.006	0.019		**0.962**	0.002
	0.0022	*0.0094*	*0.0001*	*0.0133*		*0.0160*	*0.0262*		*0.0285*	*0.0038*
Teslin	0.009	0.006	0.000	0.001		0.001	0.032		0.002	**0.948**
	0.0141	*0.0114*	*0.0001*	*0.0030*		*0.0044*	*0.0337*		*0.0057*	*0.0339*

Table 7. Mean estimates from 100 simulations for realistic stock compositions of chum salmon. Estimates for individual stocks were summed into three hierarchical levels (from Crane et al. in prep.).

		Observed			
Mixture 1	Expected	mean	SE	CV	RRMSE
Lower Summer	0.73	0.72	0.057	8%	0.08
Middle Summer	0.16	0.15	0.070	46%	0.46
Toklat	0	0.01	0.019	228%	2.49
Upper Tanana Fall	0	0.01	0.019	204%	2.27
Chandalar/Sheenjek	0.03	0.03	0.037	120%	1.20
Fishing	0.04	0.04	0.045	101%	1.02
Branch/Mainstem					
White	0.02	0.02	0.018	120%	1.24
Teslin	0.02	0.02	0.021	108%	1.08
Lower Summer	0.73	0.72	0.057	8%	0.08
Middle Summer	0.16	0.15	0.071	46%	0.46
Fall Tanana	0	0.02	0.026	149%	1.79
Border	0.07	0.08	0.048	64%	0.64
White	0.02	0.02	0.018	120%	1.24
Teslin	0.02	0.02	0.021	108%	1.08
Summer	0.89	0.86	0.050	6%	0.07
Fall	0.11	0.14	0.050	37%	0.42

		Observed			
Mixture 2	Expected	mean	SE	CV	RRMSE
Lower Summer	0.09	0.10	0.035	36%	0.37
Middle Summer	0.04	0.06	0.047	79%	0.86
Toklat	0.01	0.02	0.030	172%	1.77
Upper Tanana Fall	0.02	0.03	0.037	147%	1.48
Chandalar/Sheenjek	0.30	0.32	0.126	39%	0.40
Fishing	0.48	0.42	0.129	31%	0.34
Branch/Mainstem					
White	0.03	0.03	0.031	101%	1.01
Teslin	0.03	0.03	0.026	84%	0.84
Lower Summer	0.09	0.10	0.035	37%	0.37
Middle Summer	0.04	0.06	0.047	79%	0.86
Fall Tanana	0.03	0.04	0.042	98%	1.03
Border	0.78	0.74	0.072	10%	0.11
White	0.03	0.03	0.031	101%	1.01
Teslin	0.03	0.03	0.026	83%	0.83
Summer	0.13	0.15	0.053	34%	0.38
Fall	0.87	0.85	0.053	6%	0.07

		Observed			
Mixture 3	Expected	mean	SE	CV	RRMSE
Lower Summer	0.03	0.03	0.024	71%	0.72
Middle Summer	0.01	0.04	0.039	104%	1.27
Toklat	0.06	0.05	0.057	112%	1.13
Upper Tanana Fall	0.16	0.16	0.075	47%	0.47
Chandalar/Sheenjek	0.36	0.35	0.135	38%	0.38
Fishing	0.36	0.33	0.138	42%	0.44
Branch/Mainstem					
White	0.01	0.02	0.027	136%	1.45
Teslin	0.01	0.02	0.022	134%	1.40
Lower Summer	0.03	0.03	0.024	71%	0.72
Middle Summer	0.01	0.04	0.039	104%	1.27
Fall Tanana	0.22	0.21	0.072	34%	0.34
Border	0.72	0.68	0.083	12%	0.14
White	0.01	0.02	0.027	136%	1.45
Teslin	0.01	0.02	0.022	134%	1.40
Summer	0.04	0.07	0.041	57%	0.72
Fall	0.96	0.93	0.041	4%	0.06

		Observed			
Mixture 4	Expected	mean	SE	CV	RRMSE
Lower Summer	0.00	0.01	0.015	155%	1.84
Middle Summer	0.00	0.03	0.034	108%	1.47
Toklat	0.17	0.16	0.077	49%	0.51
Upper Tanana Fall	0.44	0.42	0.085	20%	0.21
Chandalar/Sheenjek	0.25	0.22	0.101	46%	0.48
Fishing	0.13	0.14	0.100	73%	0.73
Branch/Mainstem					
White	0.00	0.01	0.021	142%	1.
Teslin	0.00	0.01	0.010	192%	2.1,
Lower Summer	0.00	0.01	0.015	155%	1.84
Middle Summer	0.00	0.03	0.034	107%	1.47
Fall Tanana	0.62	0.58	0.077	13%	0.15
Border	0.38	0.36	0.072	20%	0.21
White	0.00	0.01	0.021	142%	1.74
Teslin	0.00	0.01	0.010	192%	2.17
Summer	1.00	0.96	0.035	4%	0.06
Fall	0.00	0.04	0.035	85%	1.31

		Observed			
Mixture 5	Expected	mean	SE	CV	RRMSE
Lower Summer	0.20	0.21	0.051	24%	0.25
Middle Summer	0.34	0.30	0.088	30%	0.34
Toklat	0.05	0.06	0.065	114%	1.14
Upper Tanana Fall	0.29	0.28	0.067	24%	0.25
Chandalar/Sheenjek	0.03	0.04	0.054	121%	1.26
Fishing	0.03	0.07	0.062	94%	1.09
Branch/Mainstem					
White	0.03	0.03	0.027	102%	1.03
Teslin	0.03	0.03	0.025	88%	0.88
Lower Summer	0.20	0.21	0.051	24%	0.25
Middle Summer	0.34	0.30	0.088	30%	0.34
Fall Tanana	0.34	0.33	0.073	22%	0.22
Border	0.06	0.11	0.071	64%	0.79
White	0.03	0.02	0.026	109%	1.11
Teslin	0.03	0.03	0.025	88%	0.88
Summer	0.54	0.50	0.076	15%	0.17
Fall	0.46	0.50	0.076	15%	0.17

Table 8. Results of simulated mixed-stock analyses[1] for fall-run chum salmon based on six nDNA loci. Analyses were conducted using each of six artificial mixed-stock data sets of different known US-Canadian proportions from baseline data from eight populations. Simulations were conducted incrementally by 20% intervals from 0% to 100% to determine the accuracy and precision of stock allocation to US and Canadian reporting groups.

Simulated Freq. of US and Canadian Stocks	Mean estimate of US contribution to simulated mixture	SE	Expected freq. of US contribution to simulated mixture	RRMSE[2]
100% US/ 0% Can	0.796	0.0816	1.0000	0.2465
80% US/ 20% Can	0.665	0.0831	0.8000	0.1944
60% US/ 40% Can	0.535	0.0823	0.6000	0.1431
40% US/ 60% Can	0.401	0.0751	0.4000	0.1186
20% US/ 80% Can	0.270	0.0746	0.2000	0.1972
0% US/ 100% Can	0.129	0.0658	0.0000	0.4032

[1]Simulated mixture analyses were conducted using the Statistical Package for Analyzing Mixtures (SPAM) developed by ADF&G using GIRLS (Masuda et al. 1991) and CONJA-S (Pella et al. 1996).
[2]The statistical standard recommended by ADF&G fisheries managers is 0.20 for analyses conducted for two reporting groups (D. Schneiderhan, pers. Comm.).

Table 9. Results of simulated mixed-stock analyses[1] for fall-run chum salmon based on mtDNA haplotype frequency. Analyses were conducted using each of six artificial mixed-stock data sets of different known US-Canadian proportions from baseline data from eight populations. Simulations were conducted incrementally by 20% intervals from 0% to 100% to determine the accuracy and precision of stock allocation to US and Canadian reporting groups.

Simulated Freq. of US and Canadian Stocks	Mean estimate of US contribution to simulated mixture	SE	Expected freq. of US contribution to simulated mixture	RRMSE[2]
100% US/ 0% Can	0.574	0.2252	1.0000	0.6365
80% US/ 20% Can	0.542	0.2171	0.8000	0.5036
60% US/ 40% Can	0.462	0.2188	0.6000	0.3804
40% US/ 60% Can	0.398	0.2189	0.4000	0.3537
20% US/ 80% Can	0.331	0.2161	0.2000	0.4392
0% US/ 100% Can	0.251	0.1785	0.0000	0.6148

[1]Simulated mixture analyses were conducted using the Statistical Package for Analyzing Mixtures (SPAM) developed by ADF&G using GIRLS (Masuda et al. 1991) and CONJA-S (Pella et al. 1996).
[2]The statistical standard recommended by ADF&G fisheries managers is 0.20 for analyses conducted for two reporting groups (D. Schneiderhan, pers. Comm.).

Table 10. Comparison of GSI and SPA estimates, SEs, and CVs of stock composition, by run, of chinook salmon commercially harvested in District 1 of the Yukon River, 1987-1991. Estimates are presented for all temporal strata used by Spearman and Wilmot (1995) in which estimates are directly comparable. Shading denotes those cases in which asymptotic normal 80% confidence intervals for the estimates do not overlap.

			Lower Run						Middle Run						Upper Run					
			GSI			SPA			GSI			SPA			GSI			SPA		
Year	Period	Harvest	Estimate	SE	CV	Estimate	SE	CV	Estimate	SE	CV	Estimate	SE	CV	Estimate	SE	CV	Estimate	SE	CV
1987	1	12,970	0.186	0.076	40.7	0.279	0.056	20.1	0.087	0.058	67.1	0.165	0.114	69.0	0.727	0.084	11.5	0.556	0.141	25.3
1987	2	22,513	0.108	0.071	66.0	0.216	0.052	24.1	0.162	0.057	35.5	0.106	0.120	113.6	0.731	0.076	10.4	0.678	0.144	21.2
1987	3-4	26,664	0.259	0.076	29.4	0.261	0.039	15.1	0.118	0.057	47.8	0.234	0.083	35.4	0.622	0.075	12.0	0.505	0.097	19.1
1987	5	7,904	0.286	0.073	25.7	0.291	0.053	18.2	0.188	0.067	35.4	0.136	0.107	78.5	0.526	0.070	13.4	0.572	0.137	24.0
1987	6	4,665	0.602	0.092	15.2	0.665	0.086	13.0	0.041	0.043	106.1	0.197	0.125	63.7	0.357	0.091	25.5	0.139	0.160	115.1
1988	1	3,330	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.289	0.076	26.5	0.206	0.116	56.2	0.613	0.081	13.3	0.415	0.142	34.2
1988	2 & 4	21,833	0.186	0.060	32.2	0.294	0.045	15.3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.590	0.058	9.8	0.695	0.048	7.0
1988	5	10,959	0.342	0.089	26.1	0.319	0.061	19.0	0.120	0.072	60.2	0.223	0.083	37.3	0.538	0.091	17.0	0.458	0.111	24.2
1988	6	8,773	0.462	0.120	25.9	0.694	0.148	21.3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.300	0.086	28.7	0.268	0.129	48.1
1988	7	3,280	0.462	0.123	26.7	0.379	0.171	45.2	0.080	0.057	71.3	0.199	0.223	111.8	0.458	0.116	25.4	0.422	0.284	67.3
1988	8	4,588	0.491	0.096	19.5	0.623	0.097	15.6	0.047	0.058	122.0	0.114	0.132	116.0	0.462	0.083	18.0	0.263	0.174	66.2
1988	9	1,610	0.541	0.120	22.3	0.525	0.157	29.9	0.028	0.040	142.1	0.224	0.214	95.9	0.431	0.113	26.1	0.251	0.266	105.8
1988	10-12	1,066	0.488	0.081	16.5	0.679	0.111	16.3	0.168	0.061	36.2	0.059	0.094	159.7	0.345	0.079	22.9	0.262	0.141	53.9
1989	2	5,862	0.111	0.060	54.4	0.223	0.041	18.5	0.264	0.058	21.8	0.192	0.063	33.0	0.626	0.061	9.8	0.585	0.081	13.9
1989	3	1,650	0.249	0.058	23.2	0.321	0.049	15.4	0.240	0.053	22.0	0.152	0.682	448.2	0.512	0.059	11.5	0.527	0.080	15.1
1989	4	15,971	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.159	0.045	28.1	0.177	0.065	36.8	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
1989	5	10,959	0.469	0.084	17.9	0.582	0.067	11.6	0.171	0.081	47.6	0.130	0.072	55.3	0.360	0.070	19.5	0.288	0.098	34.0
1989	6	8,773	0.654	0.096	14.6	0.488	0.065	13.4	0.147	0.087	58.9	0.244	0.083	34.0	0.199	0.061	30.7	0.268	0.110	41.2
1989	7	3,280	0.597	0.088	14.7	0.590	0.070	11.8	0.175	0.086	49.0	0.120	0.079	66.2	0.228	0.071	31.3	0.291	0.119	40.8
1989	8	4,588	0.576	0.105	18.3	0.502	0.079	15.7	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.364	0.104	28.6	0.191	0.132	68.9
1990	1	18,920	0.124	0.053	43.1	0.127	0.028	22.1	0.281	0.068	24.3	0.336	0.088	26.2	0.595	0.069	11.6	0.538	0.083	15.4
1990	2	8,976	0.222	0.084	37.8	0.265	0.034	12.7	0.156	0.063	40.3	0.088	0.052	59.2	0.621	0.085	13.6	0.647	0.058	9.0
1990	3	15,020	0.444	0.066	14.8	0.298	0.037	12.3	0.151	0.054	35.4	0.311	0.081	26.2	0.405	0.058	14.4	0.393	0.080	20.3
1990	4	6,487	0.594	0.070	11.7	0.399	0.038	9.6	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.321	0.056	17.4	0.276	0.069	25.0
1990	5	1,665	0.495	0.081	16.4	0.355	0.063	17.7	0.093	0.048	51.3	0.072	0.060	83.1	0.412	0.071	17.2	0.573	0.081	14.1
1991	1	17,135	0.370	0.062	16.7	0.312	0.039	12.4	0.239	0.056	23.3	0.127	0.082	64.9	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
1991	2	15,066	0.314	0.075	24.0	0.411	0.044	10.6	0.280	0.065	23.1	0.360	0.083	23.0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
1991	3	4,737	0.309	0.059	19.2	0.305	0.069	22.7	0.161	0.046	28.4	0.303	0.153	50.7	0.531	0.054	10.2	0.392	0.118	30.1
1991	4	9,264	0.427	0.078	18.3	0.402	0.045	11.2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

Table 11. Comparison of GSI and SPA annual estimates, SEs, and CVs of stock composition, by run, of chinook salmon commercially harvested in District 1 of the Yukon River, 1987-1991. Estimates exclude periods in which either GSI of SPA are unavailable or the two estimates are not directly comparable. Shading denotes cases in which asymptotic normal 80% confidence intervals for the estimates do not overlap.

		GSI			SPA		
Year	Run	Estimate	S.E.	C.V.	Estimate	S.E.	C.V.
1987	Lower	0.225	0.0383	17.0	0.279	0.0245	8.8
1987	Middle	0.128	0.0294	22.9	0.171	0.0527	30.8
1987	Upper	0.647	0.0392	6.1	0.550	0.0631	11.5
1988	Lower	0.313	0.0370	11.8	0.414	0.0349	8.4
1988	Middle	0.180	0.0302	16.8	0.096	0.0281	29.3
1988	Upper	0.508	0.0341	6.7	0.491	0.0434	8.9
1989	Lower	0.383	0.0343	9.0	0.441	0.0264	6.0
1989	Middle	0.166	0.0288	17.3	0.188	0.0389	20.8
1989	Upper	0.451	0.0290	6.4	0.372	0.0429	11.5
1990	Lower	0.310	0.0397	12.7	0.225	0.0362	16.1
1990	Middle	0.190	0.0323	17.0	0.275	0.0426	15.5
1990	Upper	0.503	0.0350	7.0	0.482	0.0410	8.5
1991	Lower	0.357	0.0376	10.5	0.361	0.0233	6.4
1991	Middle	0.206	0.0313	15.2	0.272	0.0471	17.3
1991	Upper	0.437	0.0324	7.4	0.367	0.0377	10.3

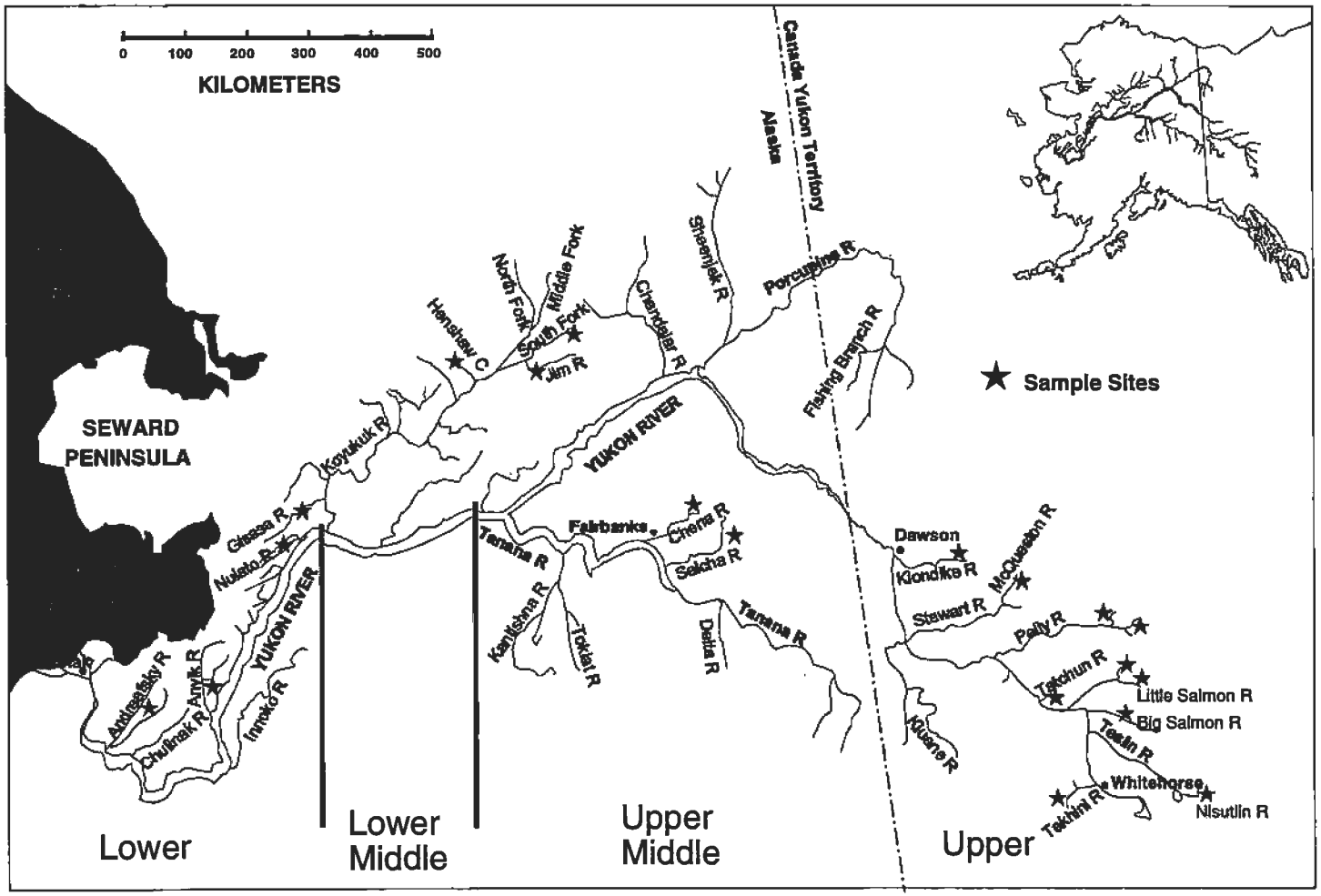

Figure 1a. Map of the Yukon River showing baseline sample locations for chinook salmon and geographic river reaches

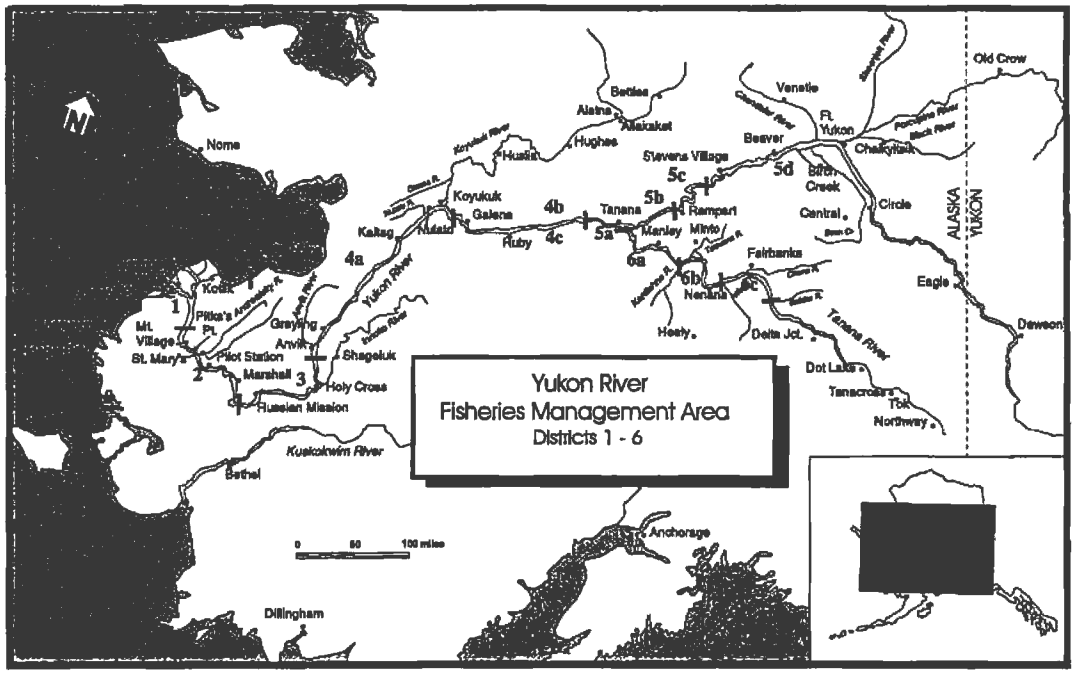

Figure 1b. Map of the Yukon River showing Alaska Department of Fish and Game fisheries management areas.

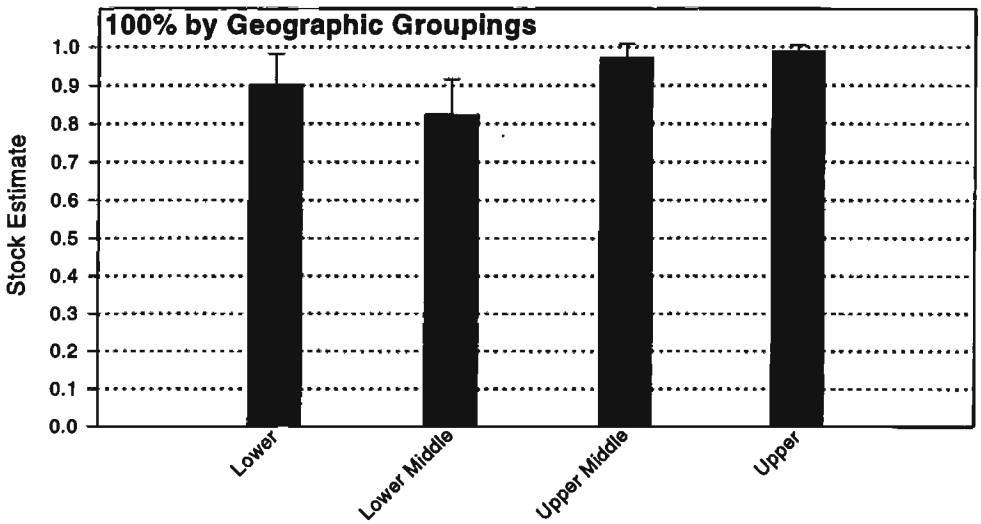

Figure 2. Results of 100% simulations based on geographic groupings of Yukon River chinook salmon stocks, where LOWER = Andreafsky + Nulato; LOWER MIDDLE = Gisasa + S.F. Koyukuk + Henshaw/Jim; UPPER MIDDLE = Chena + Salcha; and UPPER = N.F. Klondike + McQuesten + Tatchun + Little Salmon + Big Salmon + Takhini + Nisutlin.

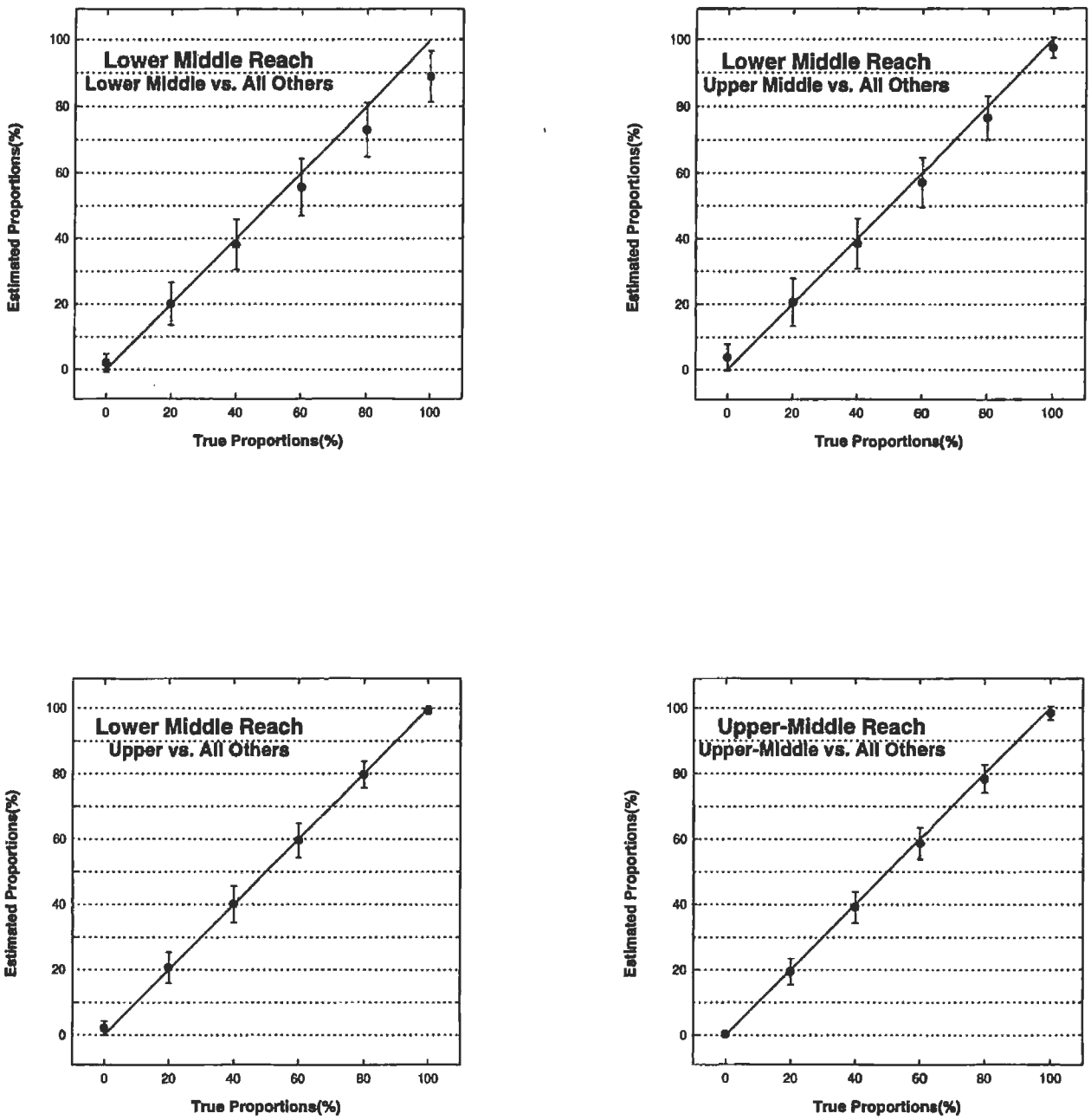

Figure 3. Accuracy graphs showing the resolution possible with geographic groups of Yukon River chinook salmon stocks in the Lower Reach.

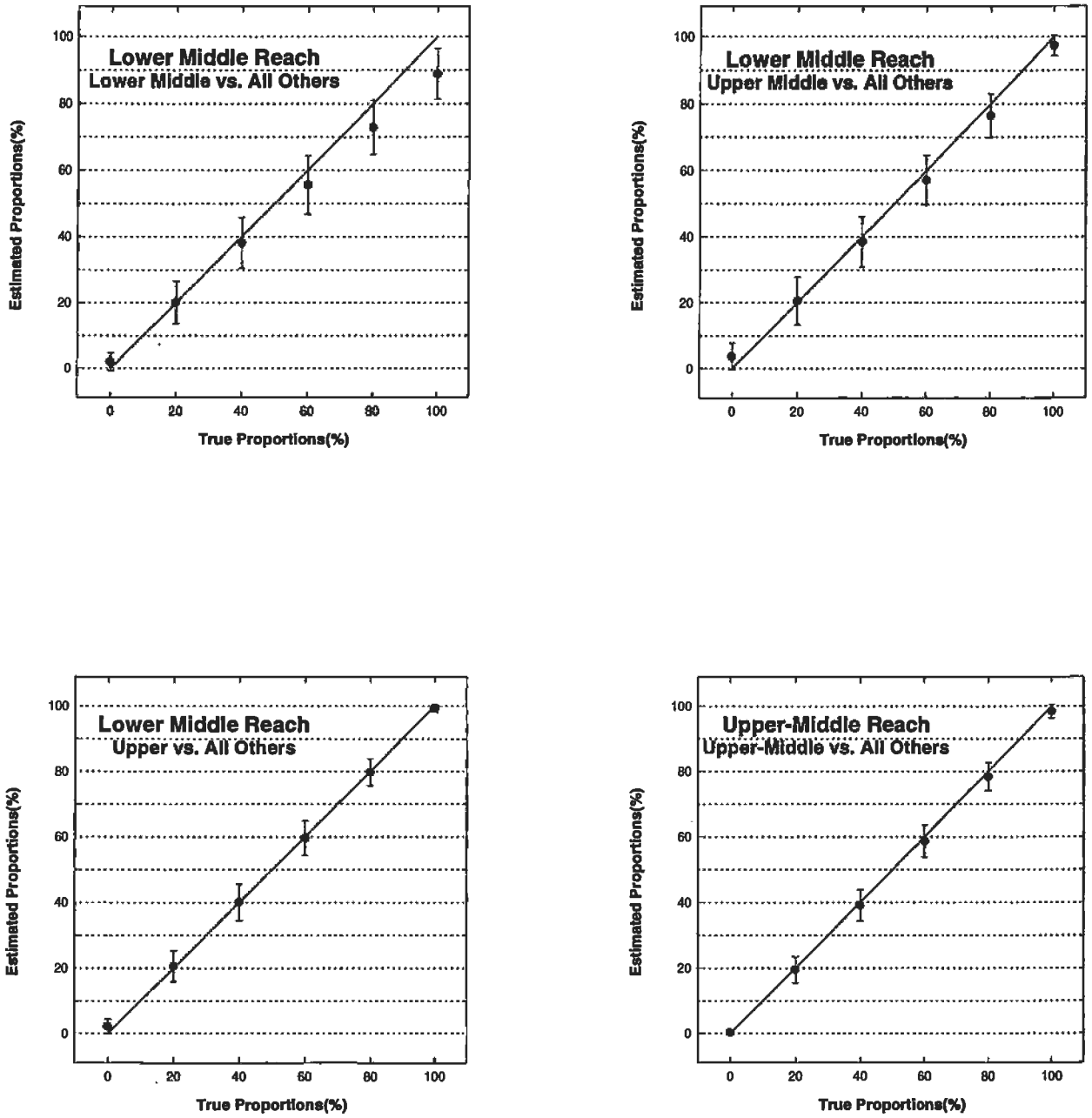

Figure 4. Accuracy graphs showing the resolution possible with geographic groups of Yukon River chinook salmon stocks in the Lower-Middle and Upper reaches.

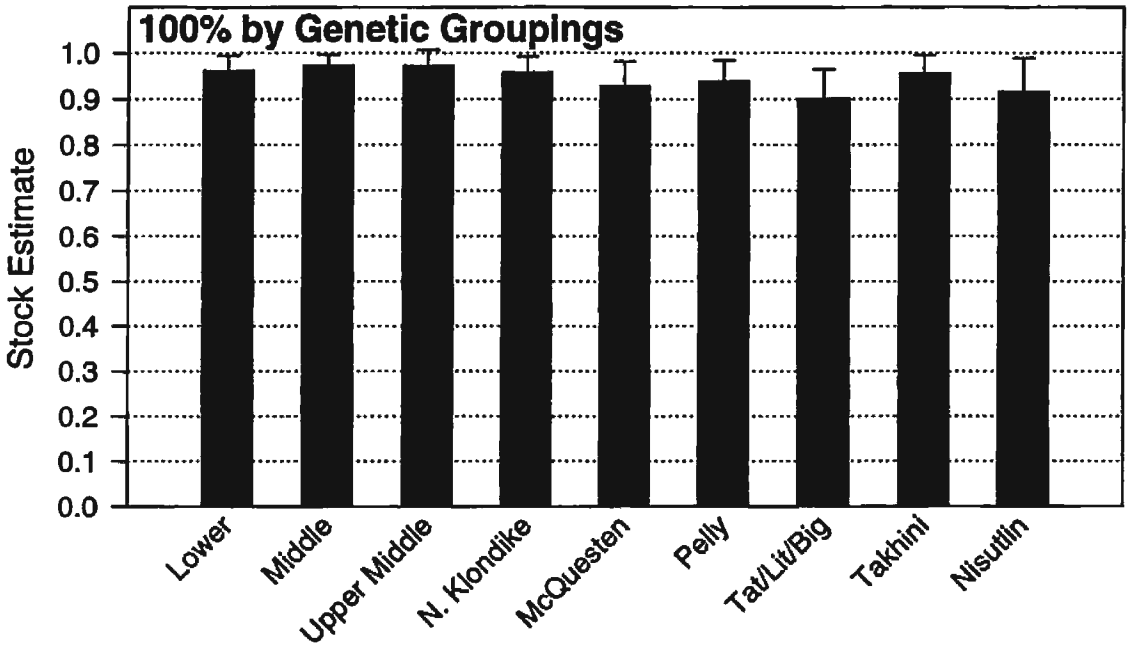

Figure 5. Results of 100% simulations based on genetic groupings of Yukon River chinook salmon stocks, where LOWER = Andreafsky + Anvik + Nulato + Gisasa; MIDDLE = S.F. Koyukuk + Henshaw/Jim + Chena + Salcha; UPPER-MIDDLE = Chena + Salcha; TAT/LIT/BIG = Tatchun + Little Salmon + Big Salmon.

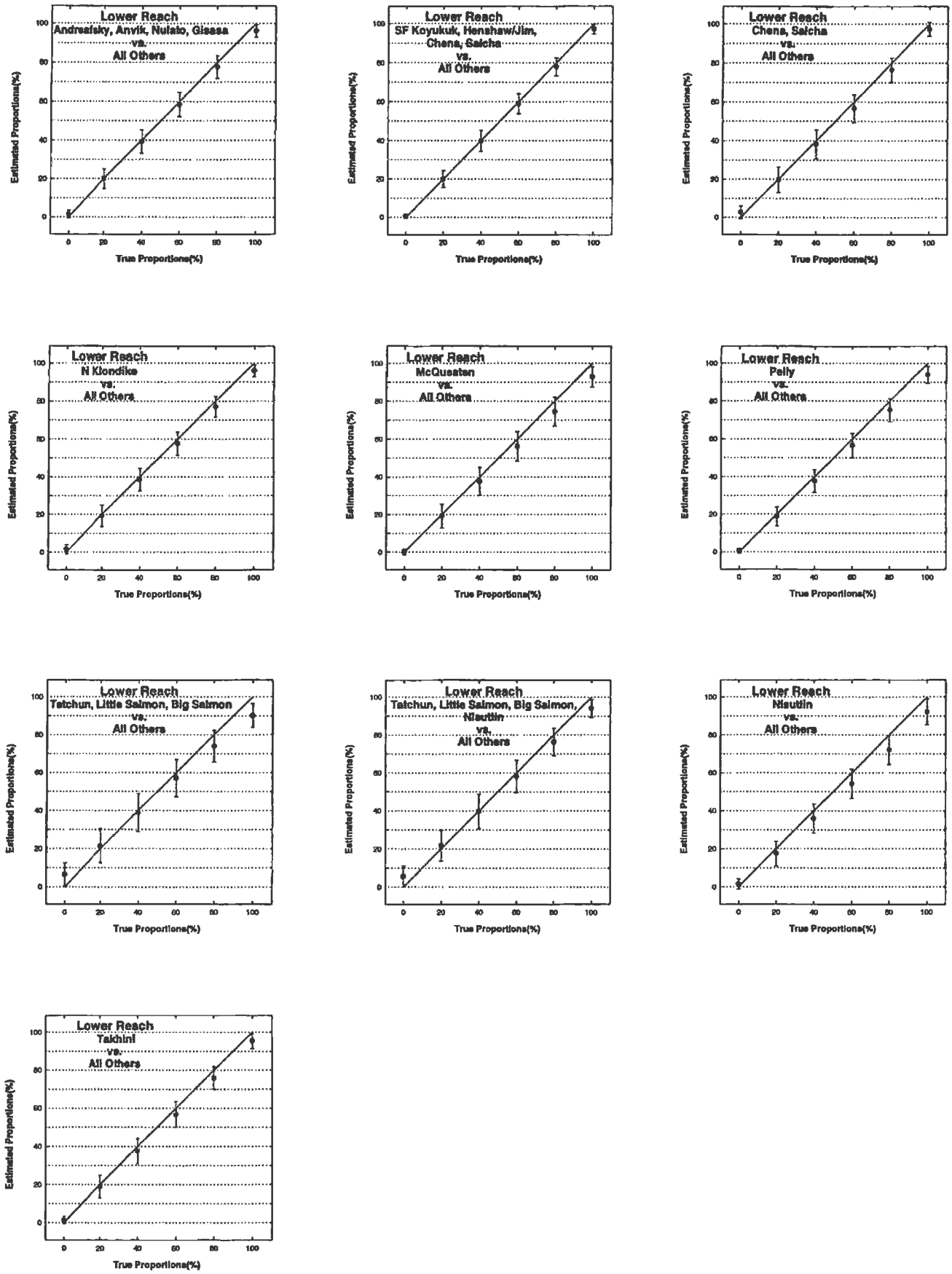

Figure 6. Accuracy graphs showing the resolution possible with genetic groupings of Yukon River chinook salmon stocks in the Lower Reach.

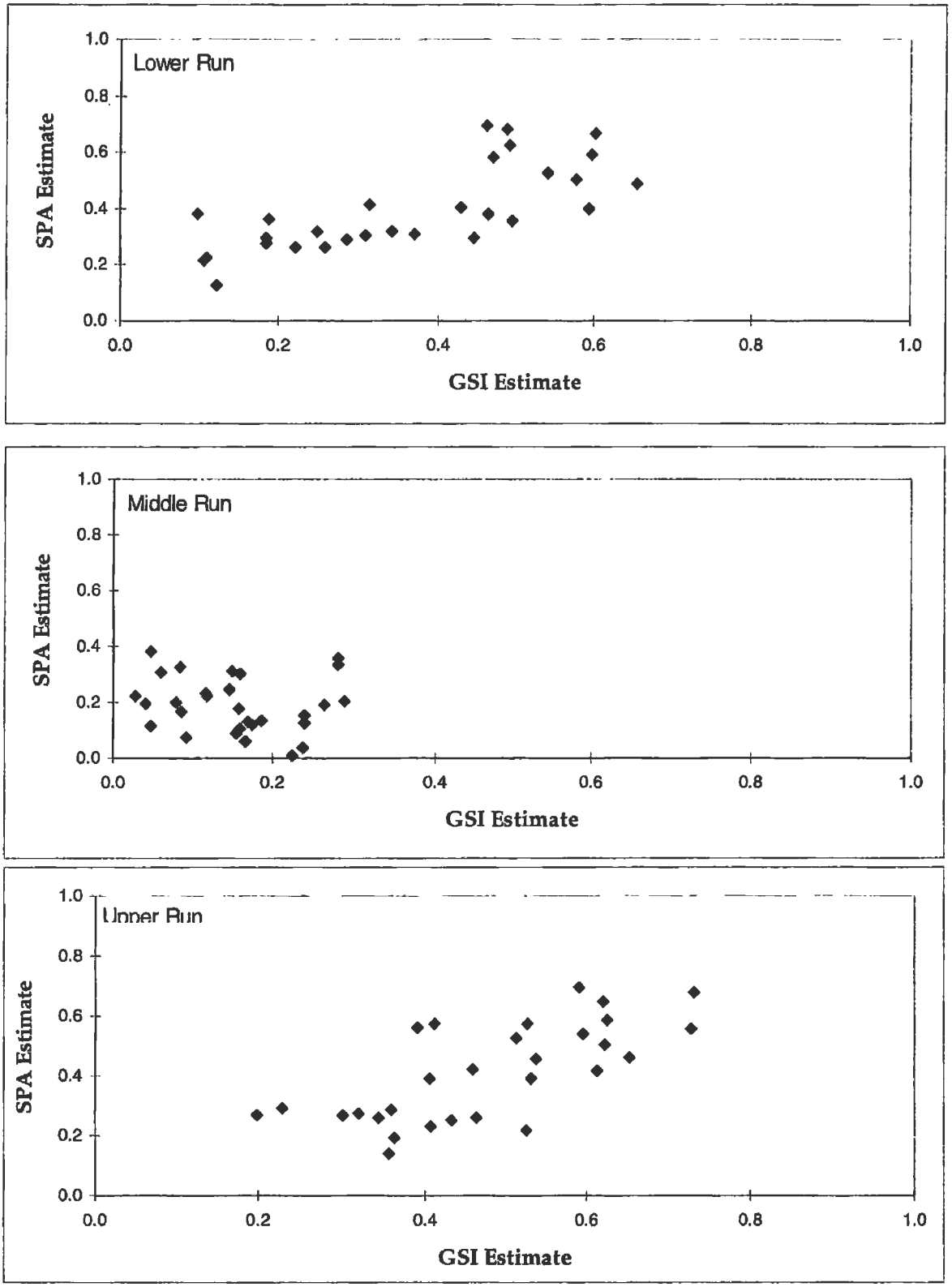

Figure 7. Scatterplots of GSI and SPA estimates of chinook salmon composition by run.