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Stock Structure and Mixed-Stock Analysis of Yukon River Chum Salmon

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Abstract

The management of Yukon River chum salmon fisheries is difficult because of the need to address a variety of complex issues, such as meeting escapements, while still providing harvest opportunities in a mixed-stock and mixed-species fishery. Yukon River chum salmon were assayed for genetic variation at 22 microsatellite loci to establish a baseline for mixed-stock analysis (MSA) applications to assist in addressing these issues. Yukon River chum salmon exhibited a relatively low degree of genetic divergence ($G_{ST} = 0.0157$) that was structured by seasonal race and geographic region. Using the 12 most informative loci, accuracies in MSA simulations for 14 of 17 reporting groups exceeded 90%, with a range of 80–98%. Stock composition estimates were within 10% of the actual proportions in a known mixture analysis. Stock specific abundance estimates, derived from combining the estimates of genetic stock composition with Pilot Station sonar abundance estimates, were concordant with upriver escapement data, after accounting for harvest. The combination of genetic MSA estimates from the baseline developed in this study and Pilot Station sonar abundance estimates provides a viable tool for assessing stock strength and assisting managers in regulating fisheries to maintain the productivity and evolutionary potential of Yukon River chum salmon.

Introduction

The Yukon River is over 3,200 kilometers long, drains 855,000 square kilometers, and encompasses 20 ecoregions (Brabets et al. 2000). It is one of only a few rivers in North America with two seasonal races of chum salmon *Oncorhynchus keta*, summer and fall (Salo 1991). The seasonal races exhibit spatial differences, with summer chum salmon primarily found in the lower and middle river and fall chum salmon in the middle and upper river. Isolation resulting from the temporal and spatial spawning fidelity has limited gene flow between the races and led to adaptations specific to each. Spawning site water temperature, not migration distance, likely controls return time, as thermal unit requirements for developing embryos are probably similar for the two races (Buklis and Barton 1984). Fry emerge and migrate at similar times. However, summer chum salmon spawn in colder runoff streams over a larger and more continuous area, allowing them to reach greater abundance, whereas

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fall chum salmon spawn in warmer spring upwellings at more specific sites (Buklis 1981; Buklis and Barton 1984). Adult fall chum salmon are distinguished from summer chum salmon by larger bodies, higher fat content, delayed freshwater sexual maturity, and a fusiform shape, all of which are attributes best suited for longer freshwater migrations (Buklis and Barton 1984; Beacham et al. 1988).

Chum salmon may comprise half of all the Pacific salmon biomass (Salo 1991), which helps explain the importance of this food resource for residents of the Yukon River drainage, whose take of chum salmon accounts for 70% of the Yukon River salmon harvested in subsistence fisheries (ADFG 2001). Returns of Yukon River chum salmon have fluctuated widely, and low returns, most notably between 1998 and 2002, have resulted in subsistence shortfalls because of fishery closures and restrictions. Such shortfalls are especially hard on residents where a subsistence lifestyle is a necessity because of limited economic opportunities.

The management of these fisheries is difficult because of the need to address a variety of complex issues, such as meeting escapements, while still providing harvest opportunities in a mixed-stock and mixed-species fishery. The transition from summer to fall management at the mouth of the Yukon River occurs on July 16, and the fall seasonal race is of special concern because of additional obligations requiring the conservation and equitable sharing of the resource with Canada, consistent with the Yukon River Salmon Agreement, an annex of the Pacific Salmon Treaty (PST). Knowledge of chum salmon origin as they enter the river would assist in meeting PST obligations. Moreover, identifying stock structure of migrating fish and determining relative stock contributions to harvests are essential for management of mixed-stock fisheries (Larkin 1981). Successful conservation can only be realized by harvesting stocks at sustainable rates to avoid the negative side effects of decreased production and diminished biodiversity that result from excessive exploitation (Allendorf et al. 1987).

Attempts to identify discrete stocks of Yukon River fall chum salmon began with tagging studies in 1976 (Buklis 1981). Those results have shown that fall chum salmon segregate by riverbank in the Galena-Ruby area (Figure 1). Specifically, Yukon River fall stocks above the Tanana River migrate earlier along the north riverbank whereas Tanana River stocks migrate later along the south riverbank. However, the resolution was insufficient to identify individual stocks.

Mixed-stock analysis (MSA; e.g., Grant et al. 1980) using genetic data has been established as an efficient and effective method for determining stock origin (Cadrin et al. 2005). The concept underlying this approach is that the natal homing of salmon can lead to reproductively isolated stocks (Salo 1991). Consequently, the genetic structures of distinct stocks vary. Application of genetic techniques for estimating stock composition of Yukon River chum salmon mixed fisheries began following the signing of the PST in 1985. Initial research of allozyme loci has revealed a stock structure defined by seasonal race and geographic region, with greater divergence between seasonal races and among regions than within them (Beacham et al. 1988; Wilmot et al. 1992; Seeb and Crane 1999a). These studies have shown that summer run stocks comprise two distinct regions, lower and middle river (Figure 1), and differ genetically from the fall run stocks. Fall stocks comprise four distinct regions: Tanana, U.S./Canada border, White, and Teslin (Figure 1). Allozyme loci did not provide

≥90% accuracy, a commonly desired threshold (Seeb and Crane 1999b), in MSA simulations for the U.S./Canada border region split by country-of-origin. Allozyme analysis is unable to detect much of the variation that exists at the DNA level because of degenerate coding, which results in low levels of allozyme variation (Weir 1996). Moreover, the available pool of variable allozyme loci has been exhausted, precluding adding loci to increase power, and allozyme samples require preservation at extremely low temperatures (i.e., in liquid nitrogen or ultra cold freezers), presenting additional logistical difficulties.

Desire for greater resolution has prompted research on DNA markers that are more variable and, therefore, potentially more informative (Kalinowski 2004; Beacham et al. 2005, 2006). Pilot studies of microsatellite variation in Yukon River chum salmon have revealed that microsatellite loci provide more accurate and precise estimates in MSA simulations (Flannery et al. 2007a). Based on these findings, we have initiated this project to develop an extensive microsatellite baseline for Yukon River chum salmon MSA. The main project objective is to develop a baseline for estimating stock composition and run timing of chum salmon collected from a lower Yukon River test fishery to assist management decisions.

Methods

Baseline Development

Sample collection and laboratory analysis—Tissue samples from returning adult chum salmon were collected from 29 stocks on or near their spawning grounds (Table 1, Figure 1). Total genomic DNA was extracted from the tissue (~25mg) using proteinase K with the Dneasy™ DNA isolation kit (Qiagen Inc., Valencia, CA) or by a chelex resin protocol (Withler et al. 2000). Polymerase chain reaction (PCR) DNA amplification was used by the U.S. Fish and Wildlife Service (USFWS) and Department of Fisheries and Oceans Canada (DFOC) laboratories to assay genetic variation. The USFWS laboratory genotyped samples at the following microsatellite loci: *Oke3*, *Oke4*, *Oke8*, *Oke11* (Buchholz et al. 2001); *Oki1*, *Oki23.1* (Smith et al. 1998); *Ots2.1*, *Ots3.1* (Banks et al. 1999); and *Ots103* (Beacham et al. 1998). The DFOC laboratory genotyped samples at the following microsatellite loci: *Oki2* (Smith et al. 1998); *Oki100* (Miller unpublished); *Omy1011* (Spies et al. 2005); *One101*, *One102*, *One103*, *One104*, *One111*, *One114* (Olsen et al. 2000); *Ssa419* (Cairney et al. 2000); and *OtsG68* (Williamson et al. 2002). The PCR product was electrophoresed and visualized on a denaturing 6% polyacrylamide gel using either a Li-Cor IR2® DNA scanner or a ABI 377 automated DNA sequencer. Genotypes were scored using sizing standards and Saga GT 3.1 (Li-Cor, Lincoln, NE) and Genotyper 2.5 (PE Biosystems, Foster City, CA) computer programs. All scores were verified by visual inspection. Genotypes were scored by two independent researchers, with any discrepancies being resolved by re-running the samples in question and repeating the double scoring process until scores matched. The USFWS merged the datasets by genotyping a common set of samples with the DFOC loci to account for cross platform allelic mobility shifts and to assess genotyping error rates.

Data analysis—The hierarchy used in likelihood and gene diversity analyses was based on the genetic structure depicted by the neighbor-joining dendrogram whereas the hierarchy for the mixed-stock analyses was based on the following fishery management regions: lower summer, Tanana summer, Tanana fall, U.S. border, Porcupine, mainstem, White, and Teslin

(Table 1, Figure 1, Figure 2). These fishery management regions do not necessarily reflect genetic lineages, and the differences between the two are indicated in Figure 1. Where multiple tests of the same hypothesis were performed, a sequential Bonferroni method was used to maintain the overall alpha at 0.05 (Rice 1989). The data were checked for duplicated genotypes using the program microsatellite toolkit (Park 2001), and any duplicates were removed. The stocks and loci were assessed for conformance to Hardy-Weinberg and gametic phase equilibrium using the program GENETIX 4.05 (Belkhir et al. 2004). Estimates of percentage polymorphic loci (95%) and expected and observed heterozygosity were calculated for the stocks with GENETIX 4.05. The program FSTAT 2.9.3 (Goudet et al. 1995) was used to calculate estimates of allelic richness for loci and stocks, estimates of gene differentiation (G_{ST}) for loci, and expected and observed heterozygosity for loci. Estimates of effective number of alleles (Hartl and Clark 1997) for stocks and loci were calculated in Microsoft Excel™. A Mann-Whitney test (Conover 1999) was used to test for significant differences ($P < 0.05$) in observed levels of genetic diversity between summer and fall stocks.

Neighbor-joining analysis (Saitou and Nei 1987) was conducted on estimates of stock pairwise chord distances (Cavalli-Sforza and Edwards 1967) calculated from allele frequencies using PHYLIP 3.57 (Felsenstein 1993). Linear regression and lowess smoothing were conducted on pairwise matrices of genetic ($F_{ST}/(1-F_{ST})$; Reynolds et al. 1983) and geographic (river kilometer) distances to assess whether isolation-by-distance (IBD; Wright 1943) existed among the stocks overall and within and between seasonal races. To assess the effect of seasonal race on genetic distance, multiple regression analysis (Ryan 1997) was conducted with genetic distance dependent on both geographic distance and seasonal race, treated as a binary variable. Significance of the correlations was determined by the Mantel test (Mantel 1967) with 2,000 randomizations using FSTAT 2.9.3.

Stock pairwise tests of the homogeneity of allele frequencies were conducted with GENEPOP 3.4 (Raymond and Rousset 1995). Hierarchical likelihood ratio tests (G -test, Sokal and Rohlf 1995) were performed to assess the homogeneity of allelic frequencies among stocks within regions, among regions, and between seasons. Alleles were pooled if expected counts overall stocks were less than three in order to maintain the G -test's approximation of the χ^2 probability distribution (Sokal and Rohlf 1995). An approximate F -statistic was used to determine whether greater heterogeneity existed between or within seasonal races (Smouse and Ward 1978). The genetic variation resulting from stock heterogeneity was assigned to the hierarchical levels through gene diversity analysis (Nei and Chesser 1983; Chakraborty and Leimar 1987). Estimates of effective migration ($N_e m$) were calculated from the gene diversity statistics using a hierarchical island model (Zhivotovsky et al. 1994).

Because more loci were available than may be needed or practical for MSA applications, analyses were first conducted to identify a subset of informative loci. The effects of the number of alleles at a locus and the overall number of alleles on the accuracy and precision of stock composition estimates were assessed through MSA simulations by analyzing each locus individually and by sequentially adding loci. Using SPAM 3.7 (Debevec et al. 2000) or GMA (Kalinowski 2003), 100 mixtures ($N = 400$) were simulated for each region, and then, with bootstrap resampling of the baseline, the stock composition of each mixture was estimated by conditional maximum likelihood (CML). Region mixtures were comprised of equal propor-

tions of the stocks within the region. A Bayesian method (Rannala and Mountain 1997) was used to estimate allele frequencies in order to prevent sampling zeros. Overall mean stock composition estimates and their square root mean squared errors were recorded. Scatter plots with lowess trend lines were used to assess the relationships between the accuracy and precision of MSA estimates and the number of alleles. Also, an analysis was conducted to rank the loci in terms of combined, rather than individual, MSA simulation information content using BELS 0.2 (Bromaghin 2007) with the following parameters: maximize mean stock composition estimation accuracy, simulations conducted on regions with stocks contributing equally, baseline bootstrapped resampled with observed sample sizes, mixture sample size set to 200, and 100 replications per simulation.

After identifying a subset of loci, 100% MSA simulations were conducted to evaluate the accuracy and precision of their stock composition estimates. Simulations were conducted with SPAM 3.7, as described above, at the following hierarchical levels: individual stock, region, seasonal race, and country. Mean stock composition estimates and their standard deviations were tabulated. Individual stock composition estimates were summed to region, seasonal race, and country to ascertain patterns of misallocation. Simulations of multistock mixtures were also conducted using likely proportions in a lower river fishery. Additionally, two hundred Yukon River chum salmon samples of known origin and independent of the baseline were genotyped with the subset of loci and treated as a mixture. The stock compositions of this mixture were estimated using the baseline data and CML and Bayesian mixture modeling (Pella and Masuda 2001). The estimated stock compositions were compared to the actual compositions to ascertain the amount of bias present in a real mixture analysis.

Baseline application

Sample collection and laboratory analysis—Tissue samples were collected from every chum salmon caught in Pilot Station sonar test fisheries (Figure 1) and sent to the USFWS every third day and at the conclusion of a designated period. Samples were stratified by pulse of fish or time period, and a subsample size of 200, selected so that the daily sample size was proportional to the daily sonar passage estimate within a stratum, was genotyped for each stratum. The sample size for genetic analysis was determined through MSA simulations of 10% contributions for each of the regions using SPAM 3.7. The sample size of 200 was selected because it was the minimum that produced regional estimates with 90% confidence intervals that excluded 0. An estimate whose 90% confidence interval does not include 0 provides evidence that the stock is actually present in the mixture at the 5% level of significance (Weir 1996). In 2004, sampling began on the first day of the fall management season, July 19 at Pilot Station due to a 3 day travel lag, and ended on the final day of test fishing, August 31. The USFWS and DFOC independently analyzed the samples using their respective suites of loci in an effort to corroborate the results. Because fall chum salmon are present prior to the first day of the fall management season, sampling was expanded in 2005 (July 1–August 31) in order to have a greater likelihood of capturing the entire fall run, and only the USFWS analyzed the samples using the most informative loci identified above.

Data analysis—The stock compositions of the mixtures were estimated using the baseline data and Bayesian mixture modeling (Pella and Masuda 2001). The estimates were summed to seasonal race, region, and country and distributed to fishery managers. The stock composi-

tion for the entire sampling period was calculated by taking a weighted average of each stratum's estimate of stock composition based on the stratum's relative abundance for the entire period as determined from Pilot Station sonar passage estimates (Seeb et al. 1997). Stock specific abundance estimates were derived by combining the Pilot Station sonar passage estimates with the genetic stock composition estimates.

A post season analysis was conducted to compare the fall stock specific abundance estimates against escapement and harvest estimates to evaluate their concordance. Summer stock specific abundance estimates were not included in the analysis. Escapements from the following projects were compiled: upper Tanana River mark and recapture (JTC 2007), Kantishna River mark and recapture (JTC 2007), Chandalar River sonar (JTC 2007), Sheenjek River sonar (JTC 2007), Canada border mark and recapture (JTC 2007), and Porcupine River mark and recapture (JTC 2005, 2006). Harvest estimates (upriver of Pilot Station) by river location were obtained from a post season survey of subsistence fishers conducted by the Alaska Department of Fish and Game (ADFG; Busher et al. 2007; JTC 2007). It was assumed that fishers were unlikely to report a summer chum salmon as a fall chum salmon. Harvest was apportioned to the U.S. and Canada fall stocks in a stepwise upstream to downstream fashion by using the escapements to estimate the relative proportions of these stocks available at the river locations and multiplying these proportions by the harvest at the river locations. These stock specific harvest estimates were then added to the appropriate escapements in order to allow a direct comparison between data sources.

Results

Baseline development

There were 14 disagreements out of 1038 allele comparisons for an overall genotyping error rate of 1%, far exceeding the standard set forth by the Pacific Salmon Commission Chinook Technical Committee (Seeb et al. 2007). Primers for *Oki1* and *Ots2.1* each amplified two loci, which were labeled *Oki1U*, *Oki1L*, *Ots2.1U*, and *Ots2.1L*. Significant Hardy-Weinberg disequilibrium was observed in 10 out of 696 tests (1.4%), less than expected due to chance alone. None of the significant tests were common to any locus or stock, so all loci and stocks were deemed to be in Hardy-Weinberg equilibrium. Significant gametic phase disequilibrium was observed in 56 out of 6,699 tests (0.8%), again less than expected due to chance, but the correlation between *One101* and *One103* was significant in every stock whereas the other significant tests were randomly distributed. Therefore, this pair was the only one judged to be in disequilibrium, and *One101* was dropped from further analyses. Unless noted, the following analyses were conducted using 21 loci (Table 2).

Measures of locus diversity ranged widely (Table 2). Genetic diversity for stocks was moderate to high (Frankham et al. 2002) with allelic richness ranging from 6.5 to 9.8, effective number of alleles from 4.5 to 8.0, and expected heterozygosity from 0.645 to 0.700 (Table 3). There was a spatial and temporal trend in levels of genetic diversity among the stocks. Summer chum salmon stocks, which reside in the lower and middle portions of the Yukon River, had significantly higher levels of diversity ($P < 0.005$) than fall stocks, which reside in the middle and upper portions of the Yukon River.

Neighbor-joining analysis of CSE distances among the stocks also revealed a spatial and temporal component to the distribution of genetic diversity (Figure 2). Roughly, summer stocks were subdivided into lower and middle river regions while fall stocks were subdivided into Tanana River, border area, White River, and Teslin River regions. Mantel tests revealed significant correlations between genetic and geographic distance overall ($r = 0.584$, $P < 0.0001$, Figure 3a), within summer ($r = 0.471$, $P < 0.0001$, Figure 3b), within fall ($r = 0.308$, $P < 0.0001$, Figure 3c) and between seasons ($r = 0.497$, $P < 0.0001$, Figure 3d). Seasonal race was also significantly correlated with genetic distance ($r = 0.485$, $P < 0.0001$) and geographic distance ($r = 0.509$, $P < 0.0001$). The partial correlation of genetic and geographic distance was significant ($r_{yx1.x2} = 0.448$, $P < 0.0001$) as was the partial correlation of genetic distance and seasonal race ($r_{yx2.x1} = 0.269$, $P < 0.0001$). Most of the variation resulting from geographic distance and seasonal race was explained once geographic distance was fitted ($R^2_{yx1} = 0.341$); nonetheless, a significant amount of information was accounted for by seasonal race, which increased explained variation to $R^2 = 0.389$. The overall and between seasonal races scatter plots revealed a pattern of increasing spread from the origin of the plot in a positive, monotonic fashion (Figure 3a,d), which suggested an equilibrium between gene flow and genetic drift (Hutchinson and Templeton 1999).

Significant allelic frequency heterogeneity was observed in 367 of the 406 pairwise tests (Table 4) and for all hierarchical levels (Table 5). Greater heterogeneity existed between seasonal races, approximately 12 times that found within seasonal races ($F_{92, 2484} = 12.03$, $P < 0.0001$). The relative magnitude of genetic variation among stocks was relatively low at 1.57% (Table 6), with 0.43% between summer and fall seasons, 0.38% among stocks within regions, and 0.76% among regions within seasons. Estimates of gene flow were high and ranged from 14.4 migrants per generation among regions within seasons to 65.0 migrants per generation among stocks within regions (Table 6). The above analyses appeared to offer contrasting views on the differences between seasonal races. This illustrates that all analyses have strengths and weaknesses, and that it is appropriate to conduct a variety of analyses to achieve a more complete understanding of the genetic relationships.

Accuracy and precision of stock composition estimates improved with the number of alleles at a locus (Figure 4) and total number of alleles in the analysis (Figure 5). Estimate improvement leveled off at 20 alleles for a locus and at 200 total alleles. Approximately 300 total alleles were required to reach 90% accuracy. Loci with 20 or more alleles were also generally ranked higher in terms of MSA information content by BELS 0.2 (Table 7).

A subset of 12 informative loci was selected (Table 7), totaling 347 alleles, and further evaluated for MSA. Simulation accuracies and standard deviations for individual stocks varied between 65.0% (5.0%) and 99% (1.0%), with the Toklat, Fishing Branch, Kluane, and Teslin stocks above 90% accuracy (individual stock results not shown). Accuracies and standard deviations improved when individual stock proportions were summed to higher hierarchical levels (Table 8) and when simulations were conducted at higher hierarchical levels (Table 9). Overall, misallocation mostly occurred among geographically proximate and genetically similar stocks, precluding the need for an exhaustive baseline for regional based MSA (Beacham et al. 2003). Stock composition estimates from simulations of multistock mixtures were within 8% of the expected value (Table 10). In the known mixture analysis,

stock composition estimates were within 10% of the expected value using Bayesian analysis and 17% using CML analysis (Table 11).

Baseline application

In 2004, identical samples for the buildup period, as the run transitioned from summer to fall, and five pulses were analyzed by both the USFWS and DFOC. Stock composition estimates were similar between the two agencies, with 41 out of 48 estimates within one standard deviation (Figure 6). During the buildup period (7/19/04–8/2/04) there was still a large component of summer run chum salmon in the test fishery harvests, with the USFWS and DFOC estimating a contribution of 43% and 42%, respectively, for the combined lower and Tanana summer regions. For Canada, Porcupine region fall chum salmon appeared to have the earliest return time, followed by fall chum salmon from the mainstem and White regions, while Teslin region fall chum salmon were not an appreciable contributor. U.S. border region fall chum salmon were fairly constant throughout the run with contributions ranging from 15% to 35%, while Tanana region fall chum salmon continued to increase their contribution throughout the run and comprised the majority of the final pulse. Overall, Tanana region fall chum salmon were the largest contributor to the fall run (Table 12).

Given the congruent results in 2004, only the USFWS provided stock composition estimates in 2005, for which two preseason periods and four pulses were analyzed (Figure 7). Fall chum salmon from the U.S. border and Porcupine regions were the first to return and started to enter the Yukon River during preseason 2 (7/10/05–7/18/05). Fall chum salmon from the Porcupine region were almost nonexistent by pulse 2 whereupon fall chum salmon from the mainstem and White regions strengthened in numbers. Tanana region fall chum salmon started to slowly enter in pulse 1 and gradually increased until comprising the largest portion of the final pulse. U.S. border region fall chum salmon were sustained throughout the run and were the largest overall contributor to the fall run (Table 12).

The post season comparison with the escapement and harvest data was performed using the stock composition estimates from the USFWS (Table 13, 14) and the Pilot Station sonar passage estimates (Table 15). Overall stock abundance based on the products of estimates of genetic stock composition and Pilot Station sonar passage ranged (in thousands) from 2 to 517 in 2004 and from 44 to 2,528 in 2005 (Table 16). Escapement totals from the upriver monitoring projects ranged (in thousands) from 38 to 200 in 2004 and 97 to 496 in 2005 (Table 17). Subsistence harvests from the fishing districts, upriver of Pilot Station, were added to the escapement totals (Table 18). The stock abundance estimates from the escapement and harvest data were in close agreement with those from the genetic and sonar data (Figure 8).

Discussion

Baseline development

Yukon River chum salmon exhibit genetic divergence. The relative magnitude of the divergence, however, is small ($G_{ST}=0.016$), less than has been observed in Yukon River Chinook ($G_{ST}=0.036$; Flannery et al. 2006a) and coho ($G_{ST}=0.103$; Flannery et al. 2006b) salmon. Restricted gene flow exists on temporal and spatial scales, with stocks genetically associated

by seasonal race and geographic region. This genetic structure has also been observed in previous studies of Yukon River chum salmon (Wilmot et al. 1994; Scribner et al. 1998; Seeb and Crane 1999a; Flannery et al. 2007a), though microsatellite loci do provide greater stock resolution than allozyme loci, revealing divergence among previously indistinct stocks, such as between the Sheenjek and Fishing Branch stocks (Crane et al. 2001). Hierarchical likelihood ratio analysis indicates that seasonal race heterogeneity is responsible for the primary subdivision. The between seasons component accounts for 12 times more heterogeneity than within, suggesting a significant barrier to gene flow. However, this analysis pools data, resulting in lost information, and though seasonal race is likely the major subdivision overall, finer scale analysis reveals that gene flow between seasons occurs according to the IBD model (Figure 3d), supporting the indirect estimates of gene flow from G_{ST} -statistics. Moreover, the IBD model adequately explains the distribution of genetic variation. Fitting the data to the isolation-by-time (IBT) model only accounted for a small increase of explained variation because seasonal race is geographically structured. Although the IBD analysis reveals that gene flow does occur between seasons, it further confirms that seasonal race is the oldest subdivision because sufficient time has elapsed to reach equilibrium between genetic drift and gene flow between seasons but not within them (Hutchinson and Templeton 1999).

The discrepancy between analyses likely results from differential effects of seasonal gene flow through differing overlaps of spawning times among stocks of summer and fall chum salmon (Coulson et al. 2006; Olsen et al. 2006). The neighbor-joining dendrogram suggests an intermediate relationship among summer and fall stocks in the middle Yukon River, with a polarity between lower river summer and upper river fall stocks (Figure 2). Moreover, there is evidence of a cline in Yukon River chum salmon (Crane et al. 2001), which can result from gene flow from two stocks, through a chain of stocks. The significant IBD between summer and fall chum salmon suggests that this is occurring. Such a relationship is not unexpected in such a large watershed (855,000 square kilometers) without fragmentation because larger systems are less subject to demographic perturbations (Reeves et al. 1995). Clinal relationships have been found in watersheds greater than 350 square kilometers but not in smaller drainages, which may be more prone to genetic drift (Li et al. 1995). Absence of lingering effects from historical range expansion and fragmentation events and the identification of restricted gene flow in a mitochondrial DNA study of Yukon River chum salmon (Flannery et al. 2007b) lend further support for the estimates of gene flow and stock structure derived from this study.

The spatial and temporal trends in genetic diversity suggest differences in gene flow and genetic drift between seasonal races. The diversity estimates indicate less gene flow, greater genetic drift, or both occur for fall chum salmon, and the reverse for summer chum salmon. These results conform to expectations based on geographic isolation, stock sizes, and habitat stability. In contrast to summer chum salmon, fall chum salmon spawn at discrete sites after extensive freshwater migrations. Stocks experiencing greater isolation will see reductions in gene flow in an IBD model (Wright 1943) and genetic diversity (Wahlund 1928). Less genetic drift would be expected in summer chum salmon if census size corresponds to effective population size (N_e), which reduces divergence and loss of genetic diversity. Considering that the mouth of the Yukon River was once much farther south and has maintained its present course for only a few thousand years (Lindsay and McPhail 1986), greater gene flow

would also be expected in summer chum salmon because habitat instability may engender greater straying and subsequent gene flow to ensure survival (Quinn 1984). Indeed, allozyme data reveal that upper Yukon River fall chum salmon are distinct while a close relationship exists between summer chum salmon of lower Yukon River and Western Alaska (Seeb and Crane 1999a), suggesting extensive gene flow, restricted to the lower Yukon River. Similar genetic diversity trends have been observed in Yukon River coho (Flannery et al. 2006b) and Chinook (Olsen et al. in review) salmon, reinforcing the effect of isolation on stocks residing in the upper Yukon River.

However, isolation has not adversely affected fall chum salmon. Levels of genetic diversity for both seasonal races are high, signifying strong evolutionary potential (Frankham et al. 2002). Lower Yukon River summer chum salmon and their connectivity with Western Alaska chum salmon constitute a large reserve of genetic diversity. This reserve may be an important source that fall chum salmon draw from by way of mediated gene flow through the middle river stocks, as indicated by the IBD results, to bring in diversity and maintain genetic health (Gharrett and Zhivotovsky 2003).

Genetic divergence, marker resolution, and sample size play important roles in the success of MSA (Pella and Milner 1987). Results from this study and others (Kalinowski 2004; Beacham et al. 2005, 2006) reveal that loci with greater variability provide more resolution to identify stocks in mixtures. However, despite selecting the most variable and informative loci, the relatively low level of genetic divergence among stocks due to high gene flow limits MSA to regions in most cases, as does the lack of a completely comprehensive baseline. Toklat, Fishing Branch, Kluane and Teslin are exceptions as they meet or exceed 90% MSA simulation accuracy, a threshold where stocks are considered highly identifiable in actual fishery mixtures (Seeb and Crane 1999b). Possible reasons for these stocks performing so well include genetic divergence and sample size. The Kluane and Teslin stocks are very divergent because of possible founder effects (Wilmot et al 1994; Flannery et al. 2007a) while larger sample sizes have likely aided Toklat ($N=250$) and Fishing Branch ($N=481$) by increasing statistical power.

In response to low genetic divergence among stocks, additional variable loci and samples may improve resolution. Although even with over 300 alleles in the analysis, allocation accuracy estimates to the U.S. border and Canada mainstem regions do not exceed 90% (Table 9), and increasing the number of alleles as high as 535 in simulation analyses did not improve the estimates (results not shown). This reflects that the country-of-origin division is political, not biological. Thus, sample sizes for the U.S. border and Canada mainstem regions will also need to be increased, considering the results for Fishing Branch, which improved from 79% allocation accuracy (Flannery et al. 2007a) to 91% by both adding highly variable loci and increasing sample size from 96 to 481. Nevertheless, the accuracies for the two regions are $\geq 80\%$, and the multistock simulations indicate that accurate estimates, within 8% of actual, for these regions in mixtures are possible. Moreover, the known mixture results demonstrate that CML is less accurate than Bayesian mixture modeling, as do other studies (Pella and Masuda 2001; Bolker et al. 2003; Beacham et al. 2005), so these MSA simulations accuracies are considered a minimum. The computational time of Bayesian mixture modeling prevents similar simulation analyses, but Bayesian allocation accuracies are anticipated to be much

higher. Therefore, the Bayesian method was used to estimate the stock compositions of real fishery mixtures.

Despite indications from simulations that accurate MSA estimates are possible, the intermediate nature of some middle river stocks and differences between management and genetic regions (Table 1, Figure 1) are potential troubling points for management. The misallocation of the intermediate middle river stocks, most notable for Big Salt (12% to summer) and South Fork Koyukuk late run (10% to fall), should not significantly bias actual fishery MSA estimates because these are minor contributing stocks. However, management regions that do not align with genetic regions may bias MSA estimates, which the known mixture analysis demonstrates with a 10% misallocation between the lower and Tanana summer regions. Lower summer includes stocks of middle river origin, and further analysis of the known mixture reveals that the misallocation is to those middle river stocks (results not shown). When the summer regions are realigned according to the genetic regions, the estimates are within 2% of expected. The division of the genetic border region into three management regions is another area of concern, particularly for the U.S. border region, which has the largest misallocation in simulations. Known mixture analyses involving samples from these management regions would be useful to further assess the bias of MSA estimates. Though the real test is to apply the baseline to actual fishery mixtures and determine whether the results are sensible because bias can still occur if the baseline is not complete, which simulations and known mixture analyses may not elucidate.

Baseline application

A major concern in baseline application to an actual fishery is ensuring random, representative sampling in order to provide unbiased stock composition estimates. Commercial and subsistence fisheries are sporadic in time, space, and level of effort, and, thus, are not necessarily representative of the run. Test fisheries, however, provide a consistent platform on which to estimate stock compositions and timing while allowing for predictions of stock compositions for subsistence and commercial harvests (Shaklee and Phelps 1990). Test fisheries operate at various locations in the lower Yukon River, but the one at Pilot Station sonar has several advantages for providing a random sample of the run as it employs a variety of mesh sizes at a location where the river flows in a single channel. Furthermore, this location simplifies the integration of the stock composition and sonar passage estimates. Although the Big Eddy and Middle Mouth test fisheries, located at the mouth, facilitate more timely stock composition estimates, collecting a random sample is problematic because there are multiple channels, and only three are covered by these test fisheries. If the stocks are not fully mixed prior to entering the Yukon River and stocks enter the river in different mouths, then MSA estimates will not account for the entire run. In addition, test fisheries at the mouth only use a single mesh size, which would contribute to non-random sampling if differences in size exist among the stocks.

Varying Yukon River chum salmon stock proportions were observed in MSA of Pilot Station sonar test fishing samples. Stock composition estimates reveal that a considerable proportion of both fall and summer chum salmon are observed before and after July 16 (Wilmot et al. 1992; ADFG 2003; present study), the break in management dates, suggesting a range, rather than a specific date, for the transition from the summer to fall run. Chum salmon of U.S.

origin consistently comprise approximately two-thirds of the fall run, but within the U.S., fall chum salmon from the Tanana and U.S. border regions return in varying proportions. Within Canada, fall chum salmon from the border region, encompassing the Porcupine and mainstem regions, consistently return in greater proportion than those from the upper region, encompassing the White and Teslin regions (Table 12; Wilmot et al. 1992; Spearman and Miller 1997). However, the ratio of proportions for fall chum salmon from the Canada border and upper Canada regions has shifted considerably. Wilmot et al. (1992) and Spearman and Miller (1997) report Canada border fall chum salmon proportions 2.8 to 4.7 times larger than upper Canada. We found Canada border fall chum salmon proportions to be only 1.3 to 1.6 times larger. This change may be a statistical artifact or may suggest a shift in regional production within Canada, possibly due to an adaptive advantage for upper Canada fall chum salmon in response to a changing environment (Kruse 1998). A similar shift in production exists in summer chum salmon, with Anvik decreasing from approximately 50% to 30% contribution to the summer run (Clark et al. 2006). The Tanana and U.S. border regions have the largest proportions of fall chum salmon, as expected, as these regions are the most productive (Buklis and Barton 1984). No specific trend appears for fall chum salmon from these regions as the ratio of their proportions varied similarly in all studies, from 0.4 to 2.3 for Tanana and 0.7 to 2.8 for the U.S. border, suggesting a natural variance associated with their abundance.

The data suggest that stocks exhibit different run timing and migratory patterns, which are important life history traits under stabilizing selection to ensure optimal reproductive success and recruitment (Hallerman 2003). Corresponding to expectations (Buklis and Barton 1984; Wilmot et al. 1992; Spearman and Miller 1997), fall chum salmon from the Porcupine and U.S. border regions are the first to migrate, followed by those from the mainstem and White River, and lastly the Tanana. The size of the stock appears to have an effect on the migratory pattern. Large stocks generally exhibit a more sustained run while smaller stocks tend to be more pulse-like. This difference is likely related to substructure within larger stocks. The sustained, even return of the U.S. border region suggests a make-up of stock components of similar size, whereas the slow buildup towards a peak suggests that the Tanana region is composed of dissimilarly sized stocks. This hypothesis does correspond with escapement data (Bue et al. 2006).

Further correspondence with escapement data is found in the comparison of stock abundance estimates to upriver escapement and harvest estimates (Figure 8), although it appears that either Pilot Station sonar is underestimating or upriver escapement projects are overestimating the total upriver passage of fish. In 2004, MSA did not begin until the start of the fall management season and, therefore, did not encompass the entire fall run because of run timing variance (Wilmot et al. 1992; ADFG 2003; present study), so underestimation by Pilot Station sonar is not unexpected. Underestimation may also result from genetic misallocation, from fall chum salmon passing the Pilot Station sonar undetected because of incomplete sonar coverage, from fall chum salmon migrating after Pilot Station sonar shuts down, from error introduced by the species apportionment test fishing program, and error from the genetic subsampling of the test fish (Carl Pfsister, pers. comm.). Conversely, the upriver escapement projects have associated error as well, but while all the projects are subject to error and none can be held as the standard, their generally close agreements substantiate one another.

Fishery Management Implications

The agreement between projects, in conjunction with the comparable stock proportions and timings with expectations from other studies, suggest that MSA along with lower river sonar are credible tools for estimating stock proportions and abundances. Additionally, the congruent results between the USFWS and DFOC, utilizing different baseline samples and loci, reveal the robustness of the method. The combination of MSA and sonar abundance provides a convenient and cost effective method to monitor all stocks simultaneously, assisting fishery managers in meeting escapements and harvesting at sustainable rates in order to maintain the productivity and evolutionary potential of Yukon River chum salmon. Moreover, MSA and sonar can provide data on total stock-specific returns for a more complete run reconstruction, allowing for improved escapement goals based on a thorough analysis of the stock dynamics.

Of particular relevance to fall chum salmon management is the run timing variance. Fall chum salmon fisheries are managed based on the projected run size, determined through preseason projections, lower river test fishing indices, and Pilot Station sonar passage. The fall run must reach certain abundance levels for fisheries to occur, but basing decisions on the abundance of chum salmon after the switch to fall management can be misleading because significant numbers of summer chum salmon are still observed, biasing the fall chum salmon projection high and potentially leading to the prosecution of unwarranted fisheries.

Project Objectives Assessment

- 1) Complete baseline sample processing.

The baseline sample processing was completed as described above.

- 2) Perform MSA on samples of known origin.

Samples of known origin were subjected to MSA and results are given above.

- 3) Estimate regional stock contributions and run timing from lower river test fishery harvests.

Regional stock contributions were estimated for Yukon River chum salmon from samples collected in the Pilot Station sonar test fishery. Estimates were distributed to fishery managers during the fishing season and are reported above along with run time information.

Conclusions

- 1) Yukon River chum salmon exhibit a relatively low degree of stock structure relative to Yukon River Chinook and coho salmon.
- 2) Fall chum salmon have lower levels of genetic diversity and greater structure than summer chum salmon.
- 3) Accurate apportionments of chum salmon to country, run, and region are possible from fishery mixtures through genetic MSA.
- 4) Mixed-stock analysis in conjunction with sonar estimates correspond to escapement and harvest data and, therefore, can be used as a management tool to monitor stocks.

Recommendations

- 1) Increase sample sizes for the following stocks of the U.S. border and Canada mainstem regions: Big Salt, Chandalar, Black, Sheenjek, Pelly, Big Creek, Minto, and Tatchun.
- 2) Continue to add samples and new stocks to the baseline as opportunities arise.

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Table 1. Stock location, stock label, seasonal race, management region, genetic region, country, sample collection years, and number of fish sampled (*N*) from 29 putative Yukon River chum salmon stocks.

Stock	Label	Seasonal Race	Management Region	Genetic Region	Country	Year	<i>N</i>
Andreafsky	1	Summer	Lower	Lower	U.S.	1987, 2004	261
Chulinak	2	Summer	Lower	Lower	U.S.	1989	100
Anvik	3	Summer	Lower	Lower	U.S.	1988	100
California	4	Summer	Lower	Lower	U.S.	1997	50
Nulato	5	Summer	Lower	Lower	U.S.	2003	100
Gisasa	6	Summer	Lower	Lower	U.S.	2003	200
Henshaw	7	Summer	Lower	Middle	U.S.	2003	200
Jim	8	Summer	Lower	Middle	U.S.	2002	160
S.F. Koyukuk Early	9	Summer	Lower	Middle	U.S.	1996	100
S.F. Koyukuk Late	10	Summer	Lower	Middle	U.S.	1996	100
Melozitna	11	Summer	Lower	Lower	U.S.	2003	146
Tozitna	12	Summer	Lower	Middle	U.S.	2002	200
Chena	13	Summer	Tanana	Middle	U.S.	1992, 1994	186
Salcha	14	Summer	Tanana	Middle	U.S.	1994, 2001	185
Delta	15	Fall	Tanana	Tanana	U.S.	1990	80
Kantishna	16	Fall	Tanana	Tanana	U.S.	2001	161
Toklat	17	Fall	Tanana	Tanana	U.S.	1990, 1994	250
Big Salt	18	Fall	U.S. Border	Border	U.S.	2001	71
Chandalar	19	Fall	U.S. Border	Border	U.S.	1989, 2001	338
Sheenjek	20	Fall	U.S. Border	Border	U.S.	1987, 1988, 1989	263
Black	21	Fall	U.S. Border	Border	U.S.	1995, 2001	112
Fishing Branch	22	Fall	Porcupine	Border	Canada	1987, 1989, 1992, 1994, 1997	481
Big Creek	23	Fall	Mainstem	Border	Canada	1992, 1995	200
Minto	24	Fall	Mainstem	Border	Canada	1989, 2002	166
Pelly	25	Fall	Mainstem	Border	Canada	1993	84
Tatchun	26	Fall	Mainstem	Border	Canada	1987, 1992	175
Donjek	27	Fall	White	White	Canada	1994	72
Kluane	28	Fall	White	White	Canada	1987, 1992, 2001	462
Teslin	29	Fall	Teslin	Teslin	Canada	1992, 2001	143

Table 2. Results across all stocks for each locus: number of alleles, allelic richness (A_R), effective number of alleles (A_E), unbiased expected heterozygosity (H_E), observed heterozygosity (H_O), and measure of stock divergence (G_{ST}).

Locus	Alleles	A_R	A_E	H_E	H_O	G_{ST}
<i>Oke8</i>	2	1.7	1.1	0.066	0.066	0.009
<i>Ots2.1L</i>	3	2.0	1.2	0.141	0.139	0.011
<i>Oki23.1</i>	4	2.9	1.7	0.392	0.397	0.020
<i>Oki1L</i>	5	2.4	1.9	0.461	0.472	0.034
<i>Oke4</i>	6	2.2	1.1	0.122	0.122	0.011
<i>Oke11</i>	7	4.4	2.4	0.574	0.570	0.007
<i>Oke3</i>	8	4.6	2.9	0.648	0.647	0.023
<i>Ots2.1U</i>	9	3.2	2.3	0.572	0.568	0.008
<i>Ssa419</i>	16	8.9	6.5	0.848	0.872	0.009
<i>Oki1U</i>	20	11.5	7.6	0.865	0.852	0.019
<i>Ots3.1</i>	20	6.6	3.4	0.698	0.689	0.024
<i>Oki2</i>	21	9.3	5.7	0.793	0.793	0.047
<i>Oki100</i>	24	11.0	6.5	0.837	0.832	0.012
<i>One104</i>	30	14.3	10.8	0.907	0.904	0.010
<i>Omy1011</i>	32	14.2	10.8	0.908	0.901	0.013
<i>One103</i>	37	11.9	7.5	0.864	0.870	0.014
<i>Ots103</i>	38	17.2	14.8	0.935	0.908	0.010
<i>One102</i>	38	11.3	9.5	0.898	0.860	0.008
<i>Ots68</i>	41	14.6	11.9	0.915	0.914	0.011
<i>One114</i>	45	12.0	9.4	0.891	0.900	0.010
<i>One111</i>	129	19.2	8.3	0.854	0.835	0.016

Table 3. Results for each stock across all loci: mean sample size (N), percentage polymorphic loci at the 95% criterion ($\%P$), allelic richness (A_R), effective number of alleles (A_E), unbiased expected heterozygosity (H_E), and observed heterozygosity (H_O). The N listed here indicates the mean number of samples across loci where data were successfully collected, which may differ from the N in Table 1. Stock names can be found in Table 1.

Stock	N	$\%P$	A_R	A_E	H_E	H_O
1	221	95.2	9.8	8.0	0.691	0.680
2	91	95.2	9.3	7.0	0.688	0.679
3	136	95.2	9.8	7.9	0.700	0.704
4	43	90.5	9.3	6.7	0.692	0.700
5	95	90.5	9.6	7.4	0.685	0.686
6	150	95.2	9.7	7.7	0.691	0.697
7	168	95.2	9.4	7.1	0.692	0.691
8	152	95.2	8.5	6.0	0.677	0.675
9	86	95.2	8.8	6.1	0.680	0.654
10	98	100.0	8.5	5.8	0.684	0.683
11	132	95.2	9.7	7.7	0.697	0.690
12	178	100.0	9.4	7.2	0.697	0.690
13	222	95.2	8.4	5.7	0.668	0.668
14	174	90.5	8.4	5.5	0.672	0.680
15	76	85.7	7.6	5.0	0.647	0.642
16	155	85.7	7.9	5.4	0.660	0.662
17	241	90.5	8.0	5.4	0.666	0.655
18	57	95.2	8.4	5.8	0.686	0.679
19	249	95.2	8.1	5.7	0.672	0.651
20	220	95.2	8.1	5.7	0.665	0.650
21	105	95.2	8.1	5.5	0.682	0.689
22	416	95.2	7.9	5.5	0.676	0.666
23	184	95.2	7.9	5.6	0.673	0.665
24	152	95.2	8.0	5.7	0.671	0.662
25	67	95.2	7.4	5.1	0.658	0.667
26	158	95.2	7.8	5.4	0.665	0.658
27	65	90.5	6.5	4.5	0.645	0.660
28	449	95.2	7.2	5.2	0.661	0.662
29	135	90.5	7.1	4.7	0.654	0.647

Table 4. Stock pairwise tests of allele frequency homogeneity. * = significant test ($P < 0.05$); NS = not significant. Reference Table 1 for stock names.

Stock	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29		
1																															
2	NS																														
3	NS	NS																													
4	*	NS	*																												
5	NS	NS	NS	*																											
6	NS	NS	NS	*	NS																										
7	*	NS	NS	*	NS	NS																									
8	*	*	*	*	*	*	*																								
9	*	*	*	*	*	*	NS	*																							
10	*	*	*	*	*	*	*	NS	*																						
11	NS	NS	NS	*	NS	NS	NS	*	*	*																					
12	*	NS	NS	*	NS	*	NS	*	*	NS	*																				
13	*	*	*	*	*	*	*	*	*	*	*	*																			
14	*	*	*	*	*	*	*	*	*	*	*	*	NS																		
15	*	*	*	*	*	*	*	*	*	*	*	*	*	*																	
16	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*																
17	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*															
18	*	*	*	*	*	*	*	NS	*	NS	*	*	*	*	*	*	*														
19	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	NS													
20	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	NS	NS												
21	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	NS	*												
22	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*											
23	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*									
24	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	NS							
25	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
26	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	NS	NS	*	*	*	*	*	
27	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
28	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	NS	*	
29	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	

Table 5. Hierarchical tests of homogeneity based on 21 loci.

Source of variation	Total df	Total G-test
Summer Lower	552	659.9*
Middle	552	1381.4*
Within Summer	1104	2041.2*
Among Summer	92	1274.8*
Total Summer	1196	3316.0*
Fall Tanana	184	377.5*
Border	736	1496.7*
White	92	140.0*
Teslin	No test	
Within Fall	1012	2014.1*
Among Fall	276	6658.5*
Total Fall	1288	8672.6*
Within seasons	2484	11988.6*
Between seasons	92	5342.0*
Total	2576	17330.6*

* $P < 0.05$

Table 6. Hierarchical gene diversity analysis based on 21 loci.

Source of variation	Gene diversity	G_{ST} -statistics	N_e
Average within stocks	$H_S=0.6758$	$H_S/H_T=0.9843$	
Average among stocks, within regions	$D_{SR}=0.0026$	$G_{SR}=0.0038^*$	65.0
Average among regions, within seasons	$D_{RC}=0.0052$	$G_{RC}=0.0076^*$	14.4
Average between seasons	$D_{CT}=0.0029$	$G_{CT}=0.0043^*$	14.6
Total gene diversity	$H_T=0.6866$	$G_{ST}=0.0157^*$	15.6

* $P < 0.05$

Table 7. Ranking of loci in terms of mixed-stock analysis (MSA) of information content, loci in bold lettering were retained for MSA applications.

Rank	Locus	No. Alleles
1	OkiIU	20
2	Ots103	38
3	Oki2	21
4	Omy1011	32
5	One103	37
6	Ots68	41
7	Oki100	24
8	Oke3	8
9	Ots3.1	20
10	Ssa419	16
11	One104	30
12	One102	38
13	One114	45
14	One111	129
15	Ots2.1L	3
16	Oki23.1	4
17	OkiIL	5
18	Ots2.1U	9
19	Oke11	7
20	Oke8	2
21	Oke4	6

Table 8. Results of allocations of individual stocks to management region, run, and country-of-origin from mixed-stock analysis of simulated mixtures developed from baseline data collected at 12 microsatellite loci. Each baseline stock was used to simulate a mixture of 400 fish. The mixture and baseline were bootstrapped 100 times. A 100% allocation to the region containing the individual stock would indicate perfect baseline performance. Allocation estimates are given above, with standard deviations below. Allocation estimates in bold indicate correct allocation.

Stock	Lower	Tanana		US Border	Porcupine	Mainstem	White	Teslin	Summer	Fall	US	Canada
		Summer	Fall									
1	0.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	1.00	0.00
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	0.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.99	0.01	1.00	0.00
	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
3	0.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.99	0.01	1.00	0.00
	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00
4	0.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.99	0.01	1.00	0.00
	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
5	0.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	1.00	0.00
	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
6	0.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	1.00	0.00
	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
7	0.97	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.99	0.01	1.00	0.00
	0.02	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00
8	0.86	0.07	0.02	0.03	0.01	0.01	0.00	0.00	0.93	0.07	0.98	0.02
	0.03	0.03	0.01	0.02	0.01	0.01	0.00	0.00	0.02	0.02	0.01	0.01
9	0.87	0.08	0.02	0.01	0.01	0.00	0.00	0.00	0.95	0.05	0.99	0.01
	0.03	0.03	0.01	0.01	0.01	0.00	0.00	0.00	0.02	0.02	0.01	0.01
10	0.85	0.06	0.04	0.03	0.01	0.02	0.00	0.00	0.90	0.10	0.98	0.02
	0.04	0.02	0.02	0.02	0.01	0.01	0.00	0.00	0.03	0.03	0.01	0.01
11	0.99	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.99	0.01	1.00	0.00
	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Continued

Table 8. Continued

Stock	Lower	Tanana		US Border	Porcupine	Mainstem	White	Teslin	Summer	Fall	US	Canada
		Summer	Fall									
12	0.97	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.99	0.01	1.00	0.00
	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00
13	0.05	0.92	0.02	0.01	0.00	0.00	0.00	0.00	0.97	0.03	1.00	0.00
	0.02	0.02	0.01	0.01	0.00	0.00	0.00	0.00	0.02	0.02	0.01	0.01
14	0.05	0.93	0.01	0.01	0.00	0.00	0.00	0.00	0.98	0.02	1.00	0.00
	0.02	0.02	0.01	0.01	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00
15	0.03	0.01	0.90	0.03	0.01	0.01	0.00	0.00	0.04	0.96	0.97	0.03
	0.01	0.01	0.02	0.01	0.01	0.01	0.00	0.00	0.01	0.01	0.01	0.01
16	0.02	0.01	0.95	0.01	0.00	0.00	0.00	0.00	0.03	0.97	0.99	0.01
	0.01	0.01	0.02	0.01	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.01
17	0.03	0.02	0.94	0.01	0.00	0.01	0.00	0.00	0.04	0.96	0.99	0.01
	0.01	0.01	0.02	0.01	0.00	0.01	0.00	0.00	0.02	0.02	0.01	0.01
18	0.09	0.03	0.02	0.78	0.05	0.03	0.00	0.00	0.12	0.88	0.92	0.08
	0.03	0.02	0.01	0.04	0.02	0.02	0.00	0.00	0.03	0.03	0.02	0.02
19	0.03	0.01	0.01	0.87	0.04	0.04	0.00	0.00	0.03	0.97	0.91	0.09
	0.01	0.01	0.01	0.03	0.02	0.02	0.00	0.00	0.01	0.01	0.02	0.02
20	0.01	0.01	0.01	0.89	0.06	0.03	0.00	0.00	0.02	0.98	0.91	0.09
	0.01	0.01	0.01	0.03	0.02	0.02	0.00	0.00	0.01	0.01	0.03	0.03
21	0.02	0.01	0.01	0.86	0.06	0.04	0.00	0.00	0.03	0.97	0.90	0.10
	0.01	0.01	0.01	0.03	0.03	0.02	0.00	0.00	0.01	0.01	0.03	0.03
22	0.01	0.00	0.00	0.04	0.91	0.04	0.00	0.00	0.01	0.99	0.05	0.95
	0.00	0.00	0.00	0.02	0.03	0.02	0.00	0.00	0.00	0.00	0.02	0.02
23	0.01	0.00	0.00	0.03	0.04	0.91	0.00	0.00	0.01	0.99	0.05	0.95
	0.01	0.00	0.00	0.02	0.02	0.02	0.00	0.00	0.01	0.01	0.02	0.02

Continued

Table 8. Continued

Stock	Lower	Tanana		US Border	Porcupine	Mainstem	White	Teslin	Summer	Fall	US	Canada
		Summer	Fall									
24	0.01	0.00	0.00	0.04	0.05	0.88	0.00	0.00	0.02	0.98	0.06	0.94
	0.01	0.00	0.01	0.02	0.02	0.03	0.00	0.00	0.01	0.01	0.02	0.02
25	0.02	0.00	0.01	0.06	0.04	0.87	0.00	0.00	0.03	0.97	0.09	0.91
	0.01	0.00	0.01	0.03	0.02	0.03	0.00	0.00	0.01	0.01	0.03	0.03
26	0.01	0.00	0.00	0.04	0.04	0.90	0.00	0.00	0.01	0.99	0.06	0.94
	0.01	0.00	0.00	0.02	0.02	0.03	0.00	0.00	0.01	0.01	0.02	0.02
27	0.01	0.00	0.00	0.01	0.01	0.01	0.96	0.00	0.01	0.99	0.02	0.98
	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.01	0.01	0.01	0.01
28	0.00	0.00	0.00	0.00	0.00	0.00	0.99	0.00	0.00	1.00	0.00	1.00
	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
29	0.01	0.00	0.00	0.01	0.00	0.03	0.00	0.94	0.01	0.99	0.02	0.98
	0.01	0.00	0.00	0.01	0.00	0.01	0.00	0.02	0.01	0.01	0.01	0.01

Table 9. Results of allocations from mixed-stock analysis of simulated mixtures developed from region, run, and country-of-origin baseline data collected at 12 microsatellite loci. Each simulated mixture (N=400) was composed of equal proportions of stocks within the management group. The mixture and baseline were bootstrapped 100 times. Allocation estimates and standard deviations are given.

	Estimate	SD
Summer	0.97	0.01
Lower	0.94	0.02
Tanana	0.91	0.02
Fall	0.95	0.02
Tanana	0.92	0.02
U.S. Border	0.80	0.04
Canada Border	0.91	0.03
Mainstem	0.87	0.03
Porcupine	0.91	0.03
Upper	0.96	0.01
White	0.98	0.01
Teslin	0.94	0.02
Fall U.S.	0.84	0.03
U.S.	0.97	0.02
Canada	0.95	0.02
U.S. Border + Canada	0.96	0.01
Mainstem + Upper	0.91	0.03

Table 10. Results of allocations from mixed-stock analysis of simulated multistock mixtures that may be encountered in a lower Yukon River fishery. Each management group represented in the simulated multistock mixtures was composed of equal proportions of stocks within the management group. Mixture sample size was 400. The mixture and baseline were bootstrapped 100 times. Allocation estimates (SD) are given.

	Mix 1		Mix 2	
	Expected	Estimate	Expected	Estimate
Summer	0.15	0.21 (0.03)	0.43	0.47 (0.03)
Lower	0.13	0.17 (0.03)	0.38	0.40 (0.03)
Tanana	0.02	0.04 (0.02)	0.05	0.07 (0.02)
Fall	0.85	0.79 (0.03)	0.57	0.53 (0.03)
Tanana	0.32	0.27 (0.03)	0.12	0.10 (0.02)
U.S. Border	0.25	0.22 (0.03)	0.27	0.22 (0.03)
Canada Border	0.17	0.19 (0.03)	0.10	0.13 (0.03)
Porcupine	0.07	0.09 (0.02)	0.03	0.06 (0.02)
Mainstem	0.10	0.10 (0.02)	0.07	0.07 (0.02)
Upper	0.11	0.11 (0.02)	0.08	0.08 (0.02)
White	0.10	0.10 (0.02)	0.06	0.06 (0.01)
Teslin	0.01	0.01 (0.01)	0.02	0.02 (0.01)
Fall U.S.	0.57	0.49 (0.03)	0.39	0.32 (0.03)
U.S.	0.72	0.70 (0.03)	0.82	0.79 (0.03)
Canada	0.28	0.30 (0.03)	0.18	0.21 (0.03)
U.S. Border + Canada	0.53	0.52 (0.03)	0.45	0.43 (0.03)
Mainstem + Upper	0.21	0.21 (0.03)	0.15	0.15 (0.03)

Table 11. Mixed-stock analysis of samples (N=200) of known origin. Bayesian and conditional maximum likelihood (CML) estimates with their standard deviations in parentheses are presented.

Stock	Expected	Bayesian Estimate	CML Estimate
Lower Summer – California	0.250	0.353 (0.053)	0.422 (0.048)
Tanana Summer – Chena	0.250	0.151 (0.045)	0.137 (0.039)
Tanana Fall – Toklat	0.250	0.236 (0.045)	0.157 (0.037)
U.S. Border	0.000	0.004 (0.008)	0.019 (0.018)
Porcupine	0.000	0.000 (0.002)	0.006 (0.012)
Mainstem	0.000	0.002 (0.005)	0.013 (0.014)
White Fall – Kluane	0.250	0.253 (0.033)	0.246 (0.032)
Teslin	0.000	0.001 (0.002)	0.001 (0.003)
Summer	0.500	0.506 (0.048)	0.560 (0.048)
Fall	0.500	0.494 (0.048)	0.440 (0.048)
U.S.	0.750	0.744 (0.033)	0.734 (0.036)
Canada	0.250	0.256 (0.033)	0.266 (0.036)

Table 12. Estimated fall chum salmon stock proportions by year.

Year	Tanana	U.S. Border	Mainstem	Porcupine	White	Teslin
2004	0.370	0.312	0.116	0.079	0.118	0.004
2005	0.209	0.494	0.117	0.048	0.108	0.024

Table 13. 2004 Pilot Station test fishery chum salmon stock composition estimates with associated standard deviations and 95% confidence intervals by pulse and management group.

	Buildup 7/19-8/2		Pulse 1 8/3-8/9	
	Estimate	SD	Estimate	SD
Summer	0.432	0.082	0.279	0.598
Lower	0.378	0.094	0.214	0.576
Tanana	0.054	0.064	0.000	0.207
Fall	0.568	0.082	0.402	0.721
Tanana	0.019	0.034	0.000	0.118
U.S. Border	0.347	0.102	0.154	0.548
Canada Border	0.171	0.067	0.055	0.316
Porcupine	0.138	0.060	0.022	0.262
Mainstem	0.033	0.058	0.000	0.201
Upper Canada	0.030	0.025	0.000	0.092
White	0.026	0.021	0.000	0.077
Teslin	0.004	0.013	0.000	0.047
Fall U.S.	0.367	0.103	0.171	0.569
U.S.	0.799	0.069	0.651	0.919
Canada	0.201	0.069	0.081	0.349
U.S. Border + Canada	0.548	0.082	0.383	0.704
Mainstem + Upper Canada	0.063	0.063	0.000	0.234
	Estimate	SD	Estimate	SD
	0.086	0.084	0.000	0.293
	0.080	0.085	0.000	0.288
	0.005	0.014	0.000	0.050
	0.914	0.084	0.707	1.000
	0.204	0.070	0.061	0.342
	0.340	0.112	0.138	0.576
	0.235	0.107	0.000	0.449
	0.132	0.102	0.000	0.337
	0.103	0.118	0.000	0.365
	0.135	0.039	0.066	0.220
	0.131	0.038	0.064	0.211
	0.004	0.012	0.000	0.044
	0.544	0.119	0.309	0.775
	0.630	0.109	0.417	0.854
	0.370	0.109	0.146	0.583
	0.711	0.084	0.529	0.857
	0.238	0.122	0.078	0.506

Continued

Table 13. Continued

	Pulse 2 8/10–8/15			Pulse 3 8/16–8/21			
	Estimate	SD	95% CI	Estimate	SD	95% CI	
Summer	0.106	0.090	0.001	0.325	0.134	0.007	0.350
Lower	0.101	0.091	0.000	0.322	0.087	0.000	0.326
Tanana	0.005	0.014	0.000	0.048	0.047	0.000	0.188
Fall	0.894	0.090	0.675	0.999	0.866	0.650	0.993
Tanana	0.312	0.066	0.185	0.445	0.323	0.166	0.492
U.S. Border	0.225	0.128	0.001	0.494	0.331	0.118	0.522
Canada Border	0.256	0.103	0.004	0.441	0.022	0.000	0.154
Porcupine	0.010	0.030	0.000	0.110	0.004	0.000	0.043
Mainstem	0.245	0.106	0.000	0.434	0.018	0.000	0.144
Upper Canada	0.102	0.035	0.043	0.181	0.191	0.104	0.291
White	0.096	0.032	0.040	0.164	0.188	0.103	0.288
Teslin	0.006	0.017	0.000	0.061	0.002	0.000	0.026
Fall U.S.	0.536	0.139	0.267	0.815	0.654	0.404	0.827
U.S.	0.642	0.105	0.451	0.874	0.788	0.640	0.888
Canada	0.358	0.105	0.126	0.549	0.212	0.112	0.360
U.S. Border + Canada	0.582	0.091	0.386	0.740	0.543	0.347	0.726
Mainstem + Upper Canada	0.347	0.108	0.106	0.541	0.209	0.110	0.352

Continued

Table 13. Continued

	Pulse 4 8/22-8/26			Pulse 5 8/27-8/31		
	Estimate	SD	95% CI	Estimate	SD	95% CI
Summer	0.099	0.091	0.000 0.320	0.029	0.044	0.000 0.160
Lower	0.082	0.091	0.000 0.308	0.025	0.043	0.000 0.156
Tanana	0.017	0.034	0.000 0.122	0.004	0.013	0.000 0.043
Fall	0.901	0.091	0.680 1.000	0.971	0.044	0.840 1.000
Tanana	0.424	0.073	0.280 0.565	0.578	0.070	0.438 0.712
U.S. Border	0.153	0.099	0.000 0.364	0.251	0.104	0.005 0.432
Canada Border	0.133	0.071	0.000 0.279	0.085	0.101	0.000 0.330
Porcupine	0.109	0.069	0.000 0.247	0.004	0.015	0.000 0.051
Mainstem	0.024	0.054	0.000 0.196	0.081	0.101	0.000 0.327
Upper Canada	0.191	0.041	0.114 0.276	0.057	0.026	0.014 0.114
White	0.189	0.041	0.113 0.274	0.054	0.024	0.013 0.107
Teslin	0.002	0.007	0.000 0.022	0.003	0.009	0.000 0.032
Fall U.S.	0.577	0.113	0.341 0.773	0.829	0.112	0.559 0.969
U.S.	0.676	0.074	0.526 0.819	0.858	0.104	0.608 0.979
Canada	0.324	0.074	0.181 0.474	0.142	0.104	0.021 0.392
U.S. Border + Canada	0.477	0.086	0.305 0.641	0.393	0.074	0.248 0.537
Mainstem + Upper Canada	0.215	0.069	0.118 0.403	0.137	0.104	0.020 0.388

Continued

Table 13. Continued

	Overall 7/19-8/31		
	Estimate	SD	95% CI
Summer	0.130	0.034	0.064 0.196
Lower	0.114	0.034	0.047 0.182
Tanana	0.016	0.012	0.000 0.039
Fall	0.870	0.034	0.804 0.936
Tanana	0.322	0.029	0.265 0.379
U.S. Border	0.272	0.048	0.177 0.367
Canada Border	0.170	0.042	0.087 0.253
Porcupine	0.069	0.028	0.014 0.123
Mainstem	0.101	0.044	0.016 0.187
Upper Canada	0.106	0.015	0.077 0.135
White	0.102	0.014	0.075 0.130
Teslin	0.004	0.005	0.000 0.014
Fall U.S.	0.594	0.052	0.492 0.696
U.S.	0.724	0.043	0.639 0.809
Canada	0.276	0.043	0.191 0.361
U.S. Border + Canada	0.548	0.036	0.477 0.619
Mainstem + Upper Canada	0.207	0.045	0.118 0.296

Table 14. 2005 Pilot Station test fishery chum salmon stock composition estimates with associated standard deviations and 95% confidence intervals by pulse and management group.

	Preseason 1 7/1-7/9			Preseason 2 7/10-7/18				
	Estimate	SD	95% CI	Estimate	SD	95% CI		
Summer	0.986	0.014	0.951	1.000	0.609	0.047	0.517	0.702
Lower	0.892	0.039	0.817	0.983	0.508	0.051	0.408	0.611
Tanana	0.095	0.038	0.000	0.166	0.101	0.038	0.033	0.180
Fall	0.014	0.014	0.000	0.049	0.391	0.047	0.299	0.483
Tanana	0.003	0.006	0.000	0.022	0.005	0.011	0.000	0.037
U.S. Border	0.002	0.005	0.000	0.017	0.245	0.054	0.144	0.356
Canada Border	0.004	0.007	0.000	0.026	0.096	0.038	0.026	0.173
Porcupine	0.000	0.002	0.000	0.004	0.090	0.037	0.019	0.164
Mainstem	0.004	0.007	0.000	0.025	0.006	0.012	0.000	0.045
Upper Canada	0.005	0.009	0.000	0.033	0.046	0.019	0.016	0.089
White	0.005	0.009	0.000	0.032	0.024	0.013	0.005	0.054
Teslin	0.000	0.002	0.000	0.004	0.023	0.014	0.003	0.056
Fall U.S.	0.005	0.008	0.000	0.028	0.250	0.054	0.150	0.363
U.S.	0.991	0.012	0.959	1.000	0.858	0.041	0.774	0.937
Canada	0.009	0.012	0.000	0.041	0.142	0.041	0.063	0.225
U.S. Border + Canada	0.011	0.013	0.000	0.044	0.386	0.047	0.294	0.480
Mainstem + Upper Canada	0.009	0.012	0.000	0.040	0.052	0.022	0.018	0.104

Continued

Table 14. Continued

	Pulse 1 7/19-7/23			Pulse 2 7/24-8/4			
	Estimate	SD	95% CI	Estimate	SD	95% CI	
Summer	0.404	0.056	0.296	0.517	0.042	0.178	0.343
Lower	0.325	0.052	0.230	0.434	0.038	0.136	0.285
Tanana	0.078	0.044	0.000	0.166	0.031	0.000	0.119
Fall	0.596	0.056	0.482	0.704	0.042	0.657	0.821
Tanana	0.073	0.039	0.000	0.158	0.042	0.000	0.153
U.S. Border	0.325	0.074	0.184	0.473	0.067	0.330	0.592
Canada Border	0.171	0.053	0.074	0.285	0.049	0.001	0.192
Porcupine	0.147	0.048	0.056	0.245	0.024	0.000	0.092
Mainstem	0.024	0.034	0.000	0.118	0.046	0.000	0.177
Upper Canada	0.028	0.019	0.004	0.077	0.028	0.084	0.194
White	0.021	0.013	0.003	0.052	0.028	0.084	0.194
Teslin	0.006	0.014	0.000	0.050	0.003	0.000	0.006
Fall U.S.	0.398	0.073	0.252	0.540	0.064	0.393	0.643
U.S.	0.802	0.055	0.685	0.902	0.055	0.663	0.877
Canada	0.198	0.055	0.097	0.315	0.055	0.123	0.337
U.S. Border + Canada	0.524	0.058	0.411	0.633	0.054	0.573	0.780
Mainstem + Upper Canada	0.051	0.038	0.006	0.147	0.053	0.116	0.320

Continued

Table 14. Continued

	Pulse 3 8/5-8/13			Pulse 4 8/14-8/31		
	Estimate	SD	95% CI	Estimate	SD	95% CI
Summer	0.026	0.031	0.000	0.050	0.038	0.005
Lower	0.016	0.026	0.000	0.049	0.038	0.004
Tanana	0.010	0.020	0.000	0.001	0.004	0.000
Fall	0.974	0.031	0.892	0.950	0.038	0.853
Tanana	0.150	0.048	0.062	0.441	0.057	0.329
U.S. Border	0.498	0.067	0.366	0.334	0.065	0.213
Canada Border	0.184	0.057	0.075	0.063	0.044	0.000
Porcupine	0.002	0.008	0.000	0.003	0.013	0.000
Mainstem	0.182	0.056	0.074	0.060	0.043	0.000
Upper Canada	0.142	0.034	0.080	0.112	0.029	0.061
White	0.118	0.030	0.066	0.092	0.025	0.049
Teslin	0.024	0.018	0.000	0.019	0.014	0.000
Fall U.S.	0.648	0.063	0.520	0.775	0.057	0.653
U.S.	0.674	0.058	0.558	0.825	0.049	0.723
Canada	0.326	0.058	0.213	0.175	0.049	0.087
U.S. Border + Canada	0.824	0.052	0.716	0.509	0.059	0.391
Mainstem + Upper Canada	0.324	0.058	0.212	0.172	0.048	0.085

Continued

Table 14. Continued

	Estimate	SD	Overall 7/1-8/31	95% CI
Summer	0.404	0.015	0.375	0.433
Lower	0.351	0.017	0.318	0.384
Tanana	0.053	0.013	0.027	0.078
Fall	0.596	0.015	0.567	0.625
Tanana	0.124	0.017	0.091	0.158
U.S. Border	0.295	0.025	0.246	0.343
Canada Border	0.098	0.019	0.060	0.136
Porcupine	0.028	0.008	0.013	0.044
Mainstem	0.070	0.018	0.035	0.105
Upper Canada	0.079	0.012	0.056	0.102
White	0.065	0.010	0.045	0.084
Teslin	0.014	0.006	0.002	0.026
Fall U.S.	0.419	0.023	0.373	0.464
U.S.	0.823	0.020	0.783	0.863
Canada	0.177	0.020	0.137	0.217
U.S. Border + Canada	0.472	0.020	0.432	0.512
Mainstem + Upper Canada	0.149	0.019	0.111	0.186

Table 15. 2004 and 2005 Pilot Station sonar passage estimates.

Year	Stratum	Passage
2004	Buildup (7/19-8/2)	83,797
	Pulse 1 (8/3-8/9)	139,891
	Pulse 2 (8/10-8/15)	119,868
	Pulse 3 (8/16-8/21)	34,173
	Pulse 4 (8/22-8/26)	79,453
	Pulse 5 (8/27-8/31)	136,878
	Total (7/19-8/31)	594,060
2005	Preseason 1 (7/1-7/9)	729,877
	Preseason 2 (7/10-7/18)	528,934
	Pulse 1 (7/19-7/23)	231,942
	Pulse 2 (7/24-8/4)	227,436
	Pulse 3 (8/5-8/13)	859,583
	Pulse 4 (8/14-8/31)	494,628
		Total (7/1-8/31)

Table 16. 2004 and 2005 stock abundance estimates derived from the products of the genetic stock composition estimates and Pilot Station sonar passage estimates. The standard deviations and 95% confidence intervals are based on the variances of the genetic estimates only.

	2004 7/19-8/31			2005 7/1-8/31		
	Estimate	SD	95% CI	Estimate	SD	95% CI
Summer	77,369	20,045	38,081	1,241,185	45,219	1,152,556
Lower	67,883	20,409	27,881	1,079,118	51,371	978,430
Tanana	9,486	7,050	0	162,230	40,218	83,403
Fall	516,691	20,045	477,404	1,831,215	45,221	1,742,582
Tanana	191,336	17,390	157,252	381,871	52,569	278,836
U.S. Border	161,435	28,795	104,997	905,028	75,400	757,243
Canada Border	100,867	25,186	51,503	301,885	59,536	185,194
Porcupine	40,726	16,581	8,227	87,441	24,827	38,779
Mainstem	60,141	25,891	9,395	214,601	54,986	106,828
Upper Canada	63,053	8,889	45,630	242,209	35,760	172,120
White	60,820	8,345	44,464	198,343	30,735	138,102
Teslin	2,234	3,183	0	43,761	18,916	6,686
Fall U.S.	352,771	30,933	292,143	1,286,734	71,211	1,147,160
U.S.	430,140	25,797	379,578	2,528,143	62,972	2,404,717
Canada	163,920	25,797	113,358	544,257	62,964	420,847
U.S. Border + Canada	325,355	21,525	283,167	1,449,316	62,448	1,326,917
Mainstem + Upper Canada	123,194	26,939	70,393	456,859	59,022	341,175

Table 17. 2004 and 2005 upriver escapement estimates.

	2004 Estimate	2005 Estimate
Upper Tanana River Mark-Recapture	123,875	318,527
Kantishna River Mark-Recapture	76,163	96,926
Total Tanana River	200,038	415,453
Chandalar Sonar	136,706	496,494
Sheenjek Sonar	37,878	438,253
Canada Border Passage (Mainstem + Upper)	163,625	451,477
Porcupine River Mark-Recapture	42,140	113,415

Table 18. 2004 and 2005 subsistence harvest apportionments. Bold numbers indicate escapements estimated by the monitoring projects. Harvest was apportioned to the U.S. and Canada fall stocks in a stepwise upstream to downstream fashion by using the escapements to estimate the relative proportions of these stocks available at the river locations and multiplying these proportions by the harvest at the river locations.

2004 Location	Harvest	Abundance of Contributing Stocks				
		Canada Mainstem + Upper	Porcupine	Sheenjek	Chandalar	Tanana
Chandalar (w/ Black)	2,562				136,706	
Y6	9,183					200,038
Y5D Above Porcupine	6,517	163,625				
Ft. Yukon	7,302	170,142	42,140	37,878		
Y5D Below Chandalar	1,128	175,108	43,370	38,984	139,268	
Y5C	43	175,606	43,493	39,094	139,664	
Y5B	18,699	175,625	43,498	39,099	139,679	
Y5A	4,419					209,221
Y4	5,593	183,879	45,542	40,936	146,243	213,640
Y3	298	185,510	45,946	41,299	147,541	215,536
Y2 (Marshall only)	291	185,597	45,968	41,319	147,610	215,637
Total	56,035	185,682	45,989	41,338	147,678	215,736

Continued

Table 18. Continued

2004 Location	Proportion of Contributing Stocks				
	Canada Mainstem + Upper	Porcupine	Sheenjek	Chandalar	Tanana
Chandalar (w/ Black)	0.00	0.00	0.00	1.00	0.00
Y6	0.00	0.00	0.00	0.00	1.00
Y5D Above Porcupine	1.00	0.00	0.00	0.00	0.00
Ft. Yukon	0.68	0.17	0.15	0.00	0.00
Y5D Below Chandalar	0.44	0.11	0.10	0.35	0.00
Y5C	0.44	0.11	0.10	0.35	0.00
Y5B	0.44	0.11	0.10	0.35	0.00
Y5A	0.00	0.00	0.00	0.00	1.00
Y4	0.29	0.07	0.06	0.23	0.34
Y3	0.29	0.07	0.06	0.23	0.34
Y2 (Marshall only)	0.29	0.07	0.06	0.23	0.34

2004 Location	Harvest Apportionment				
	Canada Mainstem + Upper	Porcupine	Sheenjek	Chandalar	Tanana
Chandalar (w/ Black)	0	0	0	2,562	0
Y6	0	0	0	0	9,183
Y5D Above Porcupine	6,517	0	0	0	0
Ft. Yukon	4,966	1,230	1,106	0	0
Y5D Below Chandalar	498	123	111	396	0
Y5C	19	5	4	15	0
Y5B	8,253	2,044	1,837	6,564	0
Y5A	0	0	0	0	4,419
Y4	1,632	404	363	1,298	1,896
Y3	87	22	19	69	101
Y2 (Marshall only)	85	21	19	68	99
Total	22,057	3,849	3,460	10,972	15,698

Continued

Table 18. Continued

2005		Abundance of Contributing Stocks				
Location	Harvest	Canada Mainstem + Upper	Porcupine	Sheenjek	Chandalar	Tanana
Chandalar (w/ Black)	2,138				496,494	
Y6	23,079					415,453
Y5D Above Porcupine	18,427	451,477				
Ft. Yukon	8,088	469,904	113,415	438,253		
Y5D Below Chandalar	425	473,624	114,313	441,723	498,632	
Y5C	2,040	473,756	114,345	441,846	498,771	
Y5B	19,907	474,388	114,497	442,435	499,436	
Y5A	638					438,532
Y4	7,073	480,558	115,986	448,189	505,931	439,170
Y3	1,304	482,266	116,399	449,782	507,730	440,731
Y2 (Marshall only)	633	482,581	116,475	450,076	508,061	441,019
Total	83,752	482,733	116,511	450,218	508,222	441,159

2005		Proportion of Contributing stocks				
Location	Canada Mainstem + Upper	Porcupine	Sheenjek	Chandalar	Tanana	
Chandalar (w/ Black)	0.00	0.00	0.00	1.00	0.00	
Y6	0.00	0.00	0.00	0.00	1.00	
Y5D Above Porcupine	1.00	0.00	0.00	0.00	0.00	
Ft. Yukon	0.46	0.11	0.43	0.00	0.00	
Y5D Below Chandalar	0.31	0.07	0.29	0.33	0.00	
Y5C	0.31	0.07	0.29	0.33	0.00	
Y5B	0.31	0.07	0.29	0.33	0.00	
Y5A	0.00	0.00	0.00	0.00	1.00	
Y4	0.24	0.06	0.23	0.25	0.22	
Y3	0.24	0.06	0.23	0.25	0.22	
Y2 (Marshall only)	0.24	0.06	0.23	0.25	0.22	

Continued

Table 18. Continued

2005 Location	Harvest Apportionment				
	Canada Mainstem + Upper	Porcupine	Sheenjek	Chandalar	Tanana
Chandalar (w/ Black)	0	0	0	2,138	0
Y6	0	0	0	0	23,079
Y5D Above Porcupine	18,427	0	0	0	0
Ft. Yukon	3,720	898	3,470	0	0
Y5D Below Chandalar	132	32	123	139	0
Y5C	632	153	590	666	0
Y5B	6,169	1,489	5,754	6,495	0
Y5A	0	0	0	0	638
Y4	1,708	412	1,593	1,798	1,561
Y3	315	76	294	332	288
Y2 (Marshall only)	153	37	143	161	140
Total	31,256	3,096	11,965	11,728	25,706

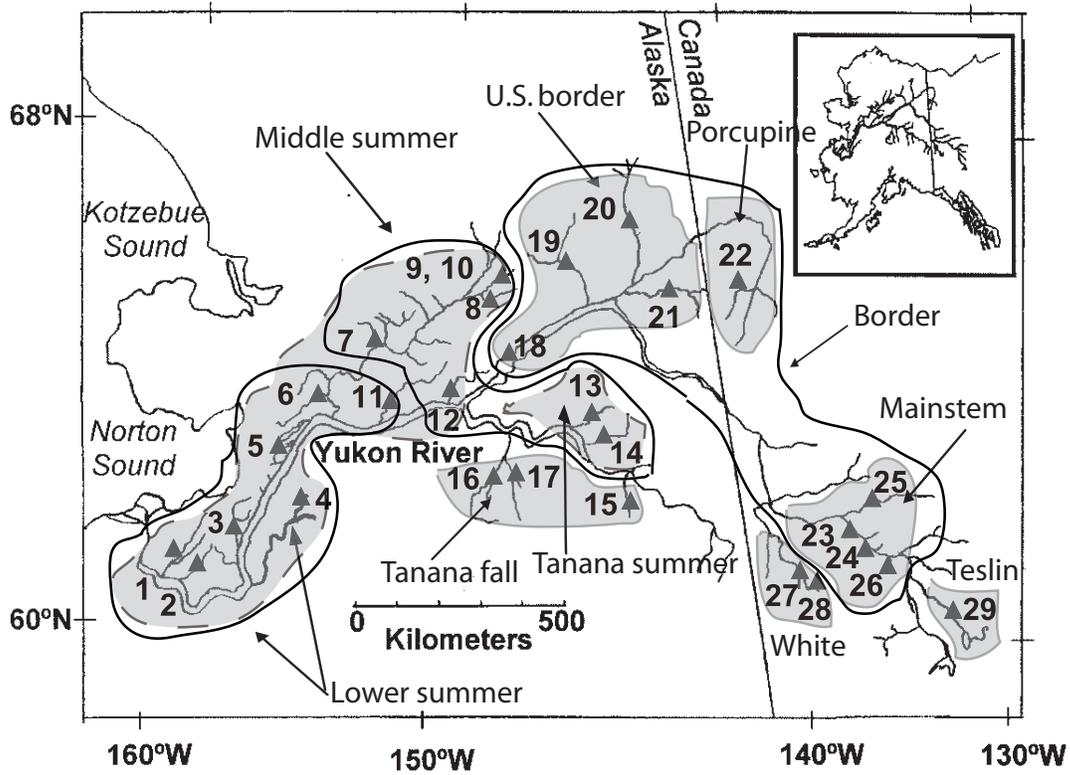


Figure 1. Sampling locations, 1 = Andreafsky, 2 = Chulinak, 3 = Anvik, 4 = California, 5 = Nulato, 6 = Gisasa, 7 = Henshaw, 8 = Jim, 9 = South Fork Koyukuk Early, 10 = South Fork Koyukuk Late, 11 = Melozitna, 12 = Tozitna, 13 = Big Salt, 14 = Chena, 15 = Salcha, 16 = Delta, 17 = Kantishna, 18 = Toklat, 19 = Chandalar, 20 = Sheenjek, 21 = Black, 22 = Fishing Branch, 23 = Big Creek, 24 = Minto, 25 = Pelly, 26 = Tatchun, 27 = Donjek, 28 = Kluane, and 29 = Teslin. The Galena–Ruby area is located near sample location 11. Pilot Station is located on the Yukon River mainstem near sample location 2. The grey shaded areas delineate fishery management regions, with summer regions outlined by dashed lines and fall regions by solid lines. The black circles delineate differences between genetic and fishery management regions.

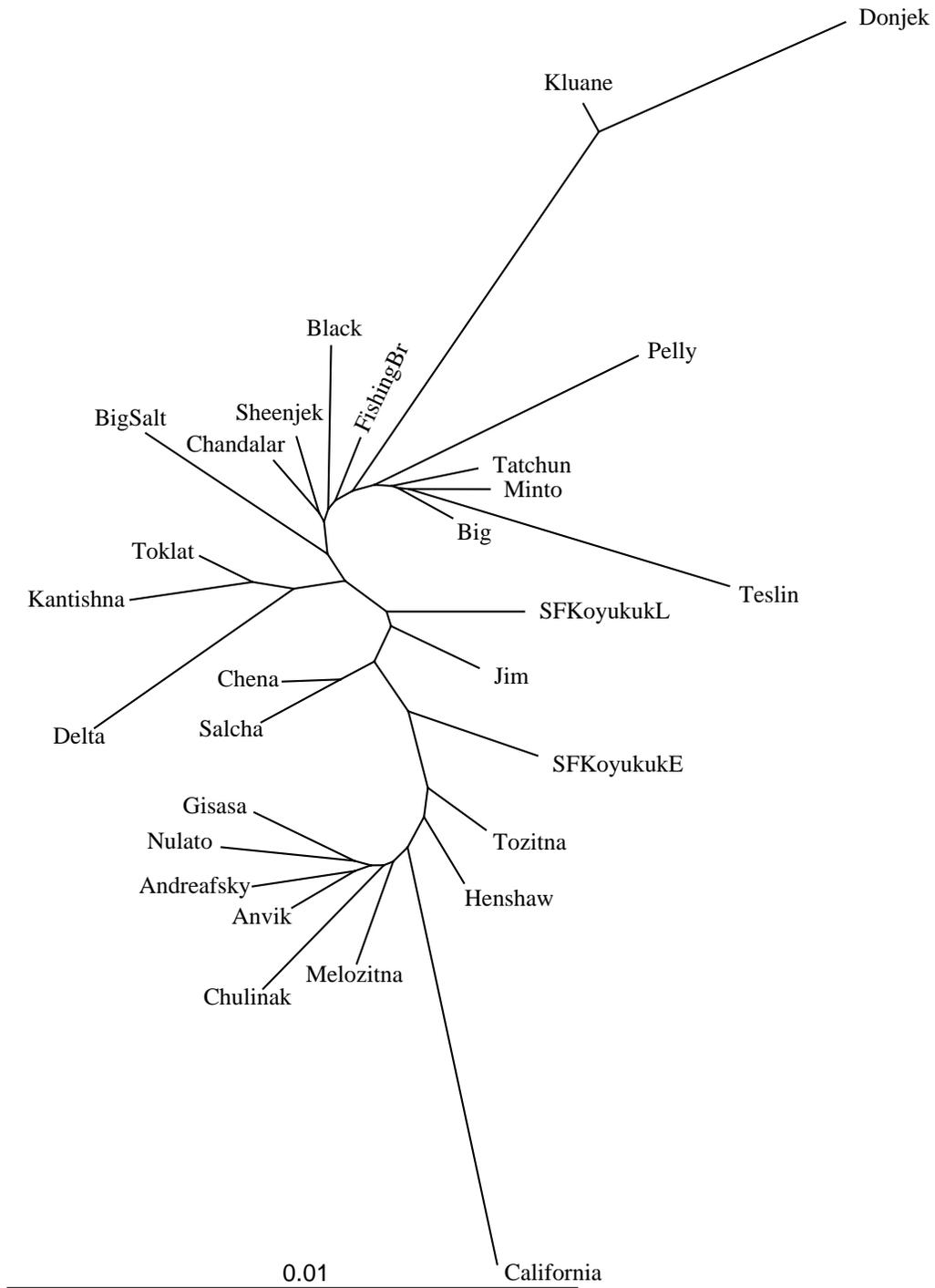


Figure 2. Neighbor-joining dendrogram of Cavelli-Sforza and Edwards (1967) chord distances calculated from allele frequencies at 21 loci.

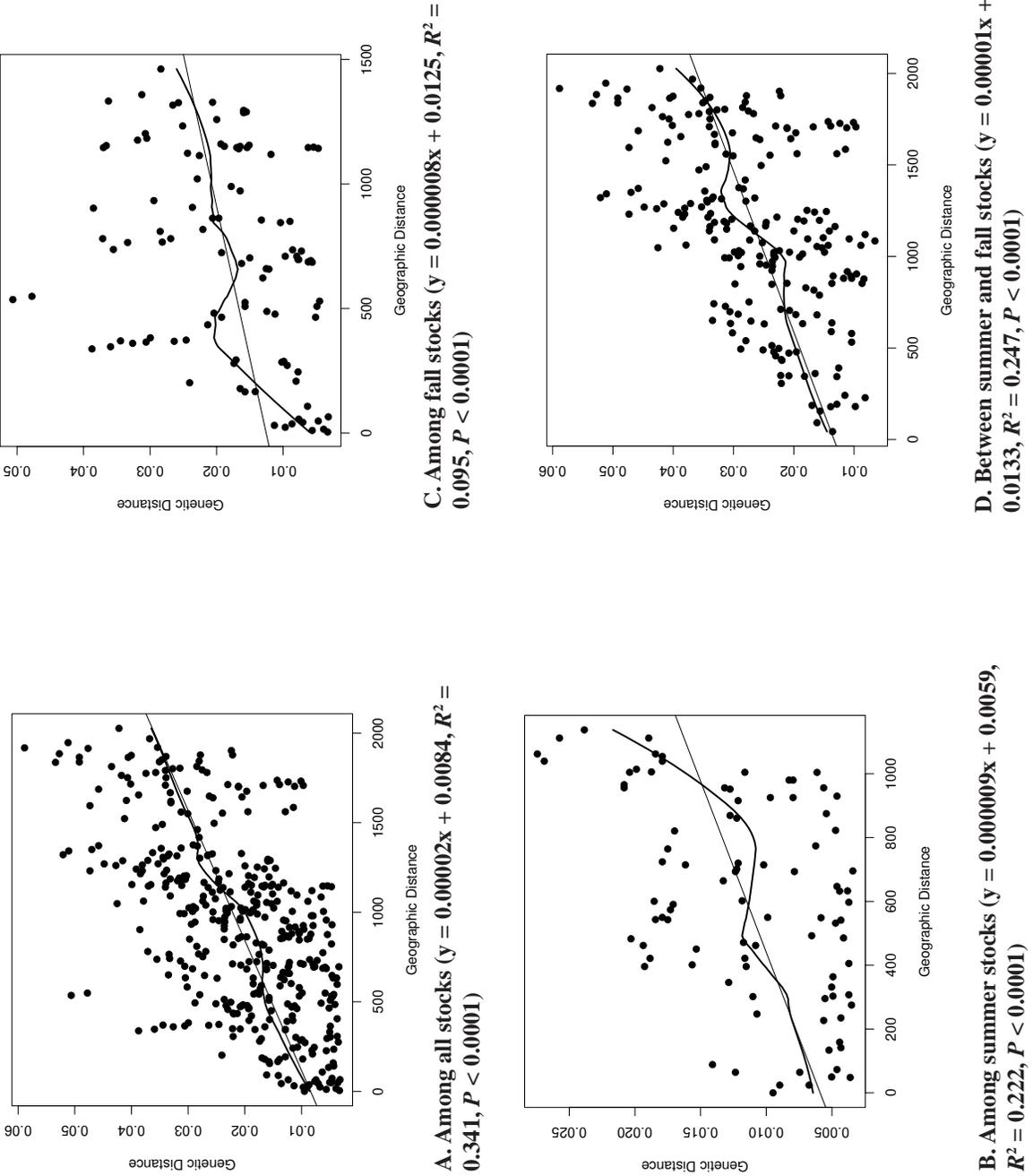
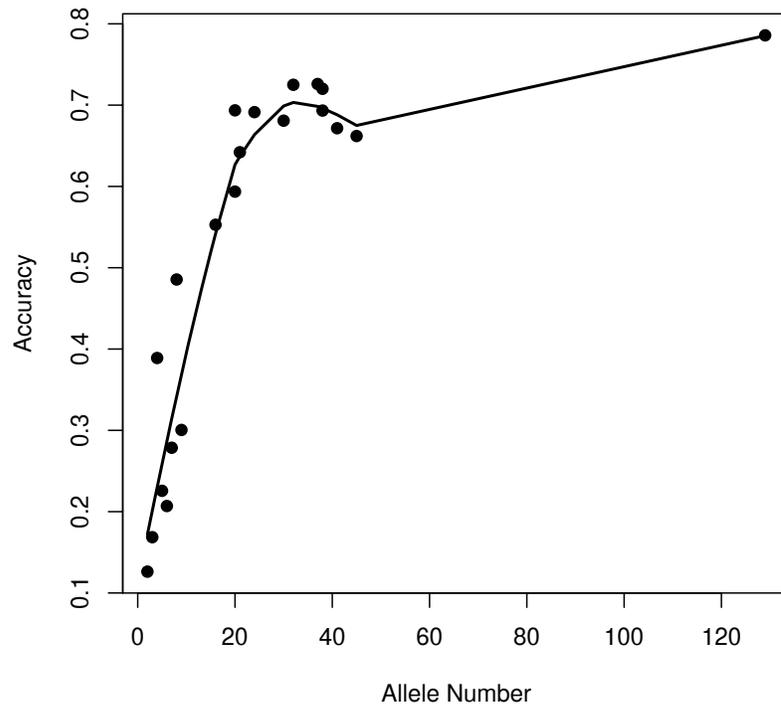


Figure 3. Stock pairwise scatter plots of genetic distance ($F_{ST}/(1-F_{ST})$) on geographic distance (kilometers). Linear and loweress trend lines are displayed.

A)



B)

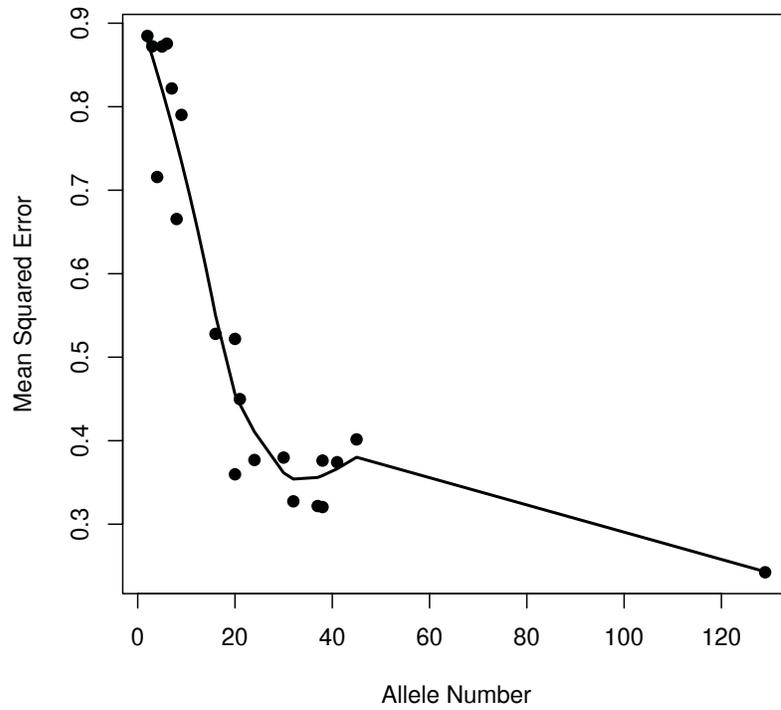


Figure 4. A) Mean accuracy and B) mean square root mean squared error for single region, single locus simulations versus the number of alleles at the locus. Lowess trend lines are displayed.

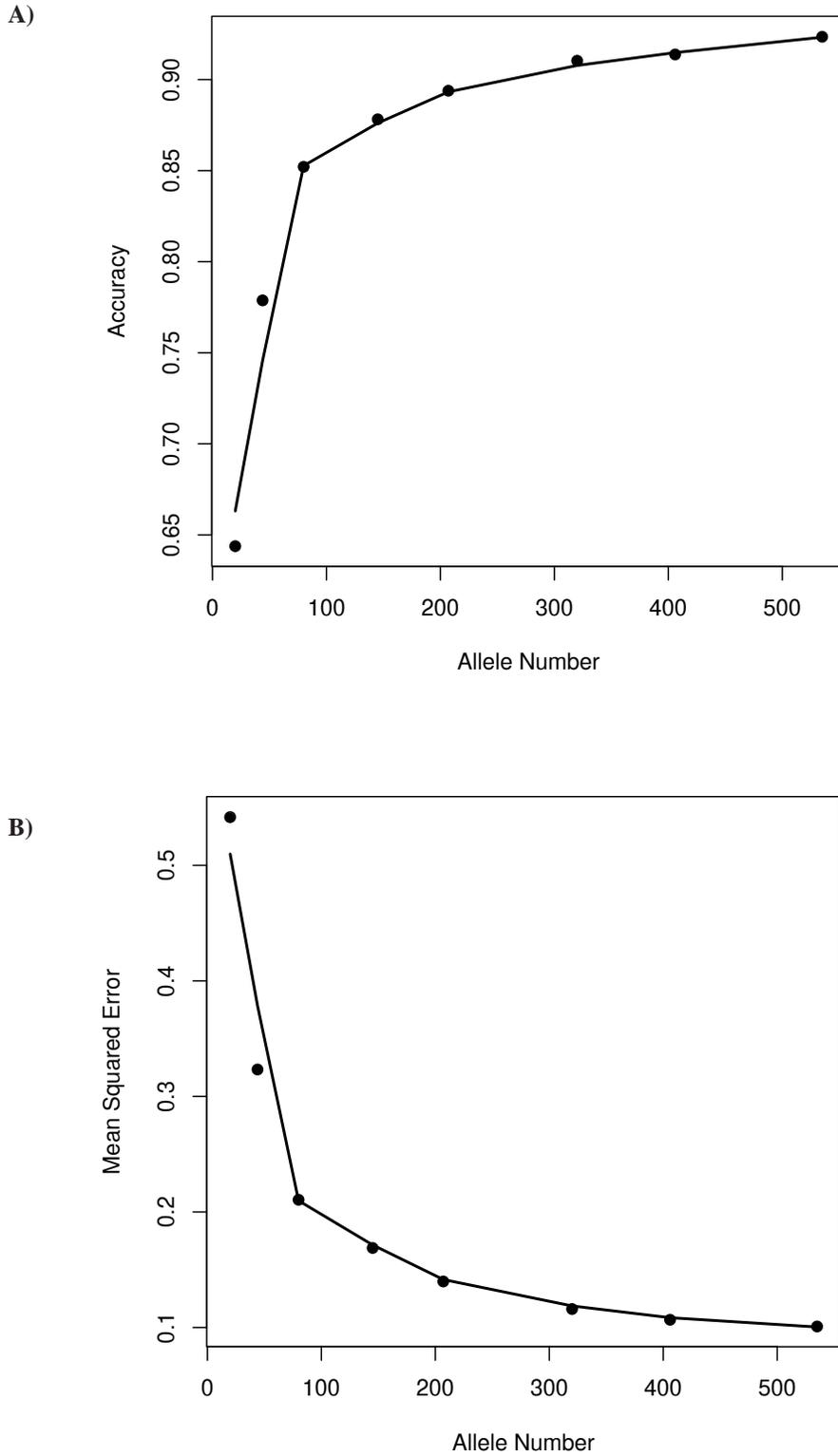


Figure 5. A) Mean accuracy and B) mean square root mean squared error for single region simulations versus the number of alleles in the analysis. Loci were sequentially added to the analysis, beginning with the least variable locus. Lowess trend lines are displayed.

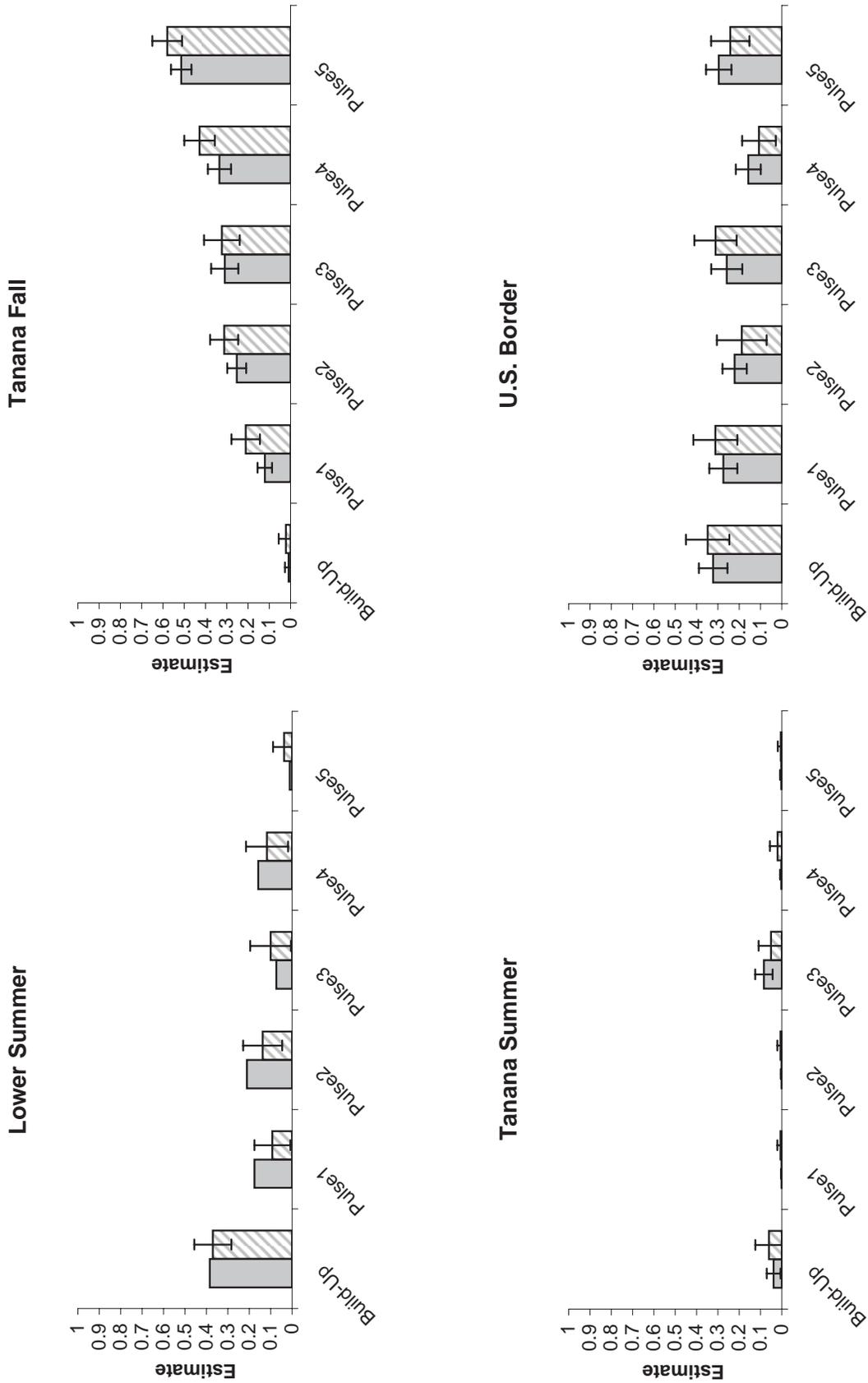


Figure 6. 2004 Pilot Station test fishery stock composition estimates, DFOC estimates (solid bar) are listed next to USFWS estimates (striped bar). Independent baselines were used. Error bars represent one standard error.

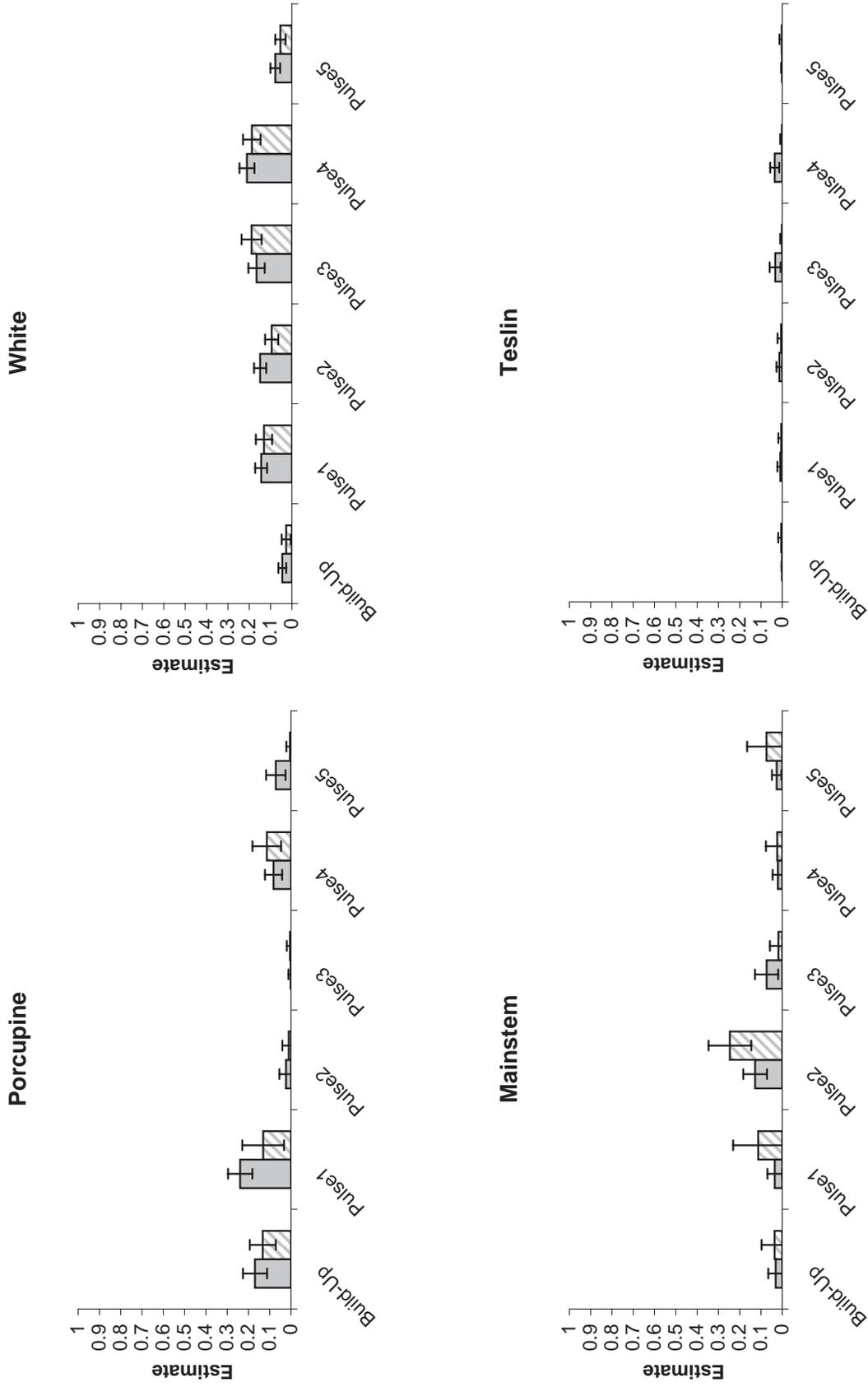


Figure 6. Continued

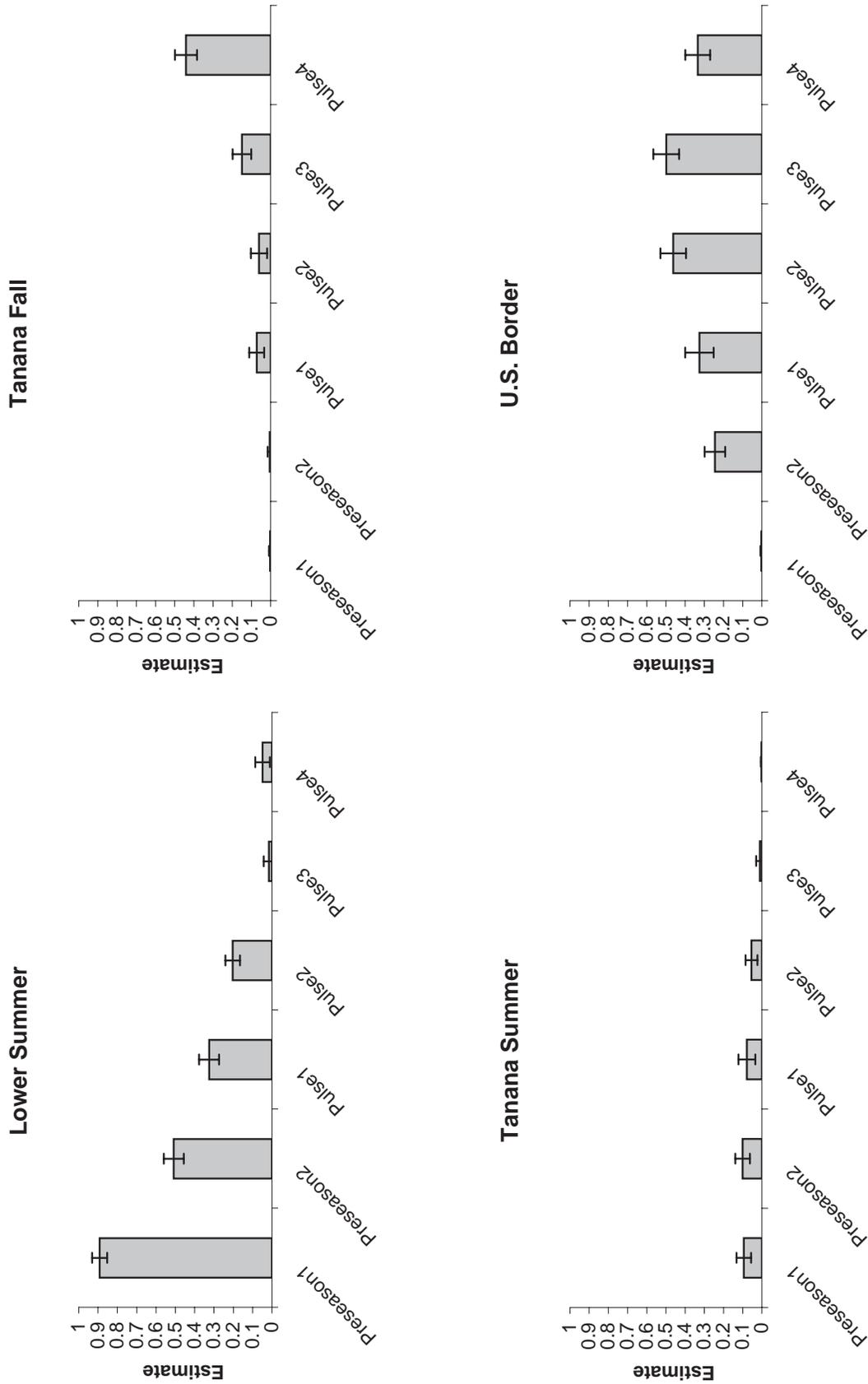


Figure 7. 2005 Pilot Station test fishery stock composition estimates. Error bars represent one standard error.

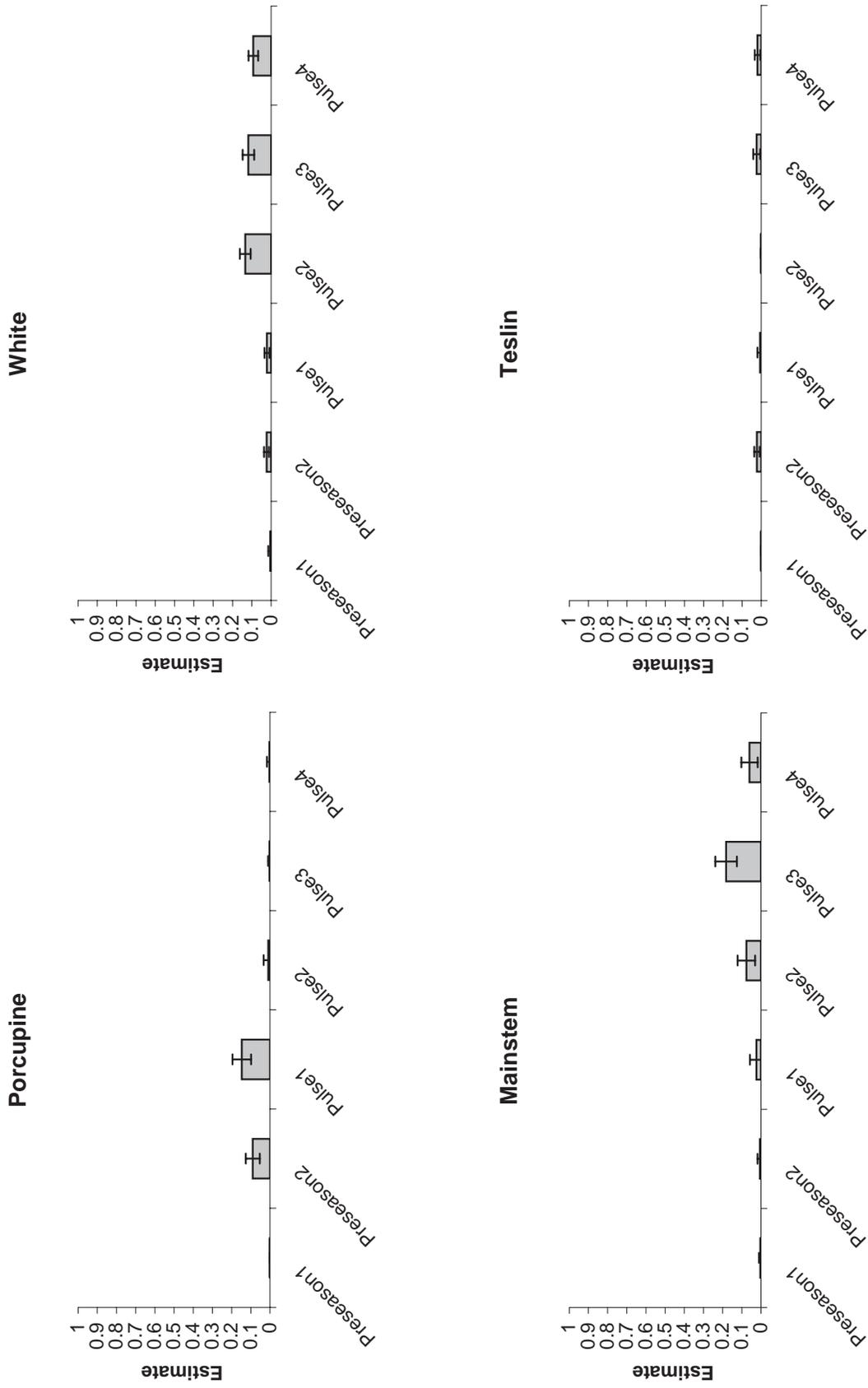


Figure 7. Continued

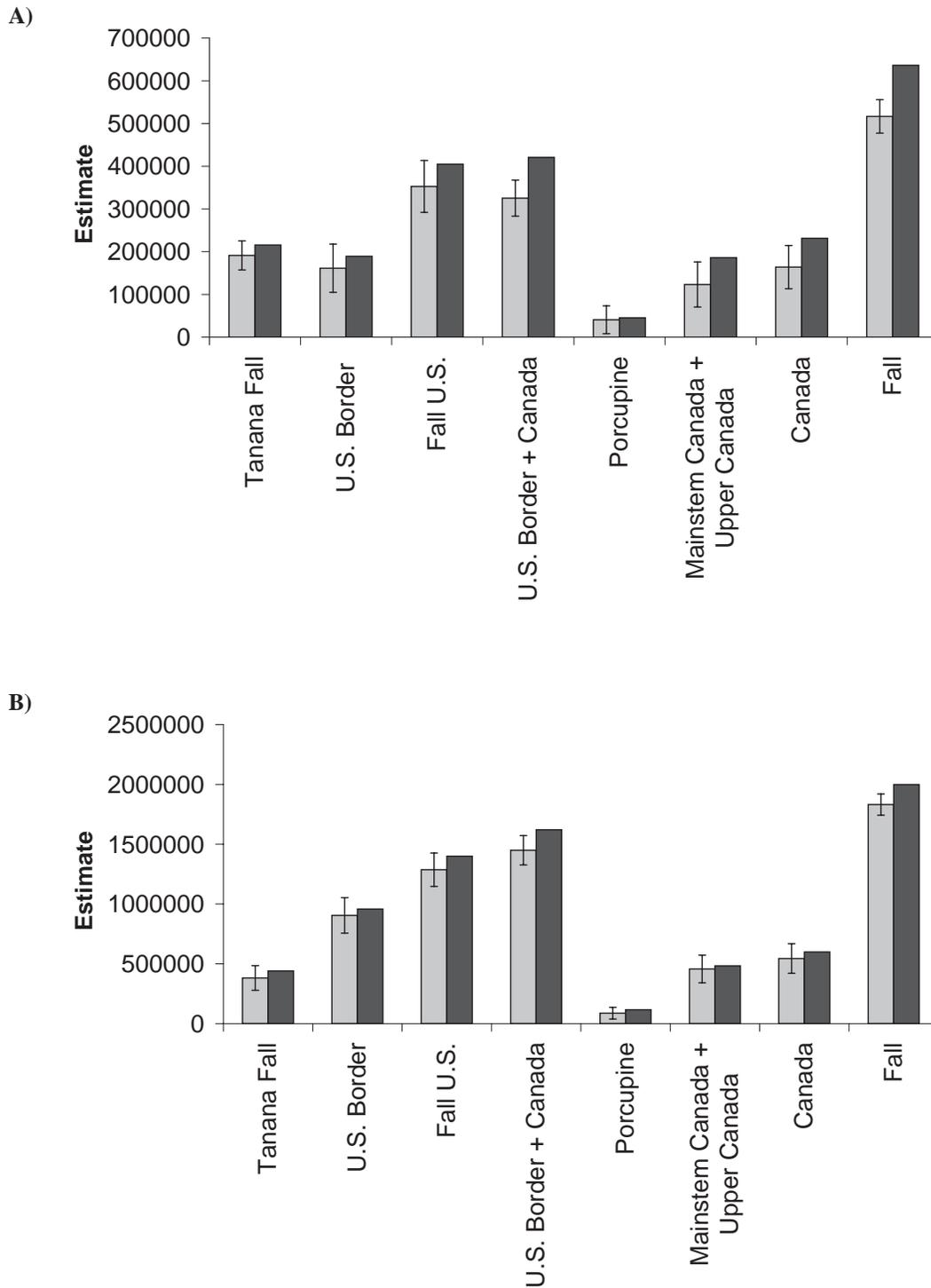


Figure 8. A) 2004 and B) 2005 comparisons of stock abundance estimates. Grey bars are genetic/sonar estimates. Black bars are escapement and harvest estimates. The 95% confidence intervals are based on the variances of the genetic estimates only.