

Evaluation and Application of Microsatellite and Major Histocompatibility Complex Variation for Stock Identification of Coho Salmon in British Columbia

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Abstract.—Variation at eight microsatellite loci and two linked exons of a major histocompatibility complex (MHC) locus was surveyed in approximately 21,000 coho salmon *Oncorhynchus kisutch* sampled from 138 localities ranging from southeast Alaska to the Columbia River, the majority of the sites being in British Columbia. The observed regional population structure enabled evaluation of the utility of using microsatellite and MHC variation for estimating the stock composition of coho salmon in mixed-stock fisheries. Both MHC exons were more effective for stock identification than any of the eight microsatellite loci examined. The two MHC exons combined were nearly as effective, on average, as the eight microsatellite loci combined. Some loci were particularly effective at discriminating stocks from specific regions. Mixed-stock analysis provided accurate estimates of contributions from the threatened Thompson River and upper Skeena River stocks, even when they composed less than 5% of the sampled fish. From about 17,000 coho salmon sampled from mixed-stock fisheries in British Columbia and Washington during 1997–1999, we found that the highest estimated proportions of coho salmon originating in southeast Alaska were in Canadian fishing areas adjacent to the international border in northern British Columbia; the highest proportions of Washington-origin coho salmon were observed closest to the international border in southern British Columbia. Within major river drainages, MHC variation within appropriately sampled fisheries can be used to determine the timing of spawning returns of specific stocks and the relative or absolute stock escapements.

The application of molecular genetic markers to stock structure analysis and mixed-stock analysis of anadromous salmonids has been extensive because of the economic importance of these fish and the relative ease of sampling temporally or spatially segregated spawning aggregations (Carvalho and Hauser 1994). For coho salmon *Oncorhynchus kisutch*, identification of coded-wire-tagged individuals (Jefferts et al. 1963) has been the primary method used to determine stock composition (Shaul and Clark 1990). Although genetic variation, as surveyed through protein electrophoresis, has been used experimentally to estimate stock composition for coho salmon (Milner 1993), the limited amount of variation observed at protein electrophoretic loci (Wehrhahn and Powell 1987; Bartley et al. 1992) has generally precluded its pragmatic application for management. Because of the low level of variation observed at allozyme loci, we examined DNA-level variation in our lab-

oratory for its potential in differentiating coho salmon populations. Differentiating among Pacific salmon populations is central to stock management (Carvalho and Hauser 1994), and thus, we chose to survey population structure of coho salmon. In initial studies, we detected high levels of polymorphism and regional population structure of coho salmon at minisatellite loci (Beacham et al. 1996; Miller et al. 1996). However, the technical complexity of surveying multiple minisatellite loci precluded their use in a high-throughput survey of coho salmon population structure throughout British Columbia and in the rapid analysis of mixed-stock fishery samples for fisheries management.

In 1995, we began to develop a comprehensive genetic database for coho salmon in British Columbia that would assist in identifying and selecting conservation and management units of British Columbia coho salmon. We believed the database would also provide sufficiently accurate and precise estimates of stock composition in mixed-stock samples and thereby enhance conservation-based fisheries management. We chose to survey variation at eight microsatellite loci and

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two exons (coding portion of a gene) of a major histocompatibility complex (MHC) locus. We used a PCR-based (polymerase chain reaction) approach to ensure cost effectiveness and speed in establishing the database and to enable nonlethal sampling for mixed-stock analysis. Microsatellite loci are abundant, highly polymorphic, and non-coding (considered selectively neutral), and provide genetic information on nonselective forces, including mutation and drift. As such, they can be used to generate estimates of gene flow, effective population size, and phylogenetic relationships. Vertebrate MHC genes encode cell-surface glycoproteins that are functional in the adaptive immune system. They evolve rapidly, are highly polymorphic, and because they encode adaptive variation, are subject to natural selection. The adaptive nature of MHC genes compromises use of MHC allele frequencies to estimate parameters for which an assumption of selective neutrality is required. However, MHC allele frequencies have the potential to enhance stock specificity and thus their utility in mixed-stock analyses. Moreover, variation in MHC allele and genotype frequencies attributable to selective forces provides quantitative information on the adaptive variation among salmonid stocks that conservation efforts are directed at preserving (Miller et al. in press). The two linked class-I MHC exons surveyed in this study exhibit high levels of polymorphism, heterozygosity, and temporally stable differentiation among coho salmon populations (Miller and Withler 1997; authors' unpublished data). The single-locus genotypes can be rapidly analyzed by denaturing gradient gel electrophoresis (DGGE; Miller et al. 1999).

After having received scientific advice in 1998 that the abundance of Thompson River and upper Skeena River coho salmon was at critically low levels (Stocker and Peacock 1998), the Minister of the Department of Fisheries and Oceans directed that the management of Canadian fisheries in 1998 was to be conducted with the objective of achieving a zero mortality of those salmon. Fisheries were curtailed in areas where Thompson River and upper Skeena River coho salmon were believed to be prevalent. Salmon fisheries in other areas could proceed if they were unlikely to intercept significant numbers of coho salmon, and generally, all coho salmon caught in any British Columbia fishery were to be released. Coded wire tag (CWT) analysis depends upon recovery of CWTs from dead fish, so under the 1998 management objectives, the traditional stock identification informa-

tion from CWTs would not be available. However, by 1998, extensive surveys of microsatellite and MHC variation had been conducted, the general units of population structure of coho salmon had been defined, and the feasibility of DNA-based MSA had been assessed (Miller and Withler 1997; Small et al. 1998a, b; Shaklee et al. 1999). Consequently, DNA analysis to determine stock contributions, especially from the Thompson River and upper Skeena River regions, was applied extensively to 1998 and 1999 samples of nonlethally collected coho salmon from fisheries in British Columbia and, to a limited extent, Washington.

In this study, we evaluate the utility of using microsatellite and MHC data for coho salmon stock identification through simulation analyses, apply the technologies to estimate stock composition of known-origin samples of coded-wire-tagged coho salmon, and outline the applications to estimating stock composition for coho salmon fisheries sampled in British Columbia and Washington during 1997–1999.

Methods

Collection of DNA samples and laboratory analysis.—Genomic DNA was extracted from either liver, scales, operculum punches, or fin clips from coho salmon sampled between 1987 and 1999 using the phenol-chloroform protocol of Miller et al. (1996; early extractions) or the chelex resin protocol of Small et al. (1998; later extractions). Samples were derived from adults in all areas except the Skeena River, where due to the paucity of adult returns, juveniles were used for some populations. For the survey of baseline populations, PCR products at four microsatellite loci—*Ots2*, *Ots3* (primers outlined by Banks et al. 1999), *Ots101*, and *Ots103* (primers outlined by Nelson and Beacham 1999)—were size fractionated on nondenaturing polyacrylamide gels, stained with 0.5 mg/mL ethidium bromide in water, and illuminated with ultraviolet light. Nelson et al. (1998) provided a more complete description of gel electrophoretic conditions. Three 20-bp (base pair) marker lanes were run on each gel, and the size of the amplified alleles was determined from the molecular size grid created with the 20-bp markers, as described by Small et al. (1998a). The PCR products at four additional loci—*Oki1* and *Oki10* (primers outlined by Smith et al. 1998), *Oki100*, and *Oki101* (primers outlined by Withler et al. in prep.)—were size fractionated on denaturing polyacrylamide gels, and allele sizes were determined with an automated DNA sequencer, the ABI 377. Variation at two

class-I MHC exons was surveyed by denaturing gradient gel electrophoresis (DGGE) (Miller et al. 1999). Two exons ($\alpha 1$, $\alpha 2$) of the MHC-Onki-A gene (primers from Miller and Withler 1998), which are homologous to the Sasa-A locus of Grimholt et al. (1994) and the Onmy-UBA locus of Shum et al. (2001), were surveyed.

Collection of the CWT sample.—In 1997, coho salmon could still be landed and retained in British Columbia fisheries. The program to recover coded-wire-tagged fish was in operation, and we were able to obtain operculum punches from coho salmon that had previously been marked with CWTs and for which the CWT had been recovered and decoded for marking location (source population). We subsequently used this sample of 264 fish to evaluate the accuracy of estimated stock compositions using a sample of known origin.

Collection of fishery samples.—In 1997, samples were collected from the recreational fishery off southwestern Vancouver Island and in test fisheries in the lower Fraser River in southern British Columbia. In 1998, when coho salmon were not to be retained in most fisheries in the province, sampling coho salmon from the fisheries was challenging. Sampling effort was expanded considerably; observers aboard troll, purse seine, and gillnet vessels sampled the bycatch of coho salmon before their release. Obtaining samples from the recreational fishery was difficult; there were no landings to sample, and it was not practical to place observers aboard individual vessels. Samples from these fisheries were generally obtained either from individual guides or charter boat operators, or from members of the British Columbia Wildlife Federation. The DNA samples from the 1998 and 1999 fisheries were obtained from either operculum punches or fin clips preserved in 70% ethanol. To facilitate rapid analysis of fishery samples, we generally screened them for variability at both MHC exons and at four microsatellite loci. The microsatellite loci screened for the 1997–1998 samples were *Ots2*, *Ots3*, *Ots101*, and *Ots103*, whereas the loci screened for the 1999 samples were *Oki1*, *Oki10*, *Oki100*, *Oki101*.

Baseline populations.—Applying DNA variation to estimates of stock composition in mixed-stock fisheries requires surveying variation in contributing populations at a sufficient number of genetic markers to provide reliable determination of population structure and, thus, estimates of stock composition. The baseline survey consisted of analysis of approximately 21,000 coho salmon in 138 populations from geographic areas where coho

salmon are likely to occur in British Columbia fisheries. These populations included 1 from Oregon, 17 from Washington, 111 from British Columbia, and 9 from southeast Alaska (Figure 1; Table 1). Regional population structure was apparent from coho salmon that formed 15 distinct groups and allowed estimation of stock composition by these groups.

Conversion of allele sizes between manual and automated sizing systems.—The ABI 377 automated sequencer was obtained in our laboratory during the 1998 fishery to shorten the processing time for the approximately 9,000 samples collected from fisheries throughout British Columbia. At that time the baseline microsatellite data consisted of manual gel data for only four (*Ots2*, *Ots3*, *Ots101*, and *Ots103*) of the eight microsatellite loci used in this analysis. For the 1998 fishery samples, we surveyed variation at *Ots3*, *Ots101*, and *Ots103* on the automated sequencer and retained *Ots2* on manual gels. Given the wide distribution of allele sizes of *Ots101* and *Ots103* and the limitation of three fluorescent dyes for microsatellites on the sequencer, we were not able at that time to analyze *Ots2* on the sequencer. Estimated allele sizes at *Ots3*, *Ots101*, and *Ots103* differed between the manual nondenaturing gels stained with ethidium bromide and the automated sequencer denaturing gels with fluorescently labeled alleles. To convert allele sizes between the two systems, we analyzed approximately 600 fish on both systems and determined the distributions of allele frequencies. By inspection of the allele frequencies, we were able to match specific allele sizes obtained from the sequencer to specific allele sizes from the manual gels and then convert the sizing in the automated sequencer data set to match that obtained from the manual gels. Estimated allele sizes from both systems were very highly correlated ($r^2 = 0.987$ for *Ots3*, 0.998 for *Ots101*, and 0.999 for *Ots103*). In general, sizes for the same allele from the sequencer were larger than those estimated from manual gels, and the differential increased directly with allele size.

Estimating stock composition.—Genotypic frequencies were determined at each locus in each population. The statistical package for the analysis of mixtures software program (SPAM; Debevec et al. 2000) was used to estimate stock composition of each mixture; this program uses maximum likelihood analysis to estimate stock composition, mainly using the convergent gradient algorithm (Pella et al. 1996). More alleles were present at the microsatellite loci than was practical for stock

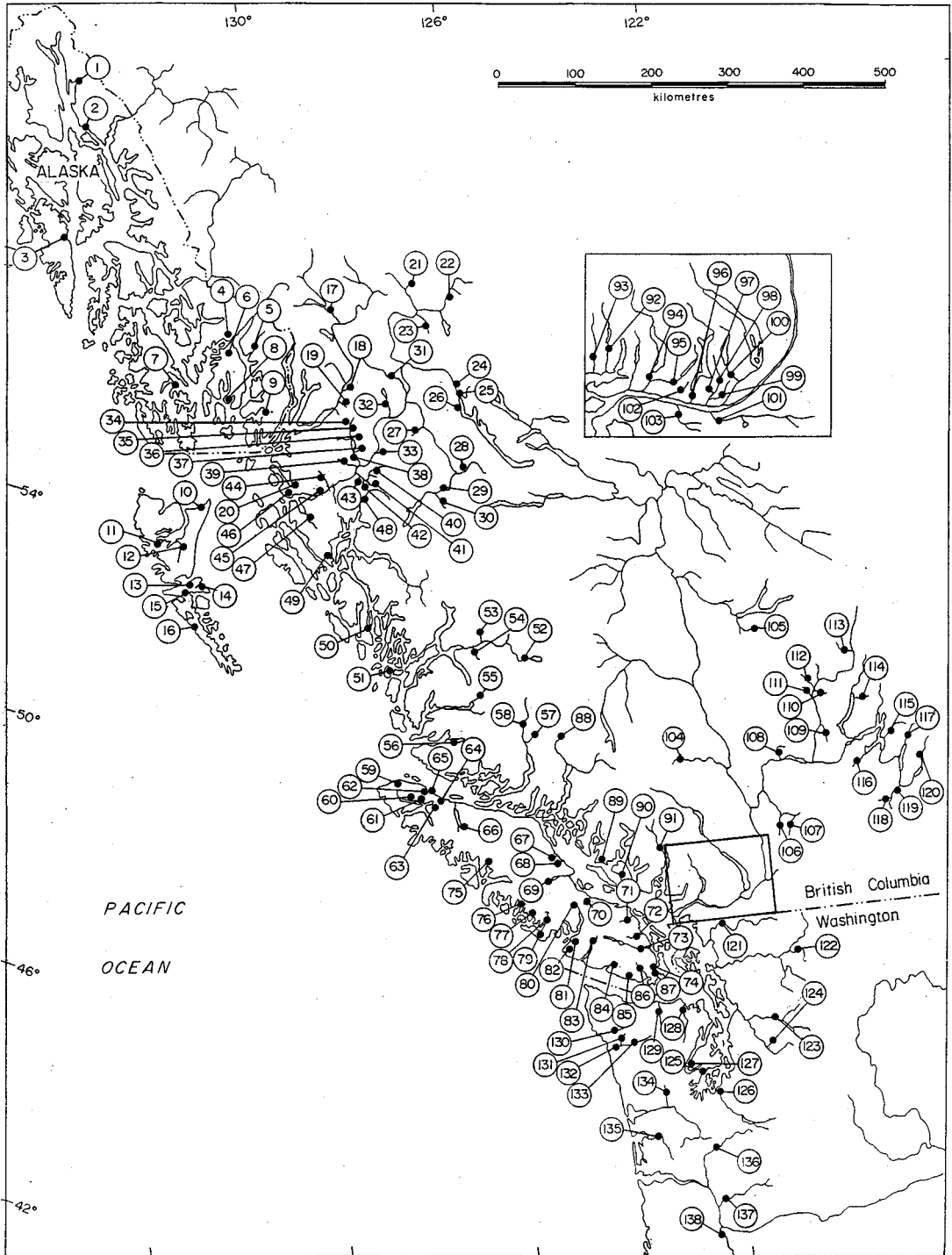


FIGURE 1.—Locations of the 138 coho salmon populations sampled to provide a genetic baseline. Numbers on the figure correspond to the population numbers in Table 1. The map inset is of the lower Fraser River.

TABLE 1.—Regions and populations within regions included in the survey of variation at eight microsatellite loci and two MHC exons in coho salmon from the Pacific Northwest. The number in parentheses after the population name refers to the location shown in Figure 1.

Region and subregion	Number of populations	Populations
Southeast Alaska (SEAK)	9	Berners (1), Gastineau Hatchery (2), Hidden Falls (3), Reflection Lake (4), Indian Creek (5), Margaret Creek (6), Karta (7), Whitman Lake (8), Hugh Smith (9)
Queen Charlotte Islands (QCI)		
North coast	3	Sangan River (10), Awun River (11), Yakoun River (12)
East coast	3	Deena (13), Copper River (14), Pallant Creek (15)
West coast	1	Tasu (16)
Nass River	3	Meziadin (17), Zolzap (18), Tseax (19)
North coast	1	Lachmach (20)
Upper Skeena River		
Upper drainage	3	Kluatantan (21), Sustut River (22), Motase (23)
Babine River	3	Babine Fence (24), Boucher (25), Upper Babine (26)
Bulkley River	4	Toboggan Creek (27), Bulkley River (28), Morice River (29), Owen (30)
Lower Skeena River		
Mid drainage	3	Kispiox (31), Kitwanga (32), Singlehurst (33)
Lower drainage	14	Hadenschild (34), Cedar (35), Clear (36), Deep (37), Kitsumkalum (38), Zymagotitz (39), Sockeye (40), Schulbuckhand (41), Clearwater (42), Coldwater (43), Exchamsiks (44), Kasiks (45), Green (46), Ecstall (47)
Central coast	11	Kitimat (48), Hartley Bay (49), Kitasoo (50), McLaughlin Bay (51), Atnarko (52), Salloomt (53), Thorsen (54), Sheemahant (55), Docee (56), Devereux (57), Klinaklini (58)
Northern Vancouver Island	8	Nahwitti (59), Wanokana (60), Stephens (61), Quatse (62), Waukwass (63), Cluxewe (64), Glen Lyon (65), Nimpkish (66)
Eastern Vancouver Island	8	Quinsam (67), Black Creek (68), Puntledge (69), Big Qualicum (70), Nanaimo (71), Chemainus (72), Cowichan (73), Goldstream (74)
Western Vancouver Island	13	Conuma (75), Cypre (76), Tranquil (77), Kennedy (78), Kootowis (79), Robertson Creek (80), Sarita (81), Pachena (82), Nitinat (83), San Juan (84), Kirby Creek (85), Sooke (86), Craigflower (87)
Southern mainland	6	Homathko (88), Lang Creek (89), Sliammon (90), Squamish (91), Seymour (92), Capilano River (93)
Fraser River		
Lower drainage	10	Pitt (94), Alouette (95), Stave (96), Inch Creek (97), Norrish (98), Nicomen (99), Chehalis (100), Chilliwack (101), Kanaka Creek (102), Salmon River (103)
Upper drainage	2	Bridge River (104), McKinley Creek (105)
Thompson River		
Lower drainage	3	Spius Creek (106), Coldwater (107), Deadman (108)
North Thompson	5	Louis Creek (109), Dunn Creek (110), Lemieux Creek (111), Mann (112), Lion (113)
South Thompson	7	Momich (114), Eagle (115), Salmon (116), Danforth (117), Duteau (118), Besette (119), Lang Channel (120)
Puget Sound	6	Nooksack (121), Marblemount (122), Wallace (123), Grizzly (124), Minter (125), Nisqually (126)
Hood Canal	1	Dewatto (127)
Juan de Fuca	2	Dungeness (128), Elwha (129)
Coastal	6	Quillayute (130), Clearwater (131), Shale (132), Queets (133), Bingham (134), Willapa (135)
Columbia River	3	Cowlitz (136), Lewis (137), Clackamas (138)

identification applications. We combined low-frequency alleles with adjacent higher-frequency alleles to reduce the number of genotypic frequencies to be estimated; loss in the ability to discriminate among stock groups was minor. Allele designations for the microsatellite loci have been outlined by Wither et al. (unpublished). The binning strategy was similar to that outlined by Small et al. (1998b). Briefly, for stock identification anal-

ysis we condensed the number of alleles: 18 alleles at *Ots2* to 8 alleles (36 genotypes), 22 at *Ots3* to 12 (78 genotypes), 31 at *Ots101* to 14 (105 genotypes), 39 at *Ots103* to 13 (91 genotypes), 26 at *Okil* to 17 (153 genotypes), 52 at *Okil0* to 21 (231 genotypes), 99 at *Okil00* to 19 (190 genotypes), and 46 at *Okil01* to 19 (190 genotypes). For the MHC loci, no compression of 17 alleles (153 genotypes) at the $\alpha 1$ locus was instituted, and 19

alleles at the $\alpha 2$ locus were condensed to 17 alleles (153 genotypes). The microsatellite loci *Ots2*, *Ots3*, *Ots101*, *Oki1*, *Oki10*, and *Oki101* were assumed to be in Hardy–Weinberg equilibrium, and expected genotypic frequencies were determined from the observed allele frequencies.

Null or nonamplifying alleles were present at *Ots103* and *Oki100* in some populations, and we investigated whether genotypic frequencies calculated for the baseline samples at these loci and used in mixed-stock analysis could be observed frequencies or those expected under Hardy–Weinberg equilibrium. Either option was possible for estimating stock compositions. For each of 15 regions surveyed, we constructed a series of hypothetical fishery samples that contained fish from just that region (Table 2). Bias was evaluated for each of the regions when model inputs were either observed or expected genotypic frequencies for each of the 138 populations. We also further binned the number of alleles at each locus, reducing the number of alleles at both *Oki100* and *Ots103* to 10 (55 genotypes). Observed and expected genotypic frequencies under Hardy–Weinberg equilibrium were used separately as model inputs for this additional allele binning strategy. Bias was reduced in estimated stock compositions for all regions under the assumption of genotypic frequencies in Hardy–Weinberg expectations (Table 2), regardless of whether observed genotypic frequencies within populations violated this assumption. Further binning of the number of alleles at these three loci had little effect on the bias observed. For subsequent estimation of stock composition, genotypic frequencies expected under Hardy–Weinberg equilibrium were used for all loci for each of the 138 populations in the baseline, and the original allele binning was employed for these two loci.

Reported stock compositions for the CWT and actual fishery samples are the point estimates of each mixture analyzed; variance estimates were derived from 100 bootstrap simulations. Each baseline population and fishery sample was sampled with replacement in order to simulate random variation involved in the collection of the baseline and fishery samples. Reported stock composition for simulated mixtures was the bootstrap mean and standard deviation.

Coastal British Columbia is divided into statistical areas for salmon catch reporting and management (Figure 2). Based upon previous recoveries of CWTs in marine fisheries (PSC 1994), we developed three baseline sets of populations for

estimating stock compositions in marine fisheries in British Columbia. The three baselines were developed to account for the likely origin of coho salmon in specific fisheries. For each baseline, we excluded population samples from geographic areas that rarely or never contributed to the fisheries based on previous CWT analyses. These population samples were excluded to reduce any bias present in the estimated stock compositions. Stock compositions for fishery samples from Statistical Areas 14–23, 123, 28–29, and Areas 3–5 in Washington were estimated with a southern baseline that included 83 populations from Oregon, Washington, the Fraser River, Vancouver Island, and the southern mainland. The southern baseline also included the two most southern populations of the central coast (Klinaklini River and Devereux Creek) as part of the mainland component. Stock compositions for fishery samples from Areas 6–13, 24–27, and 124–127 were estimated with a central baseline that included all populations surveyed, except those from southeast Alaska. Stock compositions for samples from Areas 1–6 were estimated with a northern baseline that included all 138 populations in the analysis. Drainage-specific baseline populations were used to estimate stock compositions in freshwater test fisheries or commercial fisheries in the Fraser River in southern British Columbia and the Skeena River in northern British Columbia.

Results

Population Structure

If a regional genetic structure among populations contributing to a fishery exists, then it is unnecessary to survey all individual populations that contribute to the fishery. The portion of the mixed-stock sample derived from unsampled populations is allocated to sampled populations from the same region, reducing the cost and complexity of establishing a baseline sufficient for mixture analysis. The sampled populations constitute the baseline used to estimate stock compositions in mixed-fishery samples. Regional structure was observed in the baseline populations, the Thompson River populations being the most distinct of 15 geographically based groups or stocks (Table 2; Figure 3). For estimating stock composition, the north (one population) and central coastal regions (11 populations) of British Columbia were combined into a single region, as were Hood Canal (one population) and the Strait of Juan de Fuca (two populations) in Washington.

TABLE 2.—Mean bias (%) in estimated stock compositions for 15 regional stocks of Pacific Northwest coho salmon for two sets of loci (set 1: $\alpha 1$, $\alpha 2$, *Ots2*, *Ots3*, *Ots101*, and *Ots103*; Set 2: $\alpha 1$, $\alpha 2$, *Oki1*, *Oki10*, *Oki100*, and *Oki101*). The loci *Oki100* and *Ots103* were generally not in Hardy–Weinberg equilibrium in the 138 populations surveyed. Simulations were conducted under the following conditions for these two loci: (1) genotypic distributions in conformance to Hardy–Weinberg expectations (genotypic state), (2) Hardy–Weinberg genotypic distributions with additional binning of alleles (binned genotype), (3) observed genotypic distributions (phenotype), or (4) observed genotypic distributions with binning of alleles (binned phenotype). Genotypic distributions for other loci in each set were those under Hardy–Weinberg expectations. Simulations were conducted using a 138-population baseline, 200 fish in the mixture sample, and 500 resamplings in the mixture sample and baseline populations; each mixture sample was composed solely of coho salmon from 1 of the 15 regions surveyed. Bias estimated was 100% less the bootstrap mean.

State	SE Alaska	Queen Charlotte Island	Nass River	Upper Skeena River	Lower Skeena River	Central coast	WCVI ^a	ECVI ^a
Loci: set 1								
Genotype	7	7	12	8	9	8	14	8
Binned genotype	7	8	13	7	9	8	14	9
Phenotype	19	20	23	17	19	15	23	11
Binned phenotype	16	17	19	15	16	12	20	10
Loci: set 2								
Genotype	8	10	11	11	9	8	14	3
Binned genotype	8	10	11	11	9	8	12	6
Phenotype	21	28	21	18	20	16	22	10
Binned phenotype	17	22	18	16	16	13	19	7

^a WCVI = western coast of Vancouver Island; ECVI = eastern coast of Vancouver Island; NCVI = northern coast of Vancouver Island.

Comparison of Individual Loci

Determining the relative power of individual loci for regional discrimination is of prime importance for practical stock identification applications. Of the 10 markers surveyed in our study, the MHC exons were individually more effective for stock identification than any of the eight microsatellite loci (Table 3). These two exons, although linked, differed in their ability to discriminate among fish from different regions. The exons combined were nearly as effective, on average, as the eight microsatellite loci combined for regional stock identification. The microsatellite loci *Oki10*, *Oki100*, *Oki101*, and *Ots103* were all approximately of equal utility for general applications; *Ots2* and *Ots3* were the least effective loci for regional discrimination of populations. Clearly, not all loci were equally effective in stock identification, but the usefulness of the loci varied among regions. Thus, the appropriate suite of genetic markers for coho salmon mixed-stock analysis depends on the geographic scope of the suitable baseline.

Coho salmon from some regions were more easily differentiated than those from other regions. The distinctive Thompson River coho were clearly well differentiated from coho salmon in other regions, regardless of the loci examined. When all 10 loci surveyed were used, coho salmon from the west coast of Vancouver Island (WCVI) were the

most difficult to discriminate when mixed with populations from other regions, whereas those from the east coast of Vancouver Island (ECVI) populations were accurately discriminated (Table 3). The average regional bias in estimated stock compositions for simulated fishery samples comprising fish from only a single region analyzed with the complete baseline was 8%. In marine applications, fishery samples containing fish from only a single region will rarely if ever be encountered. However, the bias in estimated stock compositions is maximized at very high or very low proportions in the mixture, so the average regional bias realized for most applications will be lower than 8%.

Some loci were particularly effective at discriminating populations from specific regions. For example, the two MHC exons were more powerful for identifying coastal Washington and Columbia River populations than were microsatellite loci. However, the combined microsatellite loci were more effective at identifying Vancouver Island coho salmon than were the MHC exons. Although the overall discriminatory ability of *Ots101* was only moderate, it was particularly effective for discriminating Thompson River coho salmon (e.g., the average estimated composition of pure samples of Thompson River coho salmon was 98% using only this single locus in the 138-population baseline; Table 3).

TABLE 2.—Extended.

State	NCVI ^a	South mainland	Lower Fraser River	Thompson River	Puget Sound	Coastal Washington	Columbia River	Mean
Loci: set 1								
Genotype	9	13	7	1	10	5	4	8
Binned genotype	9	13	7	1	9	5	4	8
Phenotype	18	23	12	6	21	20	16	17
Binned phenotype	15	19	11	3	17	13	11	14
Loci: set 2								
Genotype	6	11	4	2	8	7	4	8
Binned genotype	8	11	6	1	8	6	4	8
Phenotype	16	21	11	4	21	21	14	18
Binned phenotype	14	19	10	2	16	16	10	14

Thompson and Upper Skeena River Identifications

Since 1998, Canadian salmon fisheries have been conducted to minimize mortality of Thompson River and upper Skeena River coho salmon. Accurate estimates of these two stock components in mixed-fishery samples were thus essential for proper management. We were also interested in separating Thompson River from upper Fraser River populations, a stock of uncertain status that has genetic characteristics most similar to Thompson River populations (Figure 3). Given the low abundance and conservation concerns for the Thompson River and upper Skeena River stocks, we expected them to occur in only small proportions in mixed-fishery samples. We evaluated our ability to provide accurate estimates of these three stock components using 6 of the 10 genetic markers when any one of them composed 1, 3, or 5% of simulated fishery samples. Estimated stock compositions of the simulated fishery samples indicated that estimated Thompson River proportions were generally quite accurate even when the stock composed only 1% of the simulated sample; this accuracy was maintained over all baselines (Table 4). The Thompson River stock was distinguished from the upper Fraser River stock by using only the six genetic markers surveyed in the 1999 mixed-stock fishery samples. The upper Skeena River stock was also estimated with a high degree of accuracy with both the central and northern baselines when this stock composed 5% or less of

the mixture (Table 4). We concluded that use of microsatellite and MHC variation to estimate the Thompson River or upper Skeena River stock composition was feasible, regardless of the baseline used for estimation.

Estimates of Regional Stock Composition

We evaluated whether the genetic differentiation observed among the 138 coho salmon populations included in the baseline was sufficient for mixed-stock analysis aimed at estimating regional contributions to fishery samples. Three fishery-mixture samples were simulated, and stock compositions were estimated for 16 regions. For stock contributions ranging from 0% to 20% of the mixture, the estimated bootstrap mean of a region was usually within 0.0–1.5% of the actual composition in the mixture (Table 5). Mean estimated stock compositions of Thompson, upper Fraser, and upper Skeena rivers were all within 0.2% of the actual value in the mixture. Some bias was observed when regions not present in the mixture were included in the baseline. For example, 5% of the sample of mixture 3 was assigned to regions not present in the sample. Thus, judicious baseline selection (i.e., exclusion of baseline samples from locations that might reasonably be expected not to contribute fish to a fishery mixture) can be used to minimize bias in estimated stock compositions. We thus used three baselines to estimate stock compositions for fishery samples in British Co-

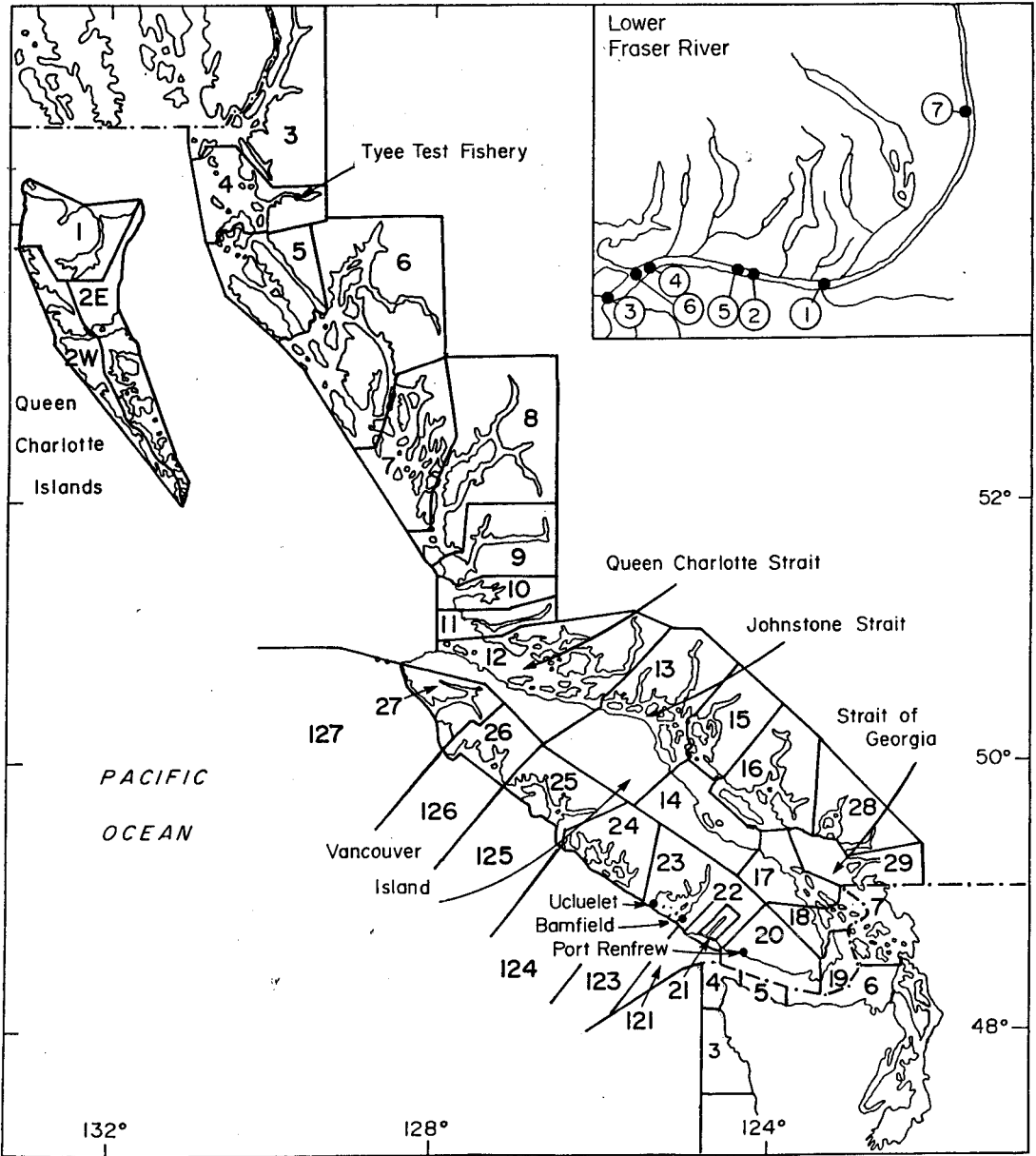


FIGURE 2.—Fishery locations and statistical areas in British Columbia and the Strait of Juan de Fuca in Washington. Inset depicts lower Fraser locations: Strawberry Island (1), Whonnock (2), selective fisheries (3), Cottonwood (4), Albion test fishery (5), tangle-net test fishery (6), and Yale fish wheel (7).

lumbia, based upon the historical presence of CWTs in the areas' fisheries.

For eight regional groups of coho salmon we evaluated the accuracy of estimated stock compositions in simulated mixtures, based on compositions of the target region ranging from 0–100% and only 6 of the 10 loci surveyed being used. Very little bias was observed when the region

composed less than 40% of the mixture (Figure 4). When specific regions composed more than 40% of the mixture sample, there was a tendency to underestimate the actual component of the target region, but the underestimation of the actual component was usually less than 5% when regional compositions were less than 80% of the mixture. We concluded that accurate estimation of regional

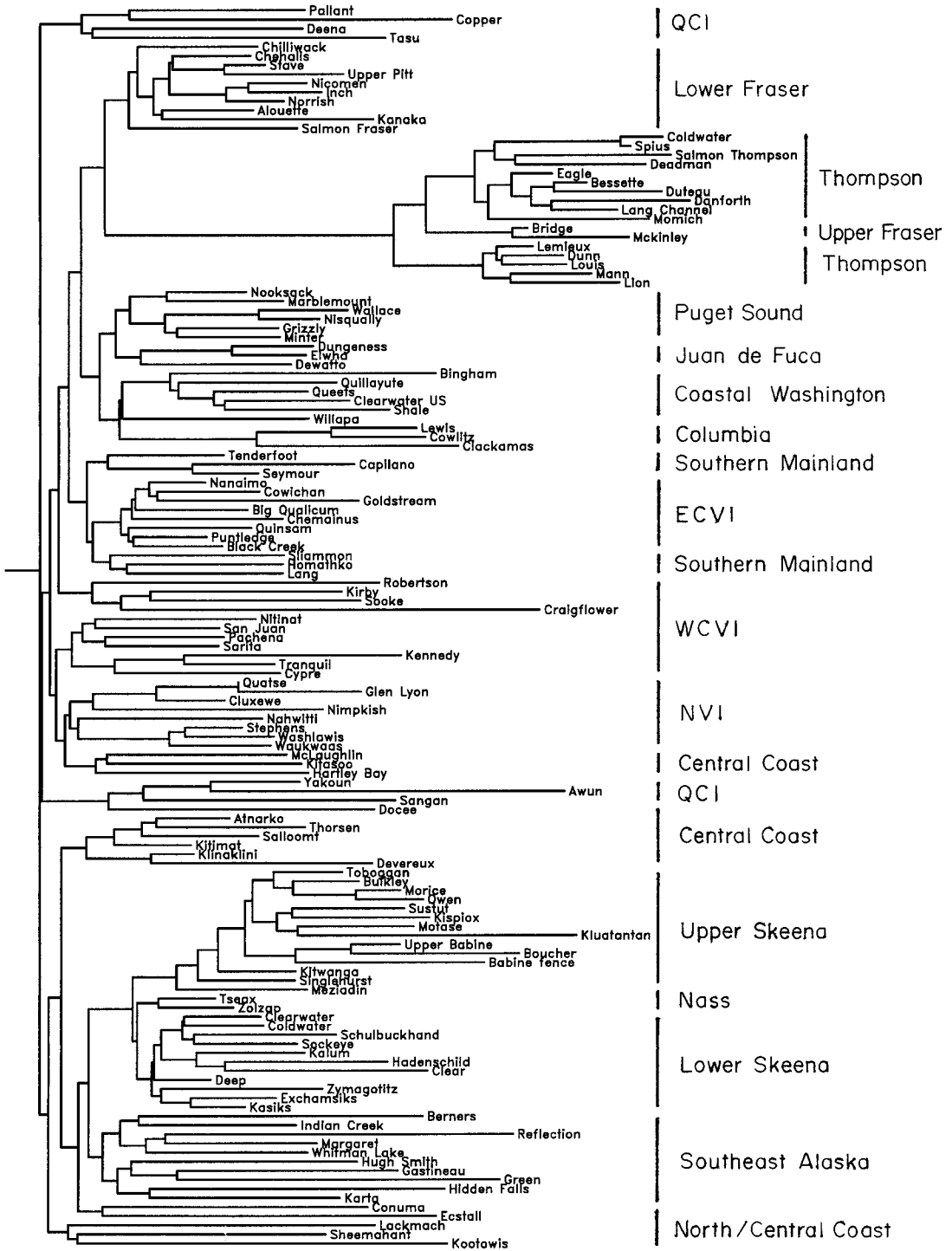


FIGURE 3.—Neighbor-joining dendrogram based on Cavalli-Sforza and Edwards (1967) chord distance for 138 coho salmon populations in southeast Alaska, British Columbia, and Washington; WCVI is the west coast of Vancouver Island, ECVI is the east coast of Vancouver Island, and QCI is Queen Charlotte Islands.

TABLE 3.—Mean bias (%) in estimated stock compositions for 15 regional stocks of coho salmon calculated with individual loci and with combinations of two MHC exons and eight microsatellite loci. Simulations were conducted using a 138-population baseline, 200 fish in the mixture sample, and 500 resamplings in the mixture sample and baseline samples; each mixture sample was composed solely of coho salmon from one region. For multiple loci, set 1 includes *Ots2*, *Ots3*, *Ots101*, and *Ots103*; set 2 includes *Oki1*, *Oki10*, *Oki100*, and *Oki101*; and set 3 includes both MHC exons and all microsatellite loci.

Locus	South-east Alaska	Queen Charlotte Island	Nass River	Upper Skeena River	Lower Skeena River	Central coast	WCVI ^a	ECVI ^a	NCVI ^a	South-main-land	Lower Fraser River	Thompson River	Puget Sound	Coastal Washington	Columbia River	Mean
Single locus																
$\alpha 2$	20	16	40	11	21	22	35	34	35	29	25	3	18	10	9	22
$\alpha 1$	25	34	32	10	21	34	42	24	29	43	32	7	33	16	12	26
<i>Oki101</i>	24	31	55	19	43	55	58	33	43	36	28	3	49	52	15	36
<i>Oki10</i>	29	32	56	27	54	49	41	43	71	52	31	5	35	22	17	38
<i>Ots103</i>	48	25	60	13	35	48	50	35	33	62	28	6	53	54	21	38
<i>Oki100</i>	32	25	44	22	57	62	51	51	49	47	41	6	58	45	25	41
<i>Ots101</i>	44	35	63	11	39	55	53	59	42	56	25	2	67	53	45	43
<i>Oki1</i>	64	57	69	20	68	56	41	54	39	68	56	13	62	50	22	49
<i>Ots3</i>	24	57	74	19	57	64	66	69	69	66	70	5	65	60	84	57
<i>Ots2</i>	64	41	89	71	72	78	60	76	84	75	68	12	67	71	13	63
Multiple loci																
$\alpha 1, \alpha 2$	11	8	18	7	13	13	19	15	18	18	13	2	13	7	4	12
Set 1	16	13	28	5	18	22	27	19	17	24	12	1	28	23	10	18
Set 2	12	15	20	8	20	19	15	12	15	17	10	1	18	17	7	14
Set 1,2	11	13	13	7	14	22	15	7	9	14	6	2	13	12	6	10
Set 3	9	12	8	8	9	6	14	3	6	11	4	2	8	7	6	8

^a WCVI = western coast of Vancouver Island; ECVI = eastern coast of Vancouver Island; NCVI = northern coast of Vancouver Island.

stock compositions should be available when the genetic data, as outlined in our study, are applied to actual mixed-fishery samples.

Identification of Specific Populations

Accurate differentiation of mixture samples to specific populations was generally not possible because not all populations contributing to a fishery sample were included in the baseline. However, situations could occur in which all populations contributing to a fishery sample could be sampled. Such a case arose for the proposed “mark-only” fishery for coho salmon in southern British Columbia and Washington State in which hatchery fish, marked by a clipped adipose fin, may be retained but naturally spawned fish, identified by the presence of an adipose fin, must be released. We evaluated the accuracy of the estimated stock composition for each Canadian population by simulating mixtures for six southern British Columbia hatcheries for which population-specific estimates of stock composition are required. The baseline was substantially reduced to include only the six Canadian populations, but all populations from Washington were retained. Analysis of three simulated mixtures indicated that accurate hatchery-specific estimates of stock composition could be

obtained if applied to samples from mark-only fisheries (Table 6).

Analysis of a Sample of Known Origin

The superiority of using expected over observed genotypic frequencies for baseline samples was confirmed for the mixture sample containing fish identified by their CWTs. The sum of errors in estimated stock composition was always less when expected genotypic frequencies for all loci were used than when observed genotypic frequencies for some loci were used (Table 7). We also estimated the stock composition of the known CWT sample for the three baselines used in estimating mixed-fishery samples and for the reduced sets of loci used for estimating stock composition in the 1997–1998 and 1999 mixed-stock fishery samples. For the 138-population northern baseline, the average regional error for the 14 indicated regions was less than 2% per region for the 264-fish CWT sample. Some differences were observed between the sets of loci used for estimated stock compositions of specific regional groups. Simulation analyses (not reported here) previously indicated that the loci used for 1997 and 1998 stock composition estimates (set 1) did not provide sufficient distinction between upper Fraser and Thompson

TABLE 4.—Estimated percentage composition of simulated mixtures of Thompson River, upper Fraser River, or upper Skeena River coho salmon. Simulated mixtures were constructed with target stocks present at 1, 3, and 5% of the mixture; three baselines (southern, central, and northern) were used to estimate compositions of the Thompson and upper Fraser mixtures and two baselines for the upper Skeena mixtures. Data for six markers were incorporated in the estimation procedure: $\alpha 1$, $\alpha 2$, *Oki1*, *Oki10*, *Oki100*, and *Oki101*. Each mixture of 200 fish was generated 500 times with replacement, and stock compositions of the mixtures were estimated by resampling each baseline population with replacement to obtain a new distribution of allele frequencies.

Baseline	Region (river)	1% mixture		3% mixture		5% mixture	
		Actual	Estimate (SD)	Actual	Estimate (SD)	Actual	Estimate (SD)
Southern	Thompson	1.0	1.2 (0.8)	3.0	2.9 (1.2)	5.0	4.9 (2.1)
	Upper Fraser	0.0	0.1 (0.2)	0.0	0.1 (0.3)	0.0	0.2 (0.4)
	Thompson	0.0	0.4 (0.4)	0.0	0.5 (0.5)	0.0	0.6 (0.7)
Central	Upper Fraser	1.0	0.8 (0.8)	3.0	2.8 (1.3)	5.0	4.3 (2.2)
	Thompson	1.0	1.1 (0.8)	3.0	2.8 (1.2)	5.0	5.2 (2.2)
	Upper Fraser	0.0	0.1 (0.3)	0.0	0.2 (0.3)	0.0	0.1 (0.4)
Northern	Thompson	0.0	0.5 (0.5)	0.0	0.7 (0.6)	0.0	0.6 (0.2)
	Upper Fraser	1.0	0.8 (0.6)	3.0	2.3 (1.1)	5.0	4.6 (1.6)
	Thompson	1.0	1.1 (0.7)	3.0	2.9 (1.2)	5.0	5.0 (1.5)
Central	Upper Fraser	0.0	0.1 (0.2)	0.0	0.1 (0.2)	0.0	0.0 (0.0)
	Thompson	0.0	0.3 (0.3)	0.0	0.4 (0.5)	0.0	0.3 (0.4)
	Upper Fraser	1.0	1.0 (0.7)	3.0	2.6 (1.1)	5.0	4.7 (1.4)
Central	Upper Skeena	1.0	1.3 (1.0)	3.0	2.9 (1.4)	5.0	5.0 (2.1)
Northern	Upper Skeena	1.0	1.1 (0.8)	3.0	3.0 (1.3)	5.0	4.8 (1.7)

River populations to provide reliable estimates of stock composition for these two regions. The upper Fraser River component tended to be overestimated using these loci in both the simulated and CWT sample. Thus, proportions for these two regions were combined in reporting of 1997 and 1998 mixed-stock results, but separated in 1999,

owing to increased interregional resolution (Table 4). Increased accuracy was obtained when all 10 loci and exons were used to estimate stock compositions, but the average regional increase in accuracy was marginal (Table 7). Analyses of the 240-fish known CWT sample with the central baseline produced results similar to the analysis with

TABLE 5.—Estimated percentage composition of three simulated mixtures of coho salmon incorporating variation at two MHC exons ($\alpha 1$, $\alpha 2$) and four microsatellite loci (*Oki1*, *Oki10*, *Oki100*, *Oki101*) and estimated with a 138-population baseline. Each mixture of 200 fish was generated 500 times with replacement, and stock compositions of the mixtures were estimated by resampling each baseline population with replacement to obtain a new distribution of allele frequencies.

Region	Mixture 1		Mixture 2		Mixture 3	
	Actual	Estimated (SD)	Actual	Estimated (SD)	Actual	Estimated (SD)
Southeast Alaska	9	7.9 (2.2)	0	0.5 (0.6)	0	0.8 (0.7)
Queen Charlotte	4	4.0 (1.6)	5	4.8 (1.7)	0	0.4 (0.5)
Nass	7	6.5 (2.4)	0	0.4 (0.6)	0	1.1 (1.3)
Upper Skeena	2	2.3 (1.2)	3	2.8 (1.3)	1	1.2 (0.9)
Lower Skeena	11	11.2 (2.8)	0	0.0 (1.2)	20	18.9 (3.1)
Northcentral coast	11	11.3 (2.5)	20	19.4 (3.4)	10	11.0 (2.7)
ECVI ^a	10	10.0 (2.7)	15	15.3 (3.3)	0	1.2 (1.1)
WCVI ^a	8	8.7 (2.3)	15	14.9 (2.9)	0	1.7 (1.3)
NCVI ^a	4	4.5 (1.9)	0	1.4 (1.2)	15	14.5 (2.9)
Southern mainland	0	1.1 (1.0)	10	9.2 (2.7)	15	12.8 (3.1)
Lower Fraser	17	16.2 (3.1)	10	9.3 (2.4)	5	4.2 (1.8)
Upper Fraser	0	0.1 (0.2)	1	0.8 (0.8)	2	1.7 (1.1)
Thompson	1	1.1 (0.8)	3	3.2 (1.3)	5	5.2 (1.6)
Puget Sound	11	9.6 (2.7)	15	12.9 (3.1)	5	5.2 (2.0)
Coastal Washington	5	5.4 (1.9)	2	2.7 (1.4)	17	15.5 (3.1)
Columbia River	0	0.1 (0.3)	1	1.0 (0.8)	5	4.8 (1.7)

^a ECVI = eastern coast of Vancouver Island; WCVI = western coast of Vancouver Island; NCVI = northern coast of Vancouver Island.

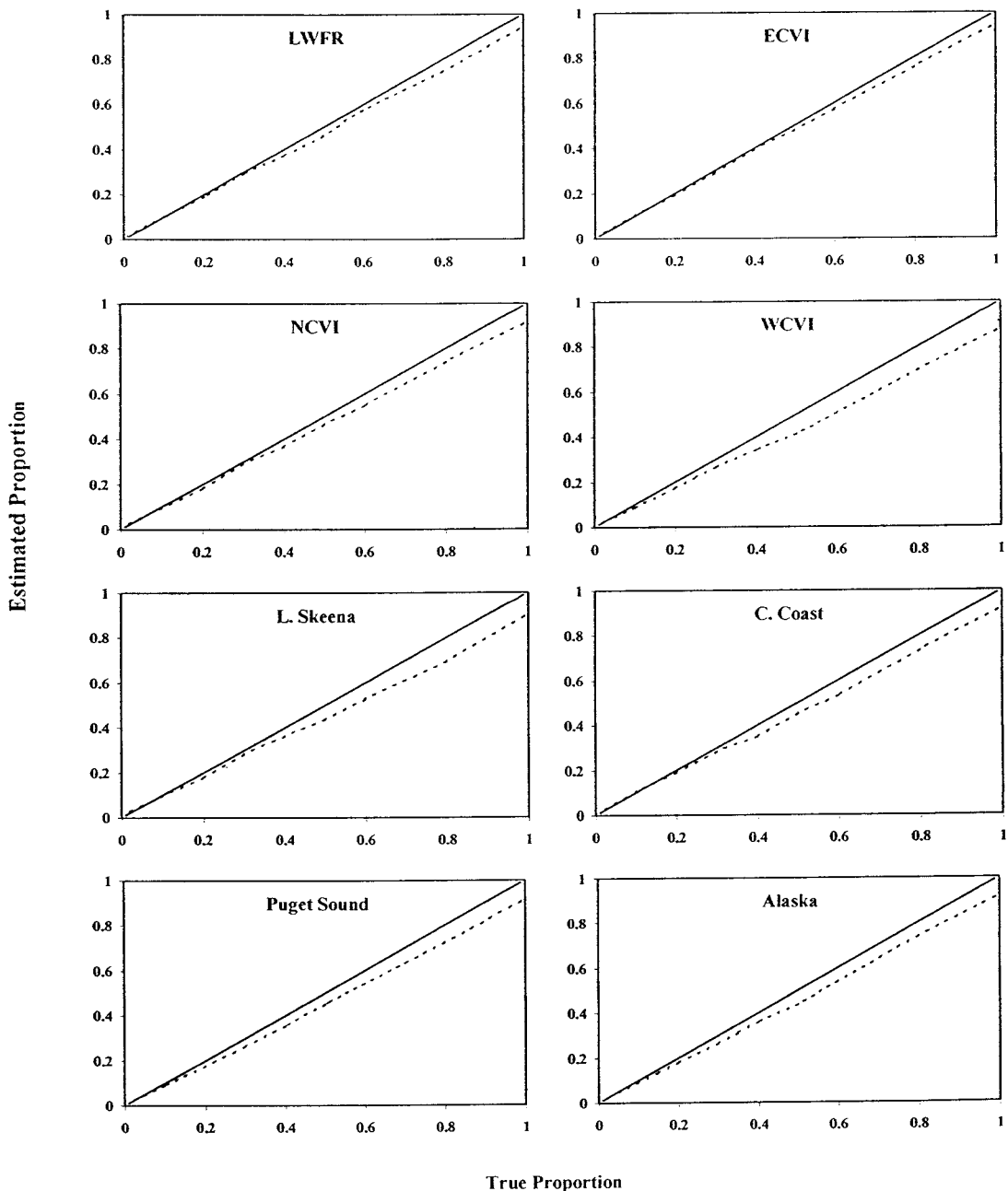


FIGURE 4.—Estimated versus true proportions for eight stocks of coho salmon for mixture sample sizes of 200 fish calculated with a 138-population baseline. Bootstrap means were derived from 500 estimated stock compositions. Abbreviations are as follows: LWFR is the lower Fraser River, ECVI is the eastern coast of Vancouver Island, NCVI is the northern coast of Vancouver Island, WCVI is the western coast of Vancouver Island, L. Skeena is the lower Skeena River, and C. Coast is the central coast.

TABLE 6.—Estimated percentage composition of three simulated mixtures of coho salmon incorporating variation at two MHC exons and eight microsatellite loci. Simulations were undertaken to examine accuracy of individual population estimates for a hypothetical mark-only fishery in southern British Columbia. Canadian populations were chosen to represent hatchery populations of adipose-clipped fish. The baseline used to estimate stock compositions includes the six Canadian populations and all Washington populations. Each mixture of 200 fish was generated 500 times with replacement, and stock compositions of the mixtures were estimated by resampling each baseline population with replacement to obtain a new distribution of allele frequencies.

Population	Mixture 1		Mixture 2		Mixture 3	
	Actual	Estimated (SD)	Actual	Estimated (SD)	Actual	Estimated (SD)
Robertson	25.0	24.2 (3.2)	0.0	0.0 (0.1)	15.0	14.5 (2.5)
Nitinat	20.0	20.2 (2.8)	10.0	10.1 (2.3)	10.0	10.2 (2.3)
Big Qualicum	0.0	0.3 (0.5)	20.0	19.8 (3.0)	25.0	24.8 (3.2)
Quinsam	10.0	10.2 (2.3)	5.0	5.6 (1.9)	25.0	25.5 (3.3)
Chehalis	10.0	10.5 (2.4)	20.0	20.6 (3.1)	5.0	5.1 (1.7)
Chilliwack	5.0	5.4 (1.8)	25.0	24.3 (3.3)	0.0	0.4 (0.5)
Washington	30.0	29.2 (3.2)	20.0	19.6 (2.8)	20.0	19.7 (2.8)

the northern baseline. In analysis with the southern baseline and the loci used in the 1999 stock composition estimate (set 2), the largest error in estimated stock compositions of the 94-fish known CWT sample was in the ECVI component (error about 8%; Table 7). However, given the results from the simulated mixtures (Figure 4), errors of this magnitude are probably restricted to the peculiarities of the 94-fish sample, rather than being caused by a systematic bias in estimated stock compositions. For all baselines, standard deviations of estimated stock compositions were, on average, lower when all 10 markers were used for estimation instead of subsets of the loci (Table 7).

Analysis of Fishery Samples: Southern Baseline

The estimated proportion of Thompson River coho salmon in mixed-stock samples was of key importance to Canadian fishery managers in 1998 and 1999. In 1998, we were unable to distinguish reliably between Thompson River and upper Fraser River using the loci surveyed in the mixed-stock sample. Indeed, it was only after the introduction of DNA analysis to the mixed-stock samples that separation of the two closely related stock groups was considered of management importance. Therefore, upper Fraser and Thompson stock estimates were combined in the 1998 mixed-fishery samples, but reported separately for the 1999 samples because of the change in the loci surveyed. Estimated stock compositions of Thompson River coho salmon were never above 2% in the Pacific Salmon Commission (PSC) seine test fishery conducted from late July to late August in Area 20 (Strait of Juan de Fuca) and rarely above 2% for the PSC gill-net test fishery conducted from early July through mid-August in a similar area

(Appendix 1). The combined upper Fraser and Thompson River component was rarely above 3%. In the recreational fishery samples from Area 20, higher proportions of upper Fraser and Thompson stocks were observed than in the seine and gill-net fisheries, but the sampling also extended longer, typically to mid-September. Analysis of recreational samples from late August through early September indicated that upper Fraser and Thompson populations could compose 5% or more of the sample. September samples from the 1998 recreational fishery in Washington's Area 5 indicated that upper Fraser and Thompson populations composed nearly 5% of the sample, and Thompson River coho salmon constituted 1–6% of the samples from the troll fishery in Washington's Area 4 (Appendix 1). Estimated stock composition of the Thompson River stock vary with the gear and time of sampling.

Recreational fishery sampling in the Strait of Georgia (Areas 14–19) indicated that coho from Vancouver Island, the lower British Columbia mainland, the lower Fraser River, and Puget Sound predominated the catch in the summer, but October samples in Area 14 indicated that ECVI stock was predominant, composing 85% of the sample (Appendix 1). By October, coho salmon from other areas have probably moved from the Strait of Georgia and closer to their respective spawning grounds.

The major contributor to fisheries in Canada's Area 20 in the Strait of Juan de Fuca was the Puget Sound stock, composing nearly 40% of the coho sampled in the seine and gill-net test fisheries (Appendix 1). However, the relative proportion of the Puget Sound stock in Canadian recreational fish-

TABLE 7.—Percentage composition (SD) of a sample of coded-wire-tagged coho salmon obtained from fisheries in British Columbia in 1997 and estimated with three sets of loci for three groups of baseline populations. Because all fish in the sample were marked with coded wire tags, the actual composition of the sample is known. Set-1 loci include $\alpha 1$, $\alpha 2$, *Ots2*, *Ots3*, *Ots101*, and *Ots103*; set-2 loci include $\alpha 1$, $\alpha 2$, *Okil*, *Okil0*, *Okil00*, and *Okil01*; set-3 loci include $\alpha 1$, $\alpha 2$, and all eight microsatellite loci. In state 1, the expected Hardy–Weinberg genotypic frequencies were used for all loci for the appropriate baseline populations. In state 2, observed genotypic frequencies for *Okil00* and *Ots103* were used.

Region	Actual	State 1			State 2		
		Set 1	Set 2	Set 3	Set 1	Set 2	Set 3
Northern baseline (138 populations)							
<i>N</i>	264	264	264	264	264	264	264
Southeast Alaska	9.1	6.8 (2.0)	4.0 (1.5)	6.0 (1.7)	5.2 (1.8)	3.8 (1.6)	4.8 (1.3)
Queen Charlotte	20.1	16.8 (2.9)	16.8 (2.8)	16.3 (2.2)	17.4 (2.6)	16.1 (2.4)	15.5 (2.3)
Nass	0.4	1.8 (1.4)	0.4 (0.6)	2.3 (1.3)	1.6 (1.4)	0.7 (1.2)	2.2 (1.1)
Upper Skeena	0.8	0.0 (0.4)	1.7 (0.9)	0.4 (0.4)	0.2 (0.4)	0.4 (0.8)	0.3 (0.6)
Lower Skeena	0.0	3.7 (2.0)	0.9 (1.2)	1.1 (1.1)	3.1 (1.7)	4.0 (1.7)	3.1 (1.7)
Northcentral coast	34.1	32.8 (3.2)	37.9 (3.6)	34.3 (3.4)	32.6 (3.5)	36.5 (3.5)	35.5 (3.7)
ECVI ^a	9.8	11.5 (3.2)	12.6 (3.1)	12.1 (3.7)	14.7 (3.4)	13.3 (3.1)	14.9 (2.8)
WCVI ^a	3.4	6.2 (2.9)	2.8 (1.9)	3.4 (1.8)	6.5 (2.4)	3.5 (2.1)	3.9 (1.8)
NCVI ^a	0.0	0.5 (1.2)	2.1 (1.4)	2.4 (1.3)	1.3 (1.9)	1.5 (1.6)	1.5 (1.7)
Southern mainland	3.8	3.7 (2.1)	1.4 (1.8)	1.6 (1.4)	0.8 (1.6)	1.2 (1.6)	0.6 (1.0)
Lower Fraser	7.2	8.3 (2.6)	8.4 (2.5)	9.7 (2.4)	8.2 (2.6)	10.1 (2.5)	9.2 (2.7)
Upper Fraser	0.0	0.4 (0.4)	0.0 (0.0)	0.0 (0.2)	0.4 (0.4)	0.0 (0.1)	0.0 (0.0)
Thompson	1.5	1.4 (0.8)	1.9 (0.8)	1.5 (0.8)	1.1 (0.9)	1.7 (0.8)	1.5 (0.7)
Washington	9.8	6.2 (2.4)	9.0 (2.4)	9.0 (2.4)	6.8 (2.7)	7.3 (2.3)	6.9 (1.8)
Σ error		23.0	24.3	21.0	30.0	29.7	30.9
Σ SD		27.4	24.4	23.0	27.1	25.3	23.1
Central baseline (128 populations)							
<i>N</i>	240	240	240	240	240	240	240
Queen Charlotte	22.1	17.5 (3.3)	17.7 (2.8)	18.0 (2.7)	18.8 (3.0)	17.8 (2.6)	17.2 (2.3)
Nass	0.4	1.3 (0.9)	1.2 (0.4)	0.9 (0.9)	1.3 (1.3)	0.5 (1.2)	1.4 (1.0)
Upper Skeena	0.8	0.5 (0.8)	1.2 (1.0)	0.4 (0.5)	0.0 (0.2)	0.4 (0.9)	0.4 (0.5)
Lower Skeena	0.0	3.7 (2.1)	0.8 (1.2)	0.9 (1.2)	2.5 (2.1)	3.7 (1.8)	3.0 (1.9)
Northcentral coast	37.5	36.1 (3.9)	41.1 (4.1)	38.4 (3.6)	35.9 (3.5)	38.6 (3.6)	38.1 (3.7)
ECVI	10.8	10.6 (2.8)	13.7 (3.3)	12.9 (3.1)	14.5 (3.4)	14.3 (3.3)	15.8 (3.6)
WCVI	3.8	6.6 (3.3)	3.0 (1.8)	3.3 (1.7)	6.8 (2.8)	2.0 (2.1)	2.6 (2.0)
NCVI	0.0	1.0 (1.0)	1.7 (1.5)	2.1 (1.1)	1.0 (1.5)	1.6 (2.0)	1.7 (1.9)
Southern mainland	4.2	4.4 (2.3)	0.9 (1.9)	1.4 (1.4)	1.1 (1.4)	1.5 (1.6)	0.3 (1.1)
Lower Fraser	7.9	9.8 (2.5)	8.8 (2.4)	10.7 (2.4)	9.0 (2.7)	10.9 (2.9)	10.5 (2.6)
Upper Fraser	0.0	0.4 (0.5)	0.0 (0.0)	0.0 (0.3)	0.4 (0.4)	0.0 (0.0)	0.0 (0.0)
Thompson	1.7	1.5 (0.8)	2.0 (1.0)	1.7 (0.7)	1.2 (0.8)	1.8 (0.9)	1.7 (0.9)
Washington	10.8	7.1 (2.5)	8.5 (2.6)	9.3 (1.8)	7.4 (2.6)	6.8 (2.6)	7.6 (2.2)
Σ error		22.1	21.8	19.0	25.8	26.6	27.7
Σ SD		26.5	23.8	21.4	25.8	25.4	23.7
Southern baseline (82 populations)							
<i>N</i>	94	94	94	94	94	94	94
ECVI	27.7	24.1 (6.0)	35.4 (6.8)	30.6 (6.0)	28.9 (7.8)	35.3 (6.2)	35.8 (4.9)
WCVI	9.6	12.5 (5.6)	7.7 (3.8)	9.5 (3.8)	14.5 (4.9)	7.5 (4.0)	8.9 (4.5)
NCVI	0.0	0.0 (1.5)	0.9 (2.0)	0.0 (1.5)	4.2 (2.9)	3.0 (2.4)	3.2 (2.8)
Southern mainland	10.6	10.0 (4.8)	7.2 (3.8)	3.5 (3.4)	3.3 (4.1)	6.9 (4.5)	6.3 (3.3)
Lower Fraser	20.2	26.0 (6.0)	21.5 (6.0)	26.8 (5.9)	21.1 (5.7)	25.5 (6.5)	22.7 (5.3)
Upper Fraser	0.0	1.0 (1.1)	0.0 (0.0)	0.0 (0.5)	1.3 (1.2)	0.0 (0.3)	0.0 (0.0)
Thompson	4.3	4.2 (2.2)	5.2 (2.4)	4.3 (1.8)	4.1 (2.8)	4.7 (2.5)	5.3 (2.5)
Washington	27.7	22.2 (5.8)	22.0 (6.3)	25.3 (5.2)	22.6 (5.1)	17.1 (5.7)	17.8 (4.2)
Σ error		19.5	21.8	19.1	25.1	32.7	29.7
Σ SD		33.0	31.1	28.0	34.4	32.0	28.4

^a ECVI = eastern coast of Vancouver Island; WCVI = western coast of Vancouver Island; NCVI = northern coast of Vancouver Island.

eries in Area 20 was less than in the seine and gill-net fisheries, ranging from 10–40% of the sample. The major Canadian stock in the fishery samples was generally the lower Fraser River

stock, although there was some variability in particular samples. As might be expected from the geographic location, there was substantial mixing of fish of Canadian and U.S. origin in Canada's

Area 20 and Washington's Areas 4 and 5 (Appendix 1).

Analysis of Fishery Samples: Central Baseline

A major interception fishery occurs in the Queen Charlotte Strait and Johnstone Strait (Areas 11–13; Figure 2). About 2% of the fish caught and subsequently released by the 1998 troll fishery were of upper Fraser and Thompson origin (Appendix 2). Sampling was more limited in the seine and gill-net fisheries, most estimates of this stock being less than 3%. The upper Skeena River stock was either not detected or estimated at less than 2% of the mixture for most of the fishery samples. Most of the fish sampled in this region originated from the central coast of British Columbia, Vancouver Island, the lower Fraser River, or Puget Sound. More northern stocks (e.g., those from the Skeena River, Nass River, or Queen Charlotte Islands) were estimated to be minor components of the samples, and these components generally declined over the sampling season.

The troll fishery is the predominant fishery occurring off the west coast of Vancouver Island (Areas 124–127). The area and time of highest Thompson River proportion in the fishery samples was the first two weeks in August in the northern (Area 125–127) troll fishery, the Thompson stock estimated at 3% in the samples. Generally, the upper Skeena stock was estimated at negligible levels in the samples. Most of the fish sampled originated from Vancouver Island, the southern mainland, the lower Fraser River, and Puget Sound. Higher proportions of Canadian-origin coho salmon were sampled in this fishery compared with the more southerly fishery in the Strait of Juan de Fuca (Area 20) (Appendix 2). Off the west coast of Vancouver Island, about 70–80% of the sample was estimated to be of Canadian origin, compared with about 40–50% for samples from the Strait of Juan de Fuca.

Analysis of Fishery Samples: Northern Baseline

In northern fisheries, the upper Skeena stock was of greatest management concern. For fisheries adjacent to the Queen Charlotte Islands (Areas 1, 2W, and 2E), this stock was only detected in a late July troll fishery on the west coast of the Queen Charlottes (2W), and then was estimated to have composed 3% of the 99-fish sample (Appendix 3). However, in Area 3, this stock composed 15% of a 153-fish sample from a seine fishery in the last half of July 1998 and 8–25% of much smaller samples from gill-net fisheries in Areas 3 and 4 taken

at the same time. The Thompson River stock was estimated to have contributed only negligible amounts to these fishery samples.

There were clear differences in stock composition between fisheries on the east coast and west coast of the Queen Charlotte Islands. On the east coast (2E), samples from both the seine and gill-net fisheries from mid-September to mid-October 1998 indicated that coho salmon from the Queen Charlotte Islands predominated the fishery, composing about 70% of the samples from both fisheries (Appendix 3). However, on the west coast (2W), the Queen Charlotte Islands stock composed less than 20% of the fishery samples from late July and August 1998.

The estimated contributions of Alaskan-origin coho salmon were highest in Canadian fishing areas closest to the northern border. Alaskan-origin coho salmon composed up to 20% of the sample from Area 3, and although only 21 fish were sampled in Area 1, nearly 20% of that sample was estimated to have been derived from Alaskan populations. In northern British Columbia, the north-central coast stock was the predominant contributor to fisheries; coho salmon from Alaska, the lower Skeena River, WCVI, and NVI composed, at times, significant proportions of samples. Central coast fishery samples (Areas 6 and 7) were predominated by the northcentral coast stock, with Vancouver Island and southern mainland populations at times making significant contributions (Appendix 3).

Analysis within Major Watersheds: Fraser River Baseline

The key question in sampling fisheries within the Fraser River drainage related to the relative abundance of Thompson River coho salmon, particularly the migration timing of the stock through the lower Fraser River. Three years of sampling by a test fishery in the lower portion of the river indicated a consistent pattern. The Thompson and upper Fraser stock composed 35% of the coho salmon in the lower Fraser River before September 22 and declined rapidly thereafter to the first week of October (Figure 5). After October 15, Thompson River fish composed less than 3% of the coho salmon in the lower Fraser River. Analysis of the samples from the fish wheel test fishery at Yale in the Fraser Canyon (Figure 2) indicated that Thompson River coho salmon composed 68% of the 1998 run at this location (Appendix 4).

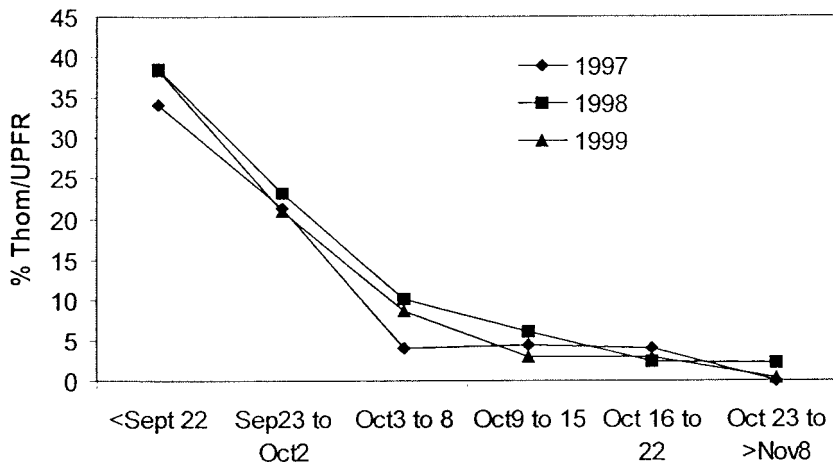


FIGURE 5.—Percentage of the Thompson and upper Fraser (UPFR) stock at specific time intervals in samples from a tangle-net test fishery in the lower Fraser River, 1997–1999.

Analysis within Major Watersheds: Skeena River Baseline

In 1998, all coho salmon caught in a test fishery in the lower Skeena River were analyzed to provide migration timing information on specific components of the run. In 1999 we analyzed a subsample of the returns that was taken over time and in proportion to run abundance. Several identifiable substocks exist within both the upper and lower portions of the watershed. The upper Skeena stock (incorporating populations upstream from the confluence of the Skeena and Babine rivers) encompasses the following substocks: upper drainage tributaries, the Babine River, and the Bulkley and Morice rivers. The lower Skeena stock encompasses the following substocks: mid-Skeena, Lakelse Lake and River tributaries, and the lower drainage tributaries. Conservation concerns over the marine fisheries addressed the entire upper Skeena stock. To satisfy local management concerns, we estimated contributions of each of the three upper Skeena substocks. Not surprisingly, coho salmon from the upper Skeena drainage were most prevalent in samples from the early portion of the returns sampled in the lower river test fishery. Composing less than 20% of the sample in the last half of July, upper drainage coho salmon declined to negligible proportions after the first week of September (Appendix 5). Both Babine River and Bulkley and Morice coho salmon were largely absent after mid-September. Conversely, the later-spawning lower river substock reached its relative peak of abundance in September, composing over 50% of the coho salmon in the river

at the time. The substock was also the predominant stock in the total return to the river, composing nearly 40% of the total return in both 1998 and 1999. The least abundant substocks were those from the upper drainage and Babine River, each composing less than 10% of the total returns in both years.

Discussion

Ideal technologies for mixed-stock analysis are those based on biological variation in characters that differ substantially among stocks, show little temporal or annual variation within stocks, and can be screened in a rapid, nonlethal, and cost-effective manner for both baseline and mixed-stock samples. The PCR-based survey of single-locus allele frequencies at microsatellite DNA and MHC loci meet these criteria and can be used for mixed-stock analysis in a species for which no alternative methodology is available. The stock composition estimates reported in this study have been derived from fisheries throughout coastal British Columbia and in the Strait of Juan de Fuca in Washington. They agree with general expectations for coho salmon distribution and migration timing. These include higher proportions of fish of U.S. origin in fishing areas closest to the northern and southern international boundaries, substantial mixing of stocks in fisheries off the west coasts of both the Queen Charlotte Islands and Vancouver Island, and higher proportions of upper drainage stocks in the early returns to both the Fraser and Skeena rivers. Stock compositions of the two stocks of greatest current management concern, the Thomp-

son River and upper Skeena River, were generally within expectations, which should enable development of effective fishery management options to conserve both stocks. This study indicated that microsatellite and MHC variation can provide reliable estimates of stock composition to any fishery in British Columbia.

The accuracy of stock composition estimates was enhanced by assuming a Hardy–Weinberg distribution of genotypic frequencies within baseline population samples for loci at which observed genotypic frequencies did not conform to expected values. This is probably because genotypes may have occurred in a mixture that was not observed in baseline samples, given the limited number of fish sampled per population and the high degree of polymorphism at the loci surveyed. Under the assumption of Hardy–Weinberg equilibrium, all possible genotypes resulting from the observed alleles at a locus are assigned some probability of occurring in the baseline population. This enables assigning, at some positive probability level, a genotype in a mixture sample to populations lacking the observed genotype in the baseline samples.

The development, evaluation, and implementation of the coho salmon genetic database provided some practical information of value to future applied studies. The inclusion of loci that may be affected by natural selection on appropriate geographic and temporal scales can increase the stock identification capabilities for a database to be used in mixed-stock analysis. In this study, an increase from four to eight microsatellite loci did not result, on average, in improved accuracy of estimates when the microsatellite data were used with the MHC data. There was, however, an increase in precision of the estimates when all 10 genetic markers were used. Similar results were observed by Beacham et al. (2000a) for analysis of six microsatellite loci in sockeye salmon *O. nerka* in Barkley Sound. For the large-scale mixed-stock analysis of coho salmon, we wanted to minimize the number of loci surveyed in the fishery samples without significantly compromising accuracy of the estimates. For analysis of 1999 samples, we chose those microsatellite loci that fit conveniently on one gel on the automated sequencer and had generally good discriminatory power. To increase the number of loci conveniently analyzed on one gel, *Oki1* and *Oki100* were multiplexed (tagged with the same fluorescent phosphoramidite). However, *Ots101* was very effective in identifying Thompson River coho salmon and should be included in future analyses of the Thompson River

component. The microsatellite loci that were least effective in estimation of stock composition (*Ots2*, *Ots3*, and *Oki1*) had the fewest number of observed alleles before binning to estimate stock composition. Whether there is a general relationship between allele number and power of the locus for stock identification needs to be evaluated for other species and applications. Clearly, judicious choice of the loci included in a survey can greatly enhance the power of microsatellite loci in stock identification applications.

Conservation concerns engender strict requirements for limiting fishing mortality of stock components that are almost certain to be present at very low abundance in mixed-stock samples. The management objective of zero mortality for Thompson River and upper Skeena River coho salmon created an urgent requirement for information on their presence in different fisheries, even those targeting other salmonid species. Mortality estimates of a nontarget stock component such as these are the product of three factors: the encounter rate of the component by a particular fishery, the assumed mortality of nontarget fish after release, and the estimated proportion of the component stock among the fish released. When projected mortalities of Thompson or upper Skeena coho salmon were considered to be contrary to the policy of zero mortality, the respective Canadian fisheries were curtailed, regardless of the species they targeted. When conservation concerns for a particular stock drive the management of a fishery, it is clear that accurate estimation of stock composition of the nontarget stock in fishery samples is vital. However, when there are conservation concerns for a particular stock, it is typically in very low abundance in fishery samples, and the accurate estimation of a stock composition of very low percentage is particularly challenging. Fortunately, in southern British Columbia, Thompson River coho salmon are very distinct genetically, and our simulation analyses and estimation of this component in the CWT sample indicated that its accurate estimation in fishery samples is possible using the DNA technology outlined in our study. Similarly, in northern British Columbia, accurate estimation of the upper Skeena River component was possible, even when the stock composed a very small (<5%) portion of the sample. In general, very little bias was observed when coho salmon from a particular region (not just Thompson River or upper Skeena River) composed 40% or less of the mixture.

The provision of stock composition estimates

for coho salmon specific to area, time, and gear allows fishery managers to evaluate the impact of options such as changing fishing boundaries or times to apply conservation measures at a local level. One such situation existed in the 1999 recreational fishery samples from Bamfield and Ucluelet in Area 23. The recreational fishery at Bamfield (situated on the southern shore of the entrance to Barkley Sound) was centered more inshore in Barkley Sound, whereas the recreational fishery at Ucluelet was at the northern shore of the entrance and more seaward. Thompson River coho salmon were not detected in the 247-fish sample from Bamfield, but 4.8% of the 115-fish sample from Ucluelet was estimated to have been of Thompson River origin.

Use of DNA analysis of freshwater test fishery samples can provide stock- and substock-specific escapement estimates and information of run timing. For example, the relative proportions of different stocks were estimated for coho salmon in the Skeena River, which combined with absolute abundance information for one of the stock components, can provide a method to estimate escapements for the other stock components. Similar applications of microsatellite variation for estimating sockeye salmon escapement have been described by Beacham and Wood (1999) and Beacham et al. (2000b).

The two technologies available for stock identification of coho salmon in mixed-stock samples (CWTs and nuclear DNA analysis) differ in their strengths and weaknesses. Coded-wire tagging normally consists of inserting a 1-mm binary-coded wire into the nasal cartilage of juvenile salmon and removing the adipose fin as a means of identifying tagged fish as adults. Only populations accessible to juvenile handling can be marked with CWTs, and the population must be tagged each year. Catches of adult salmon are usually sampled to find adults without an adipose fin, CWTs are recovered from these tagged fish, and then the data from CWT recoveries are expanded to account for the juvenile tagging rate, the catch sampling rate, and any lost heads or lost tags. The tool is very useful for providing catch estimates of tagged populations (Bernard and Clark 1996), but the application to estimating stock composition is limited by the generally low percentage of fish tagged in tagged populations and the mixed presence of untagged populations in the adult return samples. Tagged populations are assumed to be representative of the distribution of untagged populations

within the same geographic area, which may not be true.

In genetic analysis, baseline information is typically not available from all populations encountered in a fishery. However, for species in which genetic differentiation is generally based on isolation by distance, there tends to be a regional structuring of populations. Thus, for management decisions requiring regional estimates of stock composition, all contributing populations do not have to be sampled. That portion of a mixed-stock sample derived from unsampled populations is usually allocated to sampled populations from the same region, reducing the cost and complexity of establishing a sufficient baseline for mixture analysis. Thus, DNA-based mixed-stock analysis and CWTs are complementary technologies for identifying coho salmon stocks and estimating their exploitation. For regional stock composition estimates, DNA technology is more likely to provide accurate estimates of stock compositions than CWT recoveries. For estimates of catch, CWTs are more likely to provide reliable results than genetic analyses, which typically lack baseline information for all populations contributing to a fishery. Nearby unsampled populations are probably similar genetically to the sampled and CWT-marked population in question, so genetic analyses are likely to overestimate the contribution of the intended population.

When all populations contributing to a fishery sample have been included in the baseline, it may be possible to use genetic data to provide catch estimates of specific populations. Our evaluation indicated that the current genetic database for coho salmon could be used to monitor hatchery-specific catch in "mark-only" fisheries introduced to conserve wild populations. All of the limited number of hatchery populations have been included in the baseline, and 10 genetic markers have revealed sufficient differentiation among populations to enable accurate estimates of catch by hatchery. Similarly, if management needs exploitation rate estimates for specific populations, once the catch is estimated and estimates of escapement are available, then exploitation rate can be estimated without any reference to CWTs.

Widespread application of microsatellite and MHC variation to estimating stock composition of coho salmon in mixed-stock fisheries in British Columbia was conducted because of acute conservation concerns for specific stocks. The mixed-stock analysis enabled accurate estimates of stock composition in mixed-stock fishery samples, even

for stocks that were released alive after sampling, which alleviates concerns over sampling-induced mortality in the endangered stocks. The genetic database developed for coho salmon is a model that will probably be applied to an increasing number of exploited populations that give rise to the twin management concerns of identifying conservation units and detecting their presence in mixed-stock fisheries.

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References

- PSC (Pacific Salmon Commission). 1994. Interim estimates of coho stock composition for 1984–1991 southern area fisheries and for 1987–1991 northern panel area fisheries. Pacific Salmon Commission Coho Technical Committee Report TCCOHO 94-1.
- Banks, M. A., M. S. Blouin, B. A. Baldwin, V. K. Rashbrook, H. A. Fitzgerald, S. M. Blankenship, and D. Hedgecock. 1999. Isolation and inheritance of novel microsatellites in chinook salmon (*Oncorhynchus tshawytscha*). *Journal of Heredity* 90:281–288.
- Bartley, D. M., B. Bentley, P. G. Olin, and G. A. E. Gall. 1992. Population genetic structure of coho salmon (*Oncorhynchus kisutch*) in California. *California Fish and Game* 78:88–104.
- Beacham, T. D., K. M. Miller, and R. E. Withler. 1996. Minisatellite DNA variation and stock identification of coho salmon. *Journal of Fish Biology* 49:411–429.
- Beacham, T. D., and C. C. Wood. 1999. Application of microsatellite DNA variation to estimation of stock composition and escapement of Nass River sockeye salmon (*Oncorhynchus nerka*). *Canadian Journal of Fisheries and Aquatic Sciences* 56:297–310.
- Beacham, T. D., K. D. Le, M. R. Raap, K. Hyatt, W. Luedke, and R. E. Withler. 2000a. Microsatellite DNA variation and estimation of stock composition of sockeye salmon, *Oncorhynchus nerka*, in Barkley Sound, British Columbia. U.S. National Marine Fisheries Service Fishery Bulletin 98:14–24.
- Beacham, T. D., C. C. Wood, R. E. Withler, K. D. Le, and K. M. Miller. 2000b. Application of microsatellite DNA variation to estimation of stock composition, and escapement of Skeena River sockeye salmon (*Oncorhynchus nerka*). *North Pacific Anadromous Fish Commission Bulletin* 2:263–276.
- Bernard, D. R., and J. E. Clark. 1996. Estimating salmon harvest with coded-wire tags. *Canadian Journal of Fisheries and Aquatic Sciences* 53:2323–2332.
- Carvalho, G. R., and L. Hauser. 1994. Molecular genetics and the stock concept in fisheries. *Reviews in Fish Biology and Fisheries* 4:326–350.
- Cavalli-Sforza, L. L., and A. W. F. Edwards. 1967. Phylogenetic analysis: models and estimation procedures. *American Journal of Human Genetics* 19:233–257.
- Debevec, E. M., R. B. Gates, M. Masuda, J. Pella, J. Reynolds, and L. W. Seeb. 2000. SPAM (version 3.2): statistics program for analyzing mixtures. *Journal of Heredity* 91:509–510.
- Grimholt, U., I. Olsaker, F. Lingass, and O. Lie. 1994. A study of variability in the MHC class II and class I domain exons of Atlantic salmon (*Salmo salar*). *Animal Genetics* 25:147–153.
- Jefferts, K. B., P. K. Bergman, and H. F. Fiscus. 1963. A coded-wire identification system for macro-organisms. *Nature (London)* 198:460–462.
- Miller, K. M., K. H. Kaukinen, T. D. Beacham, and R. E. Withler. In press. Geographic heterogeneity in natural selection on an MHC locus in sockeye salmon. *Genetica*.
- Miller, K. M., T. J. Ming, A. D. Schulze, and R. E. Withler. 1999. Denaturing gradient gel electrophoresis (DGGE): a rapid and sensitive technique to screen nucleotide sequence variation in population surveys. *Biotechniques* 27:1016–1030.
- Miller, K. M., and R. E. Withler. 1997. MHC diversity in Pacific salmon: population structure and trans-species allelism. *Hereditas* 127:83–95.
- Miller, K. M., and R. E. Withler. 1998. The salmonid class I MHC limited diversity in a primitive teleost. *Immunological Reviews* 166:279–293.
- Miller, K. M., R. E. Withler, and T. D. Beacham. 1996. Stock identification of coho salmon (*Oncorhynchus kisutch*) using minisatellite DNA variation. *Can-*

Appendix 1: Stock Composition, Southern British Columbia and Washington

TABLE A1.1.—Estimated percentage stock compositions of coho salmon from the seine fishery in southern British Columbia and Washington during 1998–1999. Stock compositions were estimated with a 83-population southern baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses. Abbreviations are as follows: WCVI = western Vancouver Island, ECVI = eastern Vancouver Island, and NCVI = northern Vancouver Island.

Stock	Area 20 PSC test						
	Jul 21–24		Jul 25–Aug 1		Aug 2–8		Aug 9–15
	1998	1999	1998	1999	1998	1999	1998
N	184	172	310	252	153	50	168
WCVI	14.2 (3.4)	7.2 (2.9)	3.9 (2.5)	1.7 (1.2)	5.4 (3.4)	1.7 (1.2)	9.3 (3.8)
ECVI	9.3 (3.7)	4.5 (3.0)	8.4 (2.8)	12.6 (3.2)	4.6 (3.0)	12.6 (3.2)	17.6 (5.8)
NCVI	1.3 (2.2)	2.3 (2.3)	6.8 (2.0)	6.0 (2.1)	0.9 (2.2)	6.0 (2.1)	1.3 (1.7)
Southern mainland	10.2 (3.2)	10.3 (3.1)	7.0 (2.3)	14.9 (2.7)	12.4 (4.7)	14.9 (2.7)	7.5 (3.7)
Lower Fraser	15.7 (4.2)	23.9 (4.5)	13.2 (3.0)	14.7 (3.3)	9.7 (4.4)	14.7 (3.3)	3.3 (3.4)
Thompson–Upper Fraser	1.3 (1.3)		0.8 (0.7)		2.8 (1.4)		1.4 (1.1)
Thompson		1.3 (0.9)		0.0 (0.5)		0.0 (0.5)	
Upper Fraser		0.0 (0.2)		0.0 (0.2)		0.0 (0.2)	
Puget Sound	36.5 (4.7)	39.8 (5.2)	36.2 (4.5)	37.9 (4.5)	39.6 (6.7)	37.9 (4.5)	41.2 (5.1)
Juan de Fuca	4.0 (3.3)	5.6 (2.9)	12.6 (3.5)	2.9 (2.0)	17.3 (5.2)	2.9 (2.0)	5.4 (3.6)
Coastal Washington	4.1 (2.2)	2.1 (1.8)	9.5 (2.8)	4.3 (1.9)	1.1 (2.8)	4.3 (1.9)	8.8 (2.8)
Columbia	3.4 (1.5)	2.9 (1.6)	1.7 (1.2)	5.0 (1.9)	6.3 (2.3)	5.0 (1.9)	4.2 (1.9)
Canada	52.1 (5.0)	49.5 (5.6)	40.1 (4.2)	49.9 (4.8)	35.7 (6.7)	49.9 (4.8)	40.4 (5.7)
United States	47.9 (5.0)	50.5 (5.6)	59.9 (4.2)	50.1 (4.8)	64.3 (6.7)	50.1 (4.8)	59.6 (5.7)

- dian Journal of Fisheries and Aquatic Sciences 53: 181–195.
- Milner, G. B. 1993. Isozyme variation of coho salmon (*Oncorhynchus kisutch*) and its potential to estimate stock composition in mixed-stock fisheries. Pages 182–192 in L. Berg and P. W. Delaney, editors. Proceedings of the coho salmon workshop, Nanaimo, British Columbia. Department of Fisheries and Oceans, Vancouver.
- Nelson, R. J., and T. D. Beacham. 1999. Isolation and cross species amplification of microsatellite loci useful for study of Pacific salmon. *Animal Genetics* 30:228–229.
- Nelson, R. J., T. D. Beacham, and M. P. Small. 1998. Microsatellite analysis of the population structure of a Vancouver Island sockeye salmon (*Oncorhynchus nerka*) stock complex using non-denaturing gel electrophoresis. *Molecular and Marine Biotechnology* 7:312–319.
- Pella, J., M. Masuda, and S. Nelson. 1996. Search algorithms for computing stock composition of a mixture from traits of individuals by maximum likelihood. NOAA Technical Memorandum NMFS-AFSC-61.
- Shaklee, J. B., T. D. Beacham, L. Seeb, and B. A. White. 1999. Managing fisheries using genetic data: case studies from four species of Pacific salmon. *Fisheries Research* 43:45–78.
- Shaul, L. D., and J. E. Clark. 1990. Use of coded wire tag data to estimate aggregate stock composition of salmon catches in multiple mixed-stock fisheries. Pages 613–622 in N. C. Parker, A. E. Giorgi, R. C. Heidinger, D. B. Jester, Jr., E. D. Prince, and G. A. Winans, editors. Fish-marking techniques. American Fisheries Society, Symposium 7, Bethesda, Maryland.
- Shum, B. P., L. Guethlein, L. R. Flodin, M. A. Adkison, R. P. Hedrick, R. B. Nehring, R. J. M. Stet, C. Seccombe, and P. Parham. 2001. Modes of salmonid MHC class I and II evolution differ from the primate paradigm. *Journal of Immunology* 166:3297–3308.
- Small, M. P., T. D. Beacham, R. E. Withler, and R. J. Nelson. 1998a. Discriminating coho salmon (*Oncorhynchus kisutch*) populations within the Fraser River, British Columbia using microsatellite DNA markers. *Molecular Ecology* 7:141–155.
- Small, M. P., R. E. Withler, and T. D. Beacham. 1998b. Population structure and stock identification of British Columbia coho salmon (*Oncorhynchus kisutch*) based on microsatellite DNA variation. U.S. National Marine Fisheries Service Fishery Bulletin 96: 843–858.
- Smith, C. T., B. F. Koop, and R. J. Nelson. 1998. Isolation and characterization of coho salmon (*Oncorhynchus kisutch*) microsatellites and their use in other salmonids. *Molecular Ecology* 7:1614–1616.
- Stocker, M., and D. Peacock. 1998. Report of the PSARC salmon subcommittee meeting April 27–May 1, 1998 and the steering committee meeting May 4, 1998. Canadian Stock Assessment Proceedings Series 98/08. Department of Fisheries and Oceans, Nanaimo, British Columbia.
- Wehrhahn, C. F., and R. Powell. 1987. Electrophoretic variation, regional differences, and gene flow in the coho salmon (*Oncorhynchus kisutch*) of southern British Columbia. *Canadian Journal of Fisheries and Aquatic Sciences* 44:822–831.

TABLE A1.1.—Extended.

Stock	Area 20 PSC test					Commercial seine			
	Aug 9–15		Aug 16–21		Aug 22–28		Aug 6, 1999	Oct 17–24, 1998	Sep 9–11, 1998
	1999	1998	1999	1998	1999	(Area 20)	(Area 21)	(Area 23)	
<i>N</i>	99	155	207	59	63	122	153	100	
WCVI	4.5 (3.8)	6.7 (3.5)	3.9 (1.9)	8.9 (5.4)	7.4 (5.3)	2.3 (2.6)	38.2 (6.5)	89.2 (5.4)	
ECVI	22.3 (5.8)	6.7 (3.9)	19.6 (3.9)	12.5 (7.8)	20.2 (9.3)	12.5 (6.1)	18.8 (4.6)	6.5 (3.7)	
NCVI	0.0 (2.2)	3.3 (2.1)	1.4 (1.7)	4.6 (4.2)	4.7 (4.3)	1.2 (2.3)	3.6 (3.0)	2.9 (2.9)	
Southern mainland	7.4 (4.9)	4.2 (3.1)	9.5 (2.9)	5.0 (5.4)	25.9 (7.6)	10.4 (5.3)	16.9 (5.1)	0.0 (1.2)	
Lower Fraser	13.9 (5.2)	4.9 (3.3)	14.3 (3.5)	1.1 (3.3)	10.1 (6.5)	26.1 (6.7)	5.8 (3.2)	1.5 (1.6)	
Thompson–Upper Fraser		1.1 (0.9)		2.3 (2.2)			1.2 (1.1)	0.0 (0.4)	
Thompson	1.9 (1.8)		1.9 (1.1)		0.0 (0.8)	1.3 (1.7)			
Upper Fraser	0.0 (0.4)		0.7 (1.1)		0.0 (0.5)	0.0 (0.0)			
Puget Sound	29.3 (6.6)	32.3 (6.4)	41.4 (4.6)	47.8 (8.7)	25.9 (8.7)	34.1 (7.9)	6.9 (4.1)	0.0 (2.1)	
Juan de Fuca	10.7 (5.0)	18.4 (5.7)	1.9 (1.9)	7.2 (4.8)	0.0 (2.3)	8.8 (4.3)	0.1 (2.6)	0.0 (1.7)	
Coastal Washington	8.7 (4.8)	18.3 (4.4)	1.9 (1.4)	8.4 (5.2)	0.0 (2.9)	1.9 (3.8)	8.5 (4.2)	0.0 (1.2)	
Columbia	1.4 (2.0)	4.2 (2.1)	3.5 (1.5)	2.4 (2.2)	5.9 (3.2)	1.4 (2.3)	0.0 (1.0)	0.0 (0.5)	
Canada	49.9 (7.4)	26.8 (5.5)	51.3 (4.4)	34.3 (9.3)	68.2 (9.0)	53.9 (7.7)	84.5 (5.7)	100.0 (3.0)	
United States	50.1 (7.4)	73.2 (5.5)	48.7 (4.4)	65.7 (9.3)	31.8 (9.0)	46.1 (7.7)	15.5 (5.7)	0.0 (3.0)	

TABLE A1.2.—Estimated percentage stock compositions of coho salmon from the gill-net fishery in southern British Columbia and Washington during 1998–1999. Stock compositions were estimated with a 83-population southern baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses. Abbreviations are as follows: WCVI = western Vancouver Island, ECVI = eastern Vancouver Island, and NCVI = northern Vancouver Island.

Stock	Washington area 5	Area 20 PSC test						Aug 2–16, 1998
		Jul 3–18		Jul 18–25		Jul 25–Aug 1		
		Aug 4–5, 1999	1998	1999	1998	1999	1998	
<i>N</i>	44	123	111	22	116	85	58	66
WCVI	12.1 (6.0)	21.2 (5.2)	8.0 (3.9)	17.4 (9.0)	0.0 (1.5)	18.5 (6.4)	6.5 (5.5)	15.4 (6.7)
ECVI	6.8 (7.2)	6.9 (3.8)	14.2 (5.8)	4.7 (8.0)	12.3 (6.1)	12.1 (6.1)	15.6 (8.7)	4.3 (4.2)
NCVI	0.0 (3.9)	3.6 (3.1)	6.4 (3.7)	1.7 (4.6)	2.0 (2.2)	7.4 (4.5)	9.5 (6.5)	8.2 (5.9)
Southern mainland	16.6 (8.3)	9.5 (4.4)	7.7 (4.9)	13.8 (8.8)	15.9 (5.2)	9.8 (4.7)	4.8 (5.3)	16.0 (6.7)
Lower Fraser	19.9 (7.8)	7.5 (3.6)	22.0 (5.4)	0.0 (7.3)	15.3 (5.7)	4.2 (5.7)	17.1 (9.3)	5.5 (7.4)
Thompson–Upper Fraser		1.0 (0.8)		0.0 (0.0)		1.3 (1.6)		0.0 (0.6)
Thompson	4.9 (3.5)		2.1 (1.4)		0.4 (1.5)		1.1 (1.8)	
Upper Fraser	0.0 (0.0)		0.0 (0.4)		1.6 (1.5)		0.0 (0.0)	
Puget Sound	37.1 (10.3)	24.4 (5.8)	31.4 (6.9)	8.1 (11.2)	41.3 (6.6)	15.4 (6.6)	40.8 (10.4)	14.2 (7.2)
Juan de Fuca	2.6 (3.6)	4.6 (3.3)	2.8 (3.2)	31.9 (13.4)	4.9 (3.7)	14.4 (6.2)	1.7 (3.2)	14.5 (7.7)
Coastal Washington	0.0 (1.8)	13.1 (4.4)	5.6 (3.1)	22.4 (14.1)	5.2 (3.7)	9.2 (3.9)	0.0 (2.8)	20.6 (6.4)
Columbia	0.0 (2.2)	8.3 (3.1)	0.0 (0.8)	0.0 (0.6)	1.3 (1.5)	7.7 (4.1)	2.9 (2.7)	1.4 (2.6)
Canada	60.3 (10.9)	49.6 (5.5)	60.3 (7.0)	37.7 (13.5)	47.4 (6.5)	53.3 (8.2)	54.6 (11.0)	49.3 (9.3)
United States	39.7 (10.9)	50.4 (5.5)	39.7 (7.0)	62.3 (13.5)	52.6 (6.5)	46.7 (8.2)	45.4 (11.0)	50.7 (9.3)

TABLE A1.3.—Estimated percentage stock compositions of coho salmon from the troll fishery in southern British Columbia and Washington during 1999. Stock compositions were estimated with a 83-population southern baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses. Abbreviations are as follows: WCVI = western Vancouver Island, ECVI = eastern Vancouver Island, and NCVI = northern Vancouver Island.

Stock	Washington troll fishery					Canadian troll fishery		
	Aug 15–18, 1999 (Area 3)	< Aug 15, 1999 (Area 4)	Aug 16–31, 1999 (Area 4)	Sep 2, 1999 (Area 4)	Aug 22 1999 (Area 4/4b)	Jul 25–31, 1999 (Area 123)	Aug 12–13, 1999 (Area 123)	Sep 2–14, 1999 (Area 123)
<i>N</i>	56	101	180	199	207	194	204	211
WCVI	9.1 (5.4)	0.1 (2.6)	6.8 (3.5)	4.4 (2.6)	2.5 (2.7)	4.4 (2.3)	1.7 (2.3)	7.5 (2.6)
ECVI	3.6 (5.0)	9.1 (4.0)	7.0 (3.7)	11.1 (4.6)	0.0 (2.2)	9.6 (3.6)	7.6 (2.8)	12.3 (3.9)
NCVI	5.4 (4.6)	2.4 (2.3)	0.7 (1.6)	0.7 (2.3)	4.2 (2.2)	1.5 (1.5)	3.1 (2.3)	3.4 (2.5)
Southern mainland	3.9 (4.1)	1.5 (2.4)	2.9 (2.6)	1.2 (2.9)	11.1 (3.2)	7.9 (2.9)	5.9 (2.3)	7.0 (2.9)
Lower Fraser	4.4 (4.0)	15.1 (5.1)	10.5 (4.3)	21.6 (4.3)	12.8 (3.5)	24.3 (4.2)	23.6 (3.7)	32.2 (4.1)
Thompson–Upper Fraser								
Thompson	3.2 (2.6)	5.5 (2.9)	4.4 (2.1)	3.0 (1.6)	1.2 (1.2)	3.3 (1.5)	2.2 (1.2)	0.5 (0.6)
Upper Fraser	1.4 (1.1)	1.1 (0.9)	0.0 (0.2)	0.0 (0.5)	0.0 (0.3)	0.0 (0.6)	0.6 (0.6)	0.0 (0.4)
Puget Sound	19.6 (9.3)	44.9 (7.0)	25.5 (6.1)	29.5 (4.8)	30.6 (4.8)	27.4 (4.6)	36.9 (4.2)	22.0 (3.4)
Juan de Fuca	0.0 (2.1)	3.0 (3.8)	11.9 (4.1)	1.7 (1.9)	1.6 (2.4)	13.2 (3.8)	8.0 (2.4)	4.2 (2.9)
Coastal Washington	29.4 (9.1)	12.8 (4.9)	17.2 (5.6)	20.8 (4.7)	22.7 (4.2)	8.0 (2.5)	6.6 (3.0)	7.1 (2.5)
Columbia	20.0 (6.6)	4.5 (2.6)	13.0 (3.1)	6.0 (2.9)	13.3 (2.9)	0.3 (0.8)	3.6 (1.7)	3.8 (1.6)
Canada	30.9 (9.2)	34.8 (7.0)	32.4 (5.2)	42.0 (6.2)	31.7 (4.9)	51.2 (5.0)	44.8 (4.4)	62.9 (4.3)
United States	69.1 (9.2)	65.2 (7.0)	67.6 (5.2)	58.0 (6.2)	68.3 (4.9)	48.8 (5.0)	55.2 (4.4)	37.1 (4.3)

TABLE A1.4.—Estimated percentage stock compositions of coho salmon from the recreational fishery in southern British Columbia and Washington during 1997–1999. Stock compositions were estimated with a 83-population southern baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses. Abbreviations are as follows: WCVI = western Vancouver Island, ECVI = eastern Vancouver Island, and NCVI = northern Vancouver Island.

Stock	Washington			Canada		
	Aug 16, 1998 (Area 5)	Aug 23, 1998 (Area 5)	Sep 5, 1998 (Area 5)	Oct 2–29, 1998 (Area 14)	Jul 29–31, 1998 (Area 17)	Jul 5– Sep 27, 1998 (Area 19)
<i>N</i>	147	149	146	67	12	73
WCVI	8.7 (4.1)	2.9 (2.5)	3.4 (2.8)	0.2 (1.9)	7.5 (10.4)	12.6 (7.2)
ECVI	6.2 (3.9)	10.1 (3.8)	2.6 (3.4)	84.7 (6.6)	16.5 (10.7)	9.5 (6.2)
NCVI	5.5 (2.8)	7.4 (3.1)	0.7 (1.4)	2.7 (2.4)	0.0 (0.6)	5.8 (4.7)
Southern mainland	6.2 (3.8)	4.0 (2.9)	8.5 (4.3)	6.3 (5.8)	0.0 (9.1)	24.0 (8.5)
Lower Fraser	7.9 (4.5)	9.3 (3.0)	5.8 (2.4)	0.0 (1.4)	45.0 (16.9)	10.1 (5.4)
Thompson–Upper Fraser	1.1 (0.9)	1.1 (1.2)	4.6 (1.7)	0.0 (0.0)	8.3 (7.5)	3.8 (3.0)
Thompson						
Upper Fraser						
Puget Sound	43.1 (6.8)	45.4 (5.8)	59.4 (6.3)	0.0 (1.6)	22.7 (11.9)	26.3 (7.5)
Juan de Fuca	3.5 (3.3)	5.8 (3.5)	7.2 (3.8)	0.8 (1.7)	0.0 (2.5)	4.4 (3.9)
Coastal Washington	15.1 (3.8)	6.7 (4.3)	4.4 (2.5)	5.2 (3.3)	0.0 (3.1)	3.6 (4.4)
Columbia	2.7 (1.6)	7.1 (2.8)	3.3 (2.0)	0.0 (0.0)	0.0 (0.0)	0.0 (0.4)
Canada	35.6 (6.2)	34.9 (5.2)	25.6 (5.1)	94.0 (4.0)	77.3 (12.4)	65.7 (8.1)
United States	64.4 (6.2)	65.1 (5.2)	74.4 (5.1)	6.1 (4.0)	22.7 (12.4)	34.3 (8.1)

TABLE A1.4.—Continued.

Stock	Canada							
	Aug 1–24, 1997 (Area 20, Renfrew)	Aug 24– Sep 5, 1997 (Area 20, Renfrew)	Jul 26– Sep 9, 1998 (Area 20)	Aug 8–13, 1999 (Area 20)	Aug 10– Oct 1, 1999 (Area 20)	Jul 12–19, 1997 (Area 23, Ucluelet)	Aug 1– Sep 9, 1998 (Area 23, Ucluelet)	Jul 7– Sep 11, 1999 (Area 23, Ucluelet)
<i>N</i>	77	77	46	81	77	86	14	115
WCVI	7.9 (4.9)	6.4 (6.1)	18.1 (8.1)	1.5 (2.4)	4.0 (3.2)	16.3 (6.1)	52.5 (17.5)	29.5 (5.7)
ECVI	4.1 (5.3)	22.2 (7.4)	9.5 (6.0)	14.2 (7.8)	15.1 (6.7)	4.9 (5.0)	0.0 (8.9)	16.0 (5.4)
NCVI	0.9 (3.2)	8.8 (5.1)	11.2 (6.5)	7.3 (4.0)	4.3 (3.3)	2.1 (3.0)	14.6 (9.8)	10.4 (4.2)
Southern mainland	1.6 (3.6)	7.3 (6.3)	15.6 (6.9)	12.8 (4.8)	12.5 (6.2)	5.0 (4.1)	17.5 (14.4)	6.9 (3.6)
Lower Fraser	37.3 (8.5)	18.0 (7.1)	11.0 (4.5)	14.2 (6.0)	17.7 (6.2)	30.4 (7.2)	7.6 (7.8)	15.9 (5.2)
Thompson–Upper Fraser	3.7 (2.5)	5.8 (2.8)	6.3 (4.6)			1.1 (1.5)	0.0 (0.0)	
Thompson				1.2 (1.1)	5.1 (2.3)			4.8 (2.2)
Upper Fraser				0.0 (0.0)	1.3 (1.5)			0.0 (0.1)
Puget Sound	31.1 (9.8)	12.3 (7.0)	9.4 (6.7)	33.7 (7.9)	34.6 (6.4)	22.0 (7.0)	7.8 (8.1)	5.4 (2.9)
Juan de Fuca	10.4 (6.5)	6.0 (4.1)	7.3 (5.2)	5.9 (4.6)	0.0 (2.2)	6.4 (5.2)	0.0 (1.8)	2.9 (2.1)
Coastal Washington	3.0 (3.8)	9.2 (4.3)	6.4 (4.6)	4.8 (3.8)	5.4 (2.7)	6.2 (4.6)	0.0 (3.3)	8.3 (3.7)
Columbia	0.0 (1.3)	4.0 (3.1)	5.2 (3.4)	4.5 (2.7)	0.0 (1.6)	5.5 (3.2)	0.0 (0.0)	0.0 (0.7)
Canada	55.5 (8.8)	68.5 (8.4)	71.7 (8.9)	51.1 (8.2)	60.1 (6.8)	59.9 (9.0)	92.2 (8.4)	83.4 (4.7)
United States	44.5 (8.8)	31.5 (8.4)	28.3 (8.9)	48.9 (8.2)	39.9 (6.8)	40.1 (9.0)	7.8 (8.4)	16.6 (4.7)

TABLE A1.4.—Continued.

Stock	Canada				
	Jul 20–30, 1997 (Area 23, Bamfield)	Jul 31– Aug 16, 1999 (Area 23, Bamfield)	Jul 1–16, 1998 (Area 28)	Jul 15– Oct 19, 1998 (Area 29)	Aug 16– Sep 1, 1999 (Areas 123–124)
<i>N</i>	63	247	42	17	31
WCVI	15.0 (6.0)	87.3 (3.5)	4.2 (6.9)	13.3 (12.2)	14.6 (6.7)
ECVI	5.7 (4.5)	2.8 (1.8)	0.0 (3.3)	5.3 (10.8)	14.6 (6.6)
NCVI	3.0 (3.3)	1.6 (2.3)	0.0 (1.1)	0.0 (3.8)	2.5 (4.2)
Southern mainland	3.6 (4.2)	4.2 (2.1)	65.2 (15.5)	35.8 (17.3)	5.6 (5.3)
Lower Fraser	12.3 (6.7)	2.4 (1.6)	0.0 (7.0)	14.9 (12.6)	26.1 (10.9)
Thompson–Upper Fraser	2.4 (2.2)		2.2 (2.0)	6.0 (6.9)	
Thompson		0.0 (0.4)			0.0 (3.3)
Upper Fraser		0.0 (0.3)			0.0 (0.0)
Puget Sound	39.1 (8.1)	1.2 (1.1)	4.1 (6.2)	0.0 (5.4)	13.6 (7.3)
Juan de Fuca	6.4 (4.2)	0.0 (0.6)	0.0 (0.3)	0.0 (0.0)	0.0 (1.7)
Coastal Washington	10.4 (5.9)	0.2 (0.8)	22.7 (12.9)	12.0 (14.7)	19.9 (7.4)
Columbia	2.0 (1.9)	0.3 (0.4)	1.6 (6.4)	12.7 (12.2)	3.2 (3.0)
Canada	42.2 (8.6)	98.2 (1.5)	71.7 (13.5)	75.3 (15.4)	63.3 (10.4)
United States	57.8 (8.6)	1.8 (1.5)	28.3 (13.5)	24.7 (15.4)	36.7 (10.4)

Appendix 2: Stock Composition, Southcentral Coastal British Columbia, Johnstone Strait, and West Coast of Vancouver Island

TABLE A2.1.—Estimated percentage stock compositions of coho salmon from the seine, gill-net, and recreational fisheries in southcentral coastal British Columbia, Johnstone Strait, and the west coast of Vancouver Island during 1998–1999. Stock compositions were estimated with a 129-population central baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses. Abbreviations are as follows: QCI = Queen Charlotte Islands, WCVI = western Vancouver Island, ECVI = eastern Vancouver Island, and NCVI = northern Vancouver Island.

Stock	Seine fishery				Round Island test	
	Aug 30–Sep 12, 1998 (Area 7)	Jul 18–Aug 29, 1998 (Area 8)	Aug 13–Oct 24, 1999 (Areas 8–9)	Aug 3–26, 1998 (Area 12)	Aug 3–8, 1998 (Area 13)	Jul 16–31, 1998 (Area 12)
<i>N</i>	22	131	40	108	18	59
QCI	0.0 (1.3)	2.3 (1.7)	5.1 (4.6)	2.9 (2.0)	0.0 (5.2)	6.9 (4.0)
Nass	0.0 (1.9)	1.9 (1.7)	0.0 (1.0)	0.0 (1.6)	0.0 (2.7)	0.0 (1.6)
Upper Skeena	0.0 (3.4)	0.0 (0.6)	0.0 (1.3)	1.7 (1.7)	0.0 (4.5)	5.1 (3.1)
Lower Skeena	8.6 (7.9)	4.2 (2.7)	2.8 (3.7)	0.0 (2.2)	6.4 (6.2)	9.5 (4.5)
Northcentral coast	37.6 (15.3)	69.6 (6.7)	28.9 (9.1)	17.5 (7.4)	20.1 (12.7)	16.5 (7.1)
WCVI	13.4 (10.0)	10.7 (3.8)	7.2 (7.1)	7.3 (4.0)	0.0 (7.5)	11.1 (6.9)
ECVI	0.0 (5.4)	2.2 (3.1)	10.0 (6.5)	15.7 (6.3)	30.1 (14.4)	10.5 (6.4)
NCVI	35.0 (13.2)	2.0 (2.3)	9.2 (6.1)	8.2 (3.9)	0.0 (3.6)	15.3 (5.8)
Southern mainland	0.5 (9.2)	5.6 (4.0)	15.0 (7.6)	25.1 (7.7)	18.1 (12.1)	11.7 (5.2)
Lower Fraser	5.0 (6.3)	0.0 (0.9)	5.8 (5.1)	7.1 (3.0)	4.0 (7.8)	2.1 (3.0)
Thompson–Upper Fraser	0.0 (2.5)	0.0 (0.5)		2.6 (1.5)	5.6 (5.0)	0.0 (0.0)
Thompson			0.0 (0.0)			
Upper Fraser			0.0 (0.0)			
Puget Sound	0.0 (0.0)	0.0 (1.1)	10.2 (5.9)	9.0 (4.2)	15.8 (10.0)	9.1 (4.8)
Juan de Fuca	0.0 (5.0)	1.5 (1.5)	0.0 (1.6)	3.2 (2.8)	0.0 (0.0)	0.0 (1.2)
Coastal Washington	0.0 (0.0)	0.0 (0.9)	3.6 (2.7)	0.0 (2.5)	0.0 (0.0)	0.0 (3.0)
Columbia	0.0 (0.0)	0.0 (0.4)	2.2 (1.6)	0.0 (0.2)	0.0 (3.8)	2.3 (1.9)
Canada	100.0 (5.1)	98.5 (2.0)	84.0 (6.7)	87.8 (4.6)	84.2 (10.0)	88.7 (6.1)
United States	0.0 (5.1)	1.5 (2.0)	16.1 (6.7)	12.2 (4.6)	15.8 (10.0)	11.3 (6.1)

TABLE A2.1.—Extended.

Stock	Gillnet Fishery		Recreational fishery	
	Aug 1–13, 1998 (Area 12)	Aug 26–30, 1998 (Area 12)	Jul 26– Aug 1, 1998 (Area 24)	Jul 24– Sep 25, 1998 (Area 25)
	<i>N</i>	27	27	91
QCI	2.7 (4.8)	0.0 (8.2)	3.1 (2.3)	10.7 (8.9)
Nass	0.0 (1.8)	2.9 (4.8)	0.0 (0.2)	9.9 (8.0)
Upper Skeena	0.0 (2.8)	0.0 (2.9)	2.3 (1.4)	0.0 (2.9)
Lower Skeena	3.9 (5.4)	3.3 (7.4)	1.3 (1.8)	4.3 (8.0)
Northcentral coast	14.7 (7.5)	33.9 (13.2)	4.8 (2.8)	19.9 (11.2)
WCVI	21.9 (11.4)	18.0 (12.2)	74.0 (7.4)	9.3 (10.9)
ECVI	11.0 (9.8)	19.6 (13.2)	0.0 (2.6)	18.6 (13.2)
NCVI	11.0 (7.1)	7.9 (9.0)	5.9 (5.3)	13.1 (9.6)
Southern mainland	0.0 (3.7)	6.5 (7.9)	3.4 (3.6)	0.0 (4.1)
Lower Fraser	7.8 (6.3)	0.0 (5.8)	0.0 (1.0)	0.0 (1.4)
Thompson–Upper Fraser	0.0 (0.0)	0.4 (3.8)	0.0 (1.0)	5.8 (5.3)
Thompson				
Upper Fraser				
Puget Sound	14.0 (9.0)	7.7 (7.7)	3.0 (2.5)	2.5 (6.2)
Juan de Fuca	0.0 (1.1)	0.0 (4.1)	0.0 (0.0)	0.0 (2.8)
Coastal Washington	5.8 (6.9)	0.0 (3.0)	2.1 (2.2)	0.0 (6.1)
Columbia	7.3 (4.9)	0.0 (1.2)	0.0 (0.0)	5.9 (5.3)
Canada	72.9 (8.8)	92.3 (8.7)	94.8 (3.2)	91.6 (9.4)
United States	27.1 (8.8)	7.7 (8.7)	5.2 (3.2)	8.4 (9.4)

TABLE A2.2.—Estimated percentage stock compositions of coho salmon from the troll fishery in southcentral coastal British Columbia, Johnstone Strait, and the west coast of Vancouver Island during 1998–1999. Stock compositions were estimated with a 129-population central baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses. Abbreviations are as follows: QCI = Queen Charlotte Islands, WCVI = western Vancouver Island, ECVI = eastern Vancouver Island, and NCVI = northern Vancouver Island.

Stock	Jul 26– Aug 8, 1998 (Area 11)	Aug 3, 1999 (Area 11)	Jul 24–31, 1998 (Area 12)	Aug 1–7, 1998 (Area 12)	Aug 8–16, 1998 (Area 12)	Aug 17–25, 1998 (Area 12)	Jul 23– Aug 6, 1999 (Area 12)
<i>N</i>	47	23	196	68	292	44	158
QCI	7.8 (4.2)	2.7 (4.3)	0.3 (1.1)	2.6 (2.4)	1.6 (0.8)	1.4 (2.8)	0.9 (1.4)
Nass	0.0 (3.6)	4.4 (4.8)	1.4 (1.9)	1.7 (3.0)	0.0 (1.4)	0.0 (1.0)	0.0 (1.0)
Upper Skeena	3.9 (3.4)	0.0 (1.2)	1.0 (0.9)	1.6 (2.5)	0.3 (0.5)	0.0 (0.7)	0.0 (0.7)
Lower Skeena	9.8 (5.4)	4.4 (5.8)	1.6 (1.4)	5.2 (3.6)	5.1 (2.5)	1.7 (3.6)	1.4 (1.8)
Northcentral coast	19.9 (7.6)	33.6 (12.5)	7.0 (3.9)	6.5 (5.0)	19.8 (3.8)	0.0 (6.6)	23.7 (4.9)
WCVI	7.5 (6.3)	11.3 (9.0)	16.3 (4.8)	10.4 (6.5)	14.4 (4.8)	4.8 (6.9)	19.3 (5.1)
ECVI	12.8 (6.8)	2.2 (3.9)	24.6 (5.3)	21.8 (8.5)	4.1 (2.9)	22.7 (7.7)	11.1 (3.9)
NCVI	9.6 (6.2)	15.5 (10.9)	8.5 (3.2)	18.7 (7.4)	18.8 (3.3)	24.7 (8.2)	10.9 (4.4)
Southern mainland	0.4 (4.1)	4.9 (7.1)	18.0 (5.9)	12.4 (6.3)	14.9 (3.8)	9.3 (6.0)	20.0 (5.6)
Lower Fraser	14.8 (6.2)	3.8 (5.7)	5.4 (2.9)	12.5 (6.1)	3.2 (1.9)	17.2 (6.8)	5.3 (2.8)
Thompson–Upper Fraser	2.3 (2.2)		3.0 (1.3)	2.1 (1.6)	2.3 (1.0)	2.3 (2.9)	
Thompson		8.1 (5.8)					0.0 (0.5)
Upper Fraser		0.0 (1.0)					0.0 (0.1)
Puget Sound	3.4 (3.7)	0.0 (1.7)	8.8 (4.0)	3.8 (3.8)	7.5 (2.5)	7.3 (4.9)	1.6 (1.8)
Juan de Fuca	3.1 (3.0)	3.4 (3.4)	1.9 (1.7)	0.0 (2.9)	4.6 (2.2)	0.0 (3.1)	4.1 (2.1)
Coastal Washington	4.8 (4.4)	0.0 (0.0)	0.7 (1.2)	0.9 (3.5)	3.4 (1.5)	8.7 (6.3)	0.2 (2.0)
Columbia	0.0 (0.7)	5.7 (5.5)	1.6 (1.3)	0.0 (0.6)	0.0 (0.2)	0.0 (0.7)	1.6 (1.4)
Canada	88.8 (5.8)	90.9 (6.6)	87.0 (4.4)	95.3 (6.0)	84.6 (3.2)	84.0 (8.4)	92.5 (3.3)
United States	11.3 (5.8)	9.1 (6.6)	13.0 (4.4)	4.7 (6.0)	15.5 (3.2)	16.0 (8.4)	7.5 (3.3)

TABLE A2.2.—Continued.

Stock	Jul 23– Jul 31, 1999 (Area 124)	Aug 1– Aug 7, 1998 (Area 124)	Aug 1– Aug 7, 1999 (Area 124)
<i>N</i>	260	55	110
QCI	0.8 (1.0)	1.5 (1.8)	0.0 (1.0)
Nass	0.0 (0.8)	0.0 (1.0)	1.2 (1.1)
Upper Skeena	0.9 (0.7)	0.0 (0.2)	0.5 (1.3)
Lower Skeena	3.0 (1.8)	2.7 (3.2)	0.2 (1.5)
Northcentral coast	9.7 (2.7)	3.3 (2.8)	6.0 (3.1)
WCVI	19.2 (3.4)	26.8 (6.9)	25.5 (4.9)
ECVI	11.9 (3.6)	0.0 (3.2)	1.9 (3.8)
NCVI	8.5 (2.7)	8.6 (5.7)	4.1 (3.4)
Southern mainland	3.6 (2.2)	5.8 (4.0)	2.8 (2.2)
Lower Fraser	19.9 (3.4)	16.0 (7.2)	17.1 (5.0)
Thompson–Upper Fraser		1.0 (1.3)	
Thompson	1.2 (1.0)		0.9 (1.7)
Upper Fraser	1.5 (0.9)		1.5 (1.1)
Puget Sound	12.0 (3.5)	13.9 (7.8)	19.2 (4.9)
Juan de Fuca	1.9 (1.6)	3.0 (4.5)	1.8 (2.1)
Coastal Washington	4.4 (1.9)	17.3 (6.7)	15.2 (4.6)
Columbia	1.5 (0.8)	0.0 (1.4)	2.3 (1.6)
Canada	80.2 (4.4)	65.7 (8.5)	61.5 (6.1)
United States	19.8 (4.4)	34.3 (8.5)	38.5 (6.1)

TABLE A2.2.—Continued.

Stock	Aug 8–14, 1999 (Area 124)	Sep 12–15, 1999 (Area 124)	Jul 25–31, 1999 (Area 125)	Aug 1–7, 1998 (Area 125)	Aug 1–13, 1999 (Area 125)	Jul 26– Aug 13, 1999 (Area 126)	Jul 31– Aug 7, 1998 (Area 127)
<i>N</i>	199	191	264	260	142	219	155
QCI	0.3 (1.4)	1.5 (1.5)	0.8 (0.8)	1.3 (1.3)	0.8 (1.4)	0.0 (0.7)	0.1 (1.6)
Nass	0.0 (0.5)	0.3 (1.0)	0.3 (0.7)	1.2 (1.2)	0.3 (1.2)	2.0 (1.2)	0.0 (0.8)
Upper Skeena	0.0 (0.7)	0.0 (0.3)	0.7 (0.8)	0.0 (0.6)	2.0 (1.4)	0.0 (0.8)	1.2 (1.2)
Lower Skeena	4.3 (2.2)	0.2 (0.9)	2.6 (1.9)	1.0 (1.0)	2.3 (2.1)	1.8 (2.2)	0.0 (1.1)
Northcentral coast	7.5 (2.9)	2.8 (1.9)	2.1 (1.9)	3.3 (2.1)	5.2 (2.9)	4.3 (2.3)	4.8 (3.2)
WCVI	20.4 (4.4)	33.2 (5.0)	18. (3.3)	23.7 (4.0)	16.5 (4.2)	18.9 (3.9)	15.0 (5.3)
ECVI	11.8 (3.2)	17.5 (4.8)	13.3 (3.3)	12.2 (3.9)	16.4 (4.6)	11.7 (2.7)	11.9 (4.4)
NCVI	6.0 (2.7)	9.3 (3.6)	5.5 (2.2)	7.1 (3.1)	2.4 (2.2)	7.7 (2.6)	8.0 (3.6)
Southern mainland	0.0 (1.3)	5.6 (2.9)	5.7 (2.4)	2.6 (2.0)	3.8 (2.8)	6.8 (3.1)	5.7 (3.7)
Lower Fraser	20.1 (3.8)	13.8 (3.5)	24.8 (3.3)	12.3 (3.2)	29.7 (5.0)	28.9 (4.2)	16.0 (4.9)
Thompson–Upper Fraser				2.3 (1.2)			3.1 (1.6)
Thompson	0.6 (0.6)	0.6 (0.7)	0.9 (0.9)		3.1 (1.9)	3.0 (1.5)	
Upper Fraser	0.5 (0.5)	0.0 (0.2)	1.5 (1.0)		4.5 (2.1)	0.0 (0.6)	
Puget Sound	16.6 (3.7)	5.3 (2.7)	13.1 (2.9)	13.9 (3.6)	5.7 (3.0)	7.7 (2.6)	20.9 (5.6)
Juan de Fuca	4.9 (2.7)	2.4 (1.8)	2.8 (1.9)	6.3 (3.0)	2.1 (1.7)	2.3 (1.6)	6.7 (3.5)
Coastal Washington	7.2 (3.0)	6.5 (2.8)	5.3 (1.8)	8.9 (3.1)	3.6 (2.5)	4.6 (2.9)	6.1 (3.2)
Columbia	0.0 (0.2)	1.4 (1.0)	2.1 (0.9)	3.8 (1.5)	1.6 (1.7)	0.3 (0.8)	0.5 (1.2)
Canada	71.4 (4.4)	84.5 (3.9)	76.8 (3.7)	67.1 (4.9)	87.0 (4.1)	85.1 (3.8)	65.8 (5.8)
United States	28.6 (4.4)	15.6 (3.9)	23.2 (3.7)	33.0 (4.9)	13.0 (4.1)	14.9 (3.8)	34.2 (5.8)

TABLE A2.2.—Continued.

Stock	Jul 26– Aug 4, 1999 (Area 127)	Aug 1–16, 1998 (Areas 124–127)	Jul 23– Aug 2, 1999 (Areas 124–127)
<i>N</i>	177	106	195
QCI	3.6 (1.7)	0.3 (2.1)	1.3 (0.9)
Nass	0.0 (1.1)	6.9 (3.9)	0.1 (0.9)
Upper Skeena	0.0 (0.5)	1.4 (2.3)	1.1 (1.2)
Lower Skeena	3.9 (2.6)	2.6 (3.4)	2.3 (1.9)
Northcentral coast	12.3 (3.9)	8.4 (3.9)	4.1 (2.0)
WCVI	19.2 (3.9)	28.3 (6.9)	19.9 (3.5)
ECVI	12.0 (4.3)	8.6 (4.9)	10.1 (3.4)
NCVI	14.7 (4.1)	7.1 (4.2)	7.8 (2.8)
Southern mainland	7.8 (4.2)	7.9 (5.5)	3.9 (5.2)
Lower Fraser	12.9 (3.6)	15.4 (6.5)	26.8 (4.1)
Thompson–Upper Fraser		3.8 (2.1)	
Thompson	0.0 (0.4)		0.8 (0.9)
Upper Fraser	0.0 (0.6)		0.4 (0.5)
Puget Sound	5.5 (2.9)	3.0 (3.7)	15.2 (3.6)
Juan de Fuca	3.7 (2.3)	1.8 (2.6)	0.5 (1.3)
Coastal Washington	2.2 (1.9)	4.5 (3.0)	3.1 (2.1)
Columbia	2.3 (1.5)	0.0 (0.0)	2.6 (3.5)
Canada	86.4 (4.2)	90.7 (5.5)	78.6 (4.3)
United States	13.6 (4.2)	9.4 (5.5)	21.4 (4.3)

Appendix 3: Stock Composition, Northern and Northcentral British Columbia

TABLE A3.1.—Estimated percentage stock compositions of coho salmon from the seine fishery in northern and northcentral British Columbia during 1998–1999. Stock compositions were estimated with a 138–population northern baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are in parentheses. Abbreviations are as follows: QCI = Queen Charlotte Islands, WCVI = western Vancouver Island, ECVI = eastern Vancouver Island, and NCVI = northern Vancouver Island.

Stock	Aug 8–22, 1998 (Area 1)	Aug 22–29, 1998 (Area 2W)	Sep 19– Oct 10, 1998 (Area 2E)	Jul 18– Aug 1, 1998 (Area 3)	Aug 2–8, 1998 (Area 3)	Aug 15–31, 1998 (Area 3)	Jul 12–18, 1998 (Area 6)
<i>N</i>	21	12	260	153	498	90	116
Southeast Alaska	17.5 (10.5)	0.0 (3.0)	1.9 (1.4)	9.9 (4.0)	18.3 (2.8)	6.8 (7.7)	11.0 (5.3)
QCI	12.8 (9.7)	20.9 (12.1)	69.1 (4.4)	0.7 (1.2)	2.0 (0.9)	5.3 (3.4)	1.4 (3.3)
Nass	0.0 (1.8)	0.0 (4.1)	2.3 (1.6)	5.4 (3.0)	11.7 (2.3)	0.0 (4.0)	0.0 (2.3)
Upper Skeena	0.0 (0.5)	0.0 (0.0)	0.4 (0.5)	15.0 (3.8)	3.8 (1.5)	1.3 (2.7)	0.9 (2.6)
Lower Skeena	8.8 (7.6)	8.9 (10.3)	0.0 (0.9)	9.6 (4.4)	12.3 (2.8)	3.2 (5.2)	19.7 (6.7)
Northcentral coast	9.5 (10.4)	38.9 (16.5)	7.5 (2.6)	20.8 (4.8)	29.0 (3.3)	35.7 (9.7)	35.7 (8.7)
WCVI	24.3 (11.2)	21.0 (14.6)	5.6 (2.5)	5.2 (3.0)	3.0 (1.8)	5.0 (4.2)	7.6 (5.2)
ECVI	0.0 (2.4)	0.0 (10.1)	2.8 (2.3)	11.1 (4.7)	2.3 (1.9)	6.3 (4.6)	0.4 (4.2)
NCVI	10.2 (9.2)	0.0 (4.1)	3.4 (2.6)	6.2 (3.2)	9.0 (2.3)	12.8 (7.7)	4.8 (3.7)
Southern mainland	16.3 (9.2)	0.0 (6.3)	3.9 (2.0)	3.0 (2.5)	3.5 (2.3)	5.4 (4.8)	11.5 (5.8)
Lower Fraser	0.0 (1.3)	0.0 (0.0)	1.7 (1.4)	6.2 (3.3)	0.0 (0.9)	5.5 (4.5)	0.0 (2.7)
Thompson–Upper Fraser	0.0 (0.0)	0.0 (0.0)	0.0 (0.2)	0.7 (0.6)	0.3 (0.4)	0.0 (1.4)	0.0 (0.6)
Puget Sound	0.0 (5.8)	10.3 (9.1)	1.5 (1.1)	3.7 (3.3)	1.8 (1.2)	1.2 (3.6)	3.6 (4.9)
Juan de Fuca	0.0 (2.5)	0.0 (3.5)	0.0 (0.1)	1.2 (1.7)	0.7 (0.9)	0.0 (1.2)	2.1 (1.8)
Coastal Washington	0.7 (4.1)	0.0 (2.0)	0.0 (0.5)	1.3 (1.6)	2.1 (1.0)	11.6 (6.0)	1.3 (2.8)
Columbia	0.0 (0.0)	0.0 (0.0)	0.0 (0.1)	0.0 (0.7)	0.2 (0.5)	0.0 (0.4)	0.0 (0.8)
Canada	81.8 (11.4)	89.7 (10.1)	96.6 (1.9)	83.9 (5.1)	77.0 (3.3)	80.5 (8.7)	82.0 (6.7)
United States	18.2 (11.4)	10.3 (10.1)	3.4 (1.9)	16.1 (5.1)	23.0 (3.3)	19.5 (8.7)	18.0 (6.7)

TABLE A3.1.—Continued.

Stock	Jul 19–25, 1998 (Area 6)	Jul 26– Aug 1, 1998 (Area 6)	Aug 2–8, 1998 (Area 6)	Aug 16–22, 1998 (Area 6)
<i>N</i>	232	111	109	36
Southeast Alaska	3.9 (2.8)	0.9 (1.9)	5.9 (4.0)	3.4 (2.8)
QCI	0.8 (1.6)	2.3 (2.5)	2.5 (2.1)	3.9 (3.4)
Nass	0.0 (0.4)	0.0 (1.4)	4.6 (2.9)	0.0 (3.5)
Upper Skeena	0.0 (0.7)	0.3 (1.0)	1.5 (1.5)	0.0 (0.5)
Lower Skeena	9.5 (3.7)	1.4 (3.2)	4.7 (3.9)	17.3 (8.4)
Northcentral coast	55.5 (6.0)	40.6 (8.8)	61.6 (6.4)	51.7 (12.5)
WCVI	0.1 (1.5)	3.9 (4.8)	2.8 (3.2)	4.2 (5.2)
ECVI	7.2 (3.4)	0.9 (4.7)	13.5 (4.5)	8.0 (6.8)
NCVI	3.5 (2.6)	9.9 (5.3)	0.0 (1.4)	6.6 (7.5)
Southern mainland	9.1 (3.9)	19.1 (8.4)	0.1 (3.3)	0.0 (2.8)
Lower Fraser	6.5 (3.1)	5.6 (4.4)	1.7 (2.6)	0.1 (3.5)
Thompson–Upper Fraser	0.4 (0.6)	0.9 (1.2)	0.0 (0.1)	2.6 (2.6)
Puget Sound	2.5 (2.5)	4.7 (3.2)	0.0 (1.0)	0.0 (1.6)
Juan de Fuca	0.0 (0.6)	1.1 (3.1)	1.2 (1.3)	2.3 (2.3)
Coastal Washington	0.0 (1.5)	3.0 (4.1)	0.0 (1.5)	0.0 (2.1)
Columbia	1.1 (0.8)	5.4 (3.4)	0.0 (0.2)	0.0 (0.7)
Canada	92.5 (3.8)	84.9 (6.7)	93.0 (4.4)	94.4 (4.8)
United States	7.5 (3.8)	15.1 (6.7)	7.0 (4.4)	5.6 (4.8)

TABLE A3.2.—Estimated percentage stock compositions of coho salmon from the gill-net, troll, and recreational fisheries in northern and northcentral British Columbia during 1998–1999. Stock compositions were estimated with a 138-population northern baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are in parentheses. Abbreviations are as follows: QCI = Queen Charlotte Islands, WCVI = western Vancouver Island, ECVI = eastern Vancouver Island, and NCVI = northern Vancouver Island.

Stock	Gillnet fishery				Troll fishery	
	Sep 19–Oct 10, 1998	Jul 11–Aug 22, 1998	Jul 18–25, 1998	Jul 25–Aug 29, 1998	Jul 25–Aug 1, 1998	Aug 8–29, 1998
	(Area 2E)	(Area 3)	(Area 4)	(Area 6)	(Area 2W)	(Area 2W)
<i>N</i>	123	25	8	76	99	152
Southeast Alaska	3.5 (2.6)	21.8 (10.7)	8.4 (10.5)	2.1 (4.3)	4.7 (3.0)	5.1 (2.7)
QCI	68.9 (5.6)	0.0 (2.2)	26.4 (17.0)	0.0 (0.9)	7.3 (4.2)	12.6 (3.8)
Nass	0.0 (0.6)	0.0 (6.9)	0.0 (0.0)	5.4 (4.7)	1.3 (1.4)	0.0 (1.4)
Upper Skeena	0.0 (0.7)	6.6 (5.9)	23.7 (14.6)	2.5 (1.5)	3.0 (2.4)	0.0 (1.0)
Lower Skeena	2.1 (1.4)	22.7 (12.3)	0.0 (5.7)	0.0 (3.7)	6.9 (3.3)	1.1 (1.8)
Northcentral coast	3.3 (2.7)	22.0 (10.4)	0.5 (11.2)	69.7 (10.4)	10.1 (4.4)	23.5 (5.6)
WCVI	6.2 (3.9)	21.7 (8.9)	19.7 (16.8)	2.0 (2.4)	13.4 (6.3)	13.3 (4.8)
ECVI	2.3 (3.0)	0.0 (2.1)	16.2 (17.0)	0.0 (2.6)	24.2 (6.3)	11.9 (4.5)
NCVI	7.8 (3.6)	0.0 (0.7)	5.0 (10.1)	6.1 (4.0)	5.5 (4.1)	7.5 (3.9)
Southern mainland	0.6 (1.1)	0.0 (3.9)	0.0 (0.5)	7.1 (4.5)	6.2 (3.7)	10.9 (3.5)
Lower Fraser	4.8 (2.8)	0.0 (3.8)	0.0 (3.5)	0.0 (0.8)	0.1 (2.9)	2.9 (2.7)
Thompson–Upper Fraser	0.6 (0.7)	3.3 (3.4)	0.0 (4.3)	0.0 (0.0)	2.0 (1.6)	0.0 (0.4)
Thompson						
Upper Fraser						
Puget Sound	0.1 (2.3)	0.0 (5.5)	0.0 (4.7)	1.5 (3.0)	3.0 (3.2)	2.2 (2.0)
Juan de Fuca	0.0 (0.3)	0.0 (1.2)	0.0 (0.0)	2.7 (2.2)	8.1 (4.0)	2.4 (2.8)
Coastal Washington	0.0 (0.2)	0.0 (3.8)	0.0 (9.0)	0.0 (3.4)	4.2 (3.0)	6.7 (2.7)
Columbia	0.0 (0.9)	0.0 (0.0)	0.0 (0.0)	1.0 (3.0)	0.0 (1.0)	0.0 (0.4)
Canada	96.5 (3.3)	78.2 (11.1)	91.6 (13.7)	92.7 (6.7)	80.0 (5.3)	83.7 (4.0)
United States	3.6 (3.3)	21.8 (11.1)	8.4 (13.7)	7.3 (6.7)	20.0 (5.3)	16.3 (4.0)

TABLE A3.2.—Continued.

Stock	Recreational fishery				
	Jul 25–Aug 23, 1998	Jul 26, 1999	Jul 25–Aug 15, 1998	Jul 25–Aug 15, 1999	Aug 23, 1999 (Langara Island)
	(Area 3)	(Area 3)	(Area 4)	(Area 4)	
<i>N</i>	71	135	67	30	71
Southeast Alaska	5.6 (4.3)	6.0 (3.5)	2.0 (2.6)	0.0 (3.9)	0.0 (2.7)
QCI	7.2 (4.2)	3.0 (2.0)	9.0 (4.5)	5.2 (3.9)	29.8 (7.1)
Nass	6.6 (4.5)	5.2 (3.7)	0.0 (2.7)	6.5 (4.2)	10.2 (5.7)
Upper Skeena	10.2 (4.1)	12.9 (3.9)	7.5 (3.7)	6.6 (4.7)	0.0 (2.0)
Lower Skeena	7.0 (5.3)	14.7 (4.9)	16.6 (5.7)	17.3 (10.3)	8.2 (5.2)
Northcentral coast	35.7 (7.8)	29.2 (5.4)	43.4 (8.8)	28.2 (10.8)	19.4 (6.6)
WCVI	3.0 (3.2)	4.9 (2.6)	8.1 (4.4)	0.0 (0.9)	1.7 (3.0)
ECVI	1.5 (4.0)	9.3 (3.5)	0.1 (3.7)	12.7 (7.2)	0.0 (2.0)
NCVI	6.1 (4.3)	5.6 (2.8)	3.7 (4.4)	11.7 (7.9)	7.5 (4.5)
Southern mainland	7.7 (4.1)	7.2 (3.0)	3.6 (4.6)	0.0 (5.5)	6.9 (4.4)
Lower Fraser	1.8 (3.2)	1.7 (2.2)	0.1 (2.8)	0.0 (3.4)	5.4 (4.1)
Thompson–Upper Fraser	0.0 (0.1)		1.4 (1.3)		
Thompson		0.0 (0.1)		3.8 (4.3)	0.0 (0.0)
Upper Fraser		0.0 (0.0)		0.0 (0.0)	0.0 (0.2)
Puget Sound	7.7 (4.2)	0.0 (1.6)	0.0 (2.2)	3.4 (4.0)	0.0 (1.3)
Juan de Fuca	0.0 (1.4)	0.0 (0.7)	0.0 (0.6)	0.0 (1.5)	0.0 (2.6)
Coastal Washington	0.0 (0.5)	0.4 (0.9)	2.6 (2.6)	4.1 (3.6)	10.9 (4.6)
Columbia	0.0 (0.5)	0.0 (0.3)	2.1 (2.3)	0.6 (3.0)	0.0 (0.9)
Canada	86.7 (5.6)	93.6 (3.9)	93.4 (5.0)	91.9 (6.4)	89.1 (5.3)
United States	13.3 (5.6)	6.4 (3.9)	6.7 (5.0)	8.1 (6.4)	10.9 (5.3)

Appendix 4: Stock Composition, Fraser River

TABLE A4.1.—Estimated percentage stock compositions of coho salmon from the seine, gill-net, and selective recreational fisheries in Area 29 of the Fraser River during 1997–1999. Stock compositions were estimated with a Fraser River baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses.

Stock	Seine	Gill-net					Selective recreational fisheries	
	Pink tagging, Aug 29–Oct 1, 1997	Oct 15–Nov 4, 1997	Aug 1–25, 1998	Oct 10–Nov 6, 1999	Aug 26–Sep 17, 1998 (Cottonwood)	Sep 4–21, 1998 (Whonnock)	Oct 16–31, 1999 (Sel #371)	Oct 16–30, 1999 (SelKadi)
<i>N</i>	209	18	22	82	49	22	34	23
Lower Fraser	33.9 (3.3)	93.6 (6.4)	85.6 (9.1)	94.7 (2.6)	25.5 (8.5)	19.0 (10.8)	97.0 (3.6)	95.8 (4.0)
Thompson–Upper Fraser	66.1 (3.3)	6.4 (6.4)	14.4 (9.1)		74.6 (8.5)	81.0 (10.8)		
Thompson				4.6 (2.4)			2.7 (2.8)	4.2 (3.7)
Upper Fraser				0.7 (1.5)			0.3 (2.8)	0.0 (2.5)

TABLE A4.1.—Continued.

Stock	Selective recreational fisheries	
	Sep 27–Oct 22, 1999 (Sooktrap)	Sep 29–Oct 24, 1999 (Darcie Hook)
<i>N</i>	28	160
Lower Fraser	95.0 (3.9)	97.2 (1.8)
Thompson–Upper Fraser		
Thompson	0.0 (2.3)	2.8 (1.6)
Upper Fraser	5.0 (3.7)	0.0 (0.9)

TABLE A4.2.—Estimated percentage stock compositions of coho salmon from the tangle-net fishery in Area 29 of the Fraser River during 1997–1999. Stock compositions were estimated with a Fraser River baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses.

Stock	<Sep 22			Sep 23–Oct 2			Oct 3–8
	1997	1998	1999	1997	1998	1999	1997
<i>N</i>	127	59	179	244	133	66	38
Lower Fraser	65.9 (4.5)	61.5 (6.6)	61.8 (3.7)	78.6 (3.1)	76.8 (4.4)	79.0 (5.2)	95.9 (4.4)
Thompson–Upper Fraser	34.2 (4.5)	38.5 (6.6)		21.4 (3.1)	23.2 (4.4)		4.1 (4.4)
Thompson			29.9 (3.6)			7.9 (4.2)	
Upper Fraser			8.4 (3.0)			13.1 (5.0)	

TABLE A4.2.—Continued.

Stock	Oct 3–8		Oct 9–15			Oct 16–22		
	1998	1999	1997	1998	1999	1997	1998	1999
<i>N</i>	79	56	123	247	82	42	254	173
Lower Fraser	89.9 (3.9)	91.4 (4.3)	95.6 (2.3)	94.0 (2.0)	97.0 (2.1)	95.9 (3.5)	97.6 (1.6)	97.0 (1.5)
Thompson–Upper Fraser	10.1 (3.9)		4.4 (2.3)	6.1 (2.0)		4.1 (3.5)	2.4 (1.6)	
Thompson		5.4 (4.0)			1.3 (1.2)			3.0 (1.5)
Upper Fraser		3.3 (2.8)			1.6 (1.9)			0.0 (0.6)

TABLE A4.2.—Continued.

Stock	Oct 23–Nov 19			Albion test fishery		
	1997	1998	1999	<Sep 22, 1998	Sep 23–Oct 8, 1998	Oct 9–19, 1998
<i>N</i>	18	145	87	32	33	41
Lower Fraser	100.0 (4.5)	97.7 (1.9)	99.7 (2.0)	66.6 (8.6)	93.1 (5.1)	98.5 (2.4)
Thompson–Upper Fraser	0.0 (4.5)	2.3 (1.9)		33.4 (8.6)	6.9 (5.1)	1.5 (2.4)
Thompson			0.3 (1.7)			
Upper Fraser			0.0 (1.1)			

TABLE A4.3.—Estimated percentage stock compositions of coho salmon collected at the Yale Fish Wheel in Area 29 of the Fraser River during 1997–1999. Stock compositions were estimated with a Fraser River baseline. Standard deviations, estimated from 100 bootstrap resamplings of both the baseline and mixtures, are given in parentheses.

Stock	Sep 17–23, 1998	Sep 24–30, 1998	Oct 1–7, 1998	Oct 8–14, 1998	Oct 15–Nov 19, 1998	1998 season	Sep 9–Oct 3, 1999
<i>N</i>	53	81	12	103	22	271	97
Lower Fraser	7.4 (4.1)	4.2 (3.0)	5.4 (9.8)	5.3 (3.0)	14.9 (9.7)	6.3 (1.9)	2.4 (1.9)
Upper Fraser	25.6 (7.2)	30.1 (5.5)	46.8 (15.0)	22.0 (5.0)	25.0 (10.5)	25.9 (3.2)	14.5 (3.3)
Thompson	67.0 (7.6)	65.7 (6.6)	47.7 (16.6)	72.7 (6.4)	60.0 (13.6)	67.7 (4.1)	83.1 (5.5)

Appendix 5: Stock Composition, Skeena River

TABLE A5.1.—Estimated percentage stock compositions of the 1998 and 1999 Skeena River test fishery near the mouth of the Skeena River for nine periods in 1998, along with the 1998 and 1999 totals. Stock compositions were estimated with a Skeena River baseline; *N* is the number of fish analyzed in the time period, and the standard deviations are in parentheses.

Stock	Jul 15–30	Aug 1–8	Aug 9–15	Aug 16–22	Aug 23–29	Aug 30–Sep 5	Sep 6–12
<i>N</i>	51	97	89	140	108	168	155
Upper Skeena	22.6 (10.6)	17.4 (7.1)	15.7 (6.7)	6.3 (5.2)	2.9 (3.1)	4.1 (2.7)	1.1 (1.5)
Babine	24.1 (11.7)	3.8 (5.2)	18.2 (8.7)	19.8 (6.0)	26.5 (6.7)	9.2 (3.2)	5.7 (3.2)
Bulkley–Morice	21.1 (11.3)	38.5 (8.5)	40.4 (9.5)	22.0 (6.5)	20.4 (7.2)	7.3 (3.9)	6.9 (4.7)
Mid Skeena	17.2 (9.9)	18.3 (9.1)	8.9 (6.6)	25.7 (7.0)	9.9 (6.6)	1.2 (3.2)	10.4 (4.3)
Lower Skeena	3.6 (5.7)	7.4 (5.8)	10.7 (4.8)	21.6 (5.8)	14.2 (8.0)	68.0 (6.5)	54.8 (9.2)
Lakelse	11.5 (6.3)	14.6 (6.3)	6.2 (5.1)	4.6 (4.5)	26.2 (7.7)	10.2 (6.5)	21.1 (8.2)

TABLE A5.1.—Extended.

Stock	Sep 13–19	Sep 20–Oct 7	Totals	
			1998	1999
<i>N</i>	122	128	1,067	282
Upper Skeena	1.7 (2.5)	1.0 (1.7)	6.1 (1.8)	4.1 (2.5)
Babine	0.1 (1.0)	0.0 (0.8)	10.1 (2.1)	7.1 (1.9)
Bulkley–Morice	0.0 (1.6)	0.0 (0.8)	16.3 (2.4)	15.9 (3.5)
Mid Skeena	3.8 (3.0)	1.1 (2.3)	10.3 (2.4)	22.6 (4.0)
Lower Skeena	67.2 (10.9)	52.5 (8.0)	38.2 (3.2)	36.4 (4.9)
Lakelse	27.3 (10.8)	45.4 (8.2)	19.0 (3.4)	14.0 (4.2)