# Origin of Juvenile Chum Salmon
# From Gulf of Alaska Coastal Waters, 2001

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**Juvenile chum salmon and jellies from a trawl catch in Shelikof Strait, Alaska, summer 2001.**

**P**revious migration models of juvenile chum salmon, Oncorhynchus keta, in the Gulf of Alaska (GOA) indicate a counter-clockwise movement pattern where the juveniles migrate along the GOA continental shelf corridor, typically north and then west, before entering offshore waters in fall and winter. Little is known, however, about many of the specific aspects of this migration such as migration rates, the abundance and distribution of specific stock-groupings along this corridor, and point of debarkation where the juveniles move from coastal to offshore waters.

In the past several years, new survey and laboratory methods employed by the Auke Bay Laboratory's (ABL) Ocean Carrying Capacity Program (OCC) in conjunction with oceanographic investigations through GLOBEC (Global Ocean Ecosystem Dynam-

ics) research initiatives have overcome key data limitations encountered by previous research, thereby allowing new insight into salmon migration characteristics in the GOA. Many of the weather limitations encountered by purse seine operations in the past have been overcome by the use of rope trawls towed at the surface. Past reliance on limited recoveries of tags from salmon tagged at sea has given way to new tools that provide robust methods of identifying stocks or regional stock-groupings in mixtures of fish. Large-scale hatchery thermal mark programs recently developed at several hatcheries in North America have made it possible to study the migration, distribution, growth, and survival of these individual stocks. A broader-scale perspective of salmon migration along the GOA coastal corridor is possible
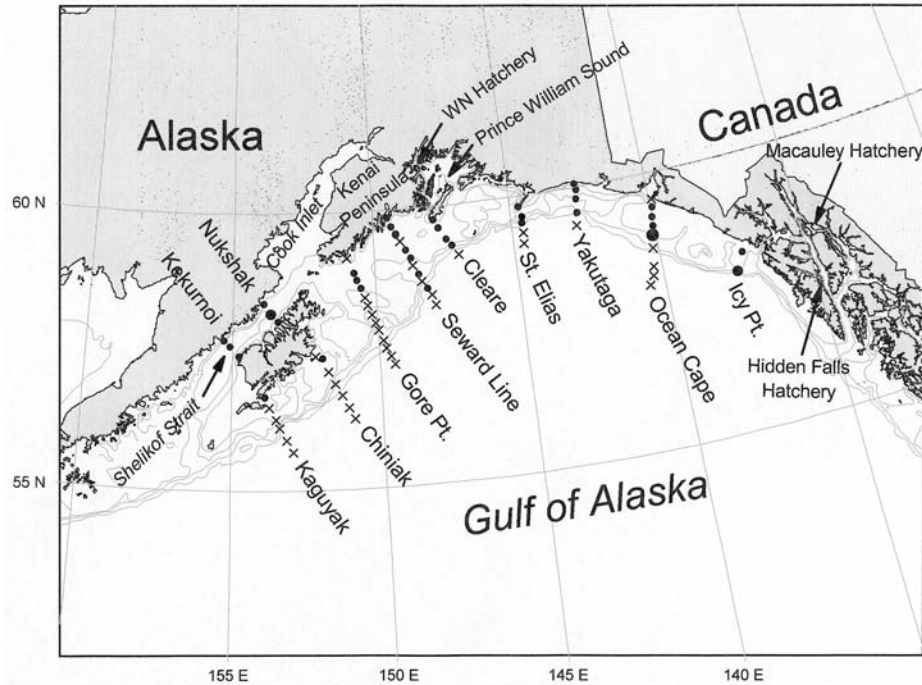
**Figure 1. Juvenile chum salmon collections taken during the July-August 2001 OCC/GLOBEC research cruise along Gulf of Alaska transects. An X indicates a station where no chum salmon were caught; circles, the size of which represent catch size, indicate stations where juvenile chum salmon were caught.**

through the use of genetic analyses that take advantage of the genetic divergence that exists among regional groups of populations.

In this report, we provide updated information on salmon migration patterns in the GOA, relying upon migration and distribution data from thermally marked chum salmon hatchery stocks and the first genetic stock identification analysis of juvenile salmon migrating through this coastal corridor.

## Methods

Sampling was conducted aboard the 38-m chartered fishing vessel Great Pacific between 17 July and 6 August 2001. Eleven transects with a total of 75 stations extended perpendicular from nearshore sites, across the continental shelf to oceanic waters beyond the 200-m shelf break (Fig. 1). Stations were generally less than 20 km apart. Fish were collected in a 198-m long mid-water rope trawl that had a typical spread of 10-m vertical and 45-m horizontal. The net was towed at the surface for 30 minutes between 3.5-5 knots, primarily during daylight hours. Sampling and catch information is not reported in this article but is summarized in other OCC documents.

Whole juvenile chum salmon were stored in ultra-cold freezers onboard and then shipped to the ABL for processing. Heart, liver, eye, and muscle tissues were extracted for genetic analysis, and the heads removed for otolith thermal mark analysis. The otoliths were extracted and analyzed by the Mark, Tag, and Age Laboratory, Division of Commercial Fisheries, Alaska Department of Fish and Game (ADF&G), Juneau, Alaska. The tissue samples were analyzed with protein electrophoresis to identify the genetic characteristics of 20 allozyme loci. Specific laboratory protocol followed is not within the scope of this article but is available at the request of the authors.

The genetic variation in the collections was then compared to a genetic baseline to deter-

Table 1. Number of hatchery thermally marked and unmarked juvenile chum salmon collected in 2001 at each OCC/GLOBEC transect in the Gulf of Alaska. The number of fish examined at each transect for otolith thermal marks by the ADF&G laboratory (total = 1,035) differs slightly from the number of fish analyzed for genetic characters.

| | | Hatchery | | | | |
|---|---|---|---|---|---|---|
| Location | Date | Macaulay | Hidden Falls | Wally Noerenberg | Unmarked | Total |
| *East of Prince William Sound* | | | | | | |
| Icy Point | July 17 | 23 | 37 | 0 | 110 | 170 |
| Ocean Cape | July 18-19 | 32 | 18 | 0 | 85 | 135 |
| Cape Yakutaga | July 22 | 19 | 2 | 0 | 17 | 38 |
| Cape St. Elias | July 23 | 13 | 1 | 0 | 7 | 21 |
| *West of Prince William Sound* | | | | | | |
| Cape Cleare | July 24 | 33 | 0 | 18 | 9 | 60 |
| Seward Line | July 25-27 | 23 | 0 | 92 | 28 | 143 |
| Gore Point | July 29-31 | 1 | 0 | 56 | 15 | 72 |
| *Shelikof Strait* | | | | | | |
| Cape Nukshak | Aug 3 | 0 | 0 | 5 | 281 | 286 |
| Cape Kekurnoi | Aug 4 | 0 | 0 | 0 | 104 | 104 |
| *South of Kodiak Island* | | | | | | |
| Cape Chiniak | Aug 1-2 | 0 | 0 | 0 | 0 | 0 |
| Cape Kaguyak | Aug 5-6 | 0 | 0 | 0 | 6 | 6 |
| *Total* | | 144 | 58 | 171 | 662 | 1,035 |

mine the origin of fish in the mixture. This Pacific Rim allozyme baseline is one of the most extensive genetic baselines in existence and has been developed since the mid-1980s with the cooperation of several domestic and foreign fisheries agencies. The primary distribution of populations in Asia and North America is now represented by allele frequency data for 20 loci from 356 populations. Regional origin estimates and 90% confidence intervals were made for each mixture collection or group of collections using a conditional maximum likelihood model in the software program SPAM.

## Results and Discussion

Hatchery thermal marks

Of 1,035 juvenile chum salmon examined for thermal marks, 373 (36%) were marked at one of three Alaskan hatcheries: the Wally Noerenberg Hatchery in western Prince William Sound (PWS) and the Macaulay (for-

merly Gastineau) and Hidden Falls Hatcheries in Southeast Alaska (Table 1). Together, these three hatcheries thermally marked 100% of the more than 260 million fish released in 2001. Some of the fish that were assigned to the Macaulay Hatchery may actually be from the Nitinat River Hatchery, Canadian Department of Fisheries and Oceans, on southwestern Vancouver Island, British Columbia. Unfortunately, the chum salmon released from these hatcheries shared the same otolith mark patterns in 2001 (Peter Hagen, ADF&G, personal communication).

The fraction of marked hatchery fish in each collection ranged from 0% to 85%. In collections east of PWS, 40% of the chum salmon were marked from Southeast Alaska Hatcheries. The highest concentration of hatchery fish occurred in the collections just beyond the western exit corridor of PWS; 81% of the catch along the Kenai Peninsula were marked from the Wally Noerenberg and Macaulay Hatch-
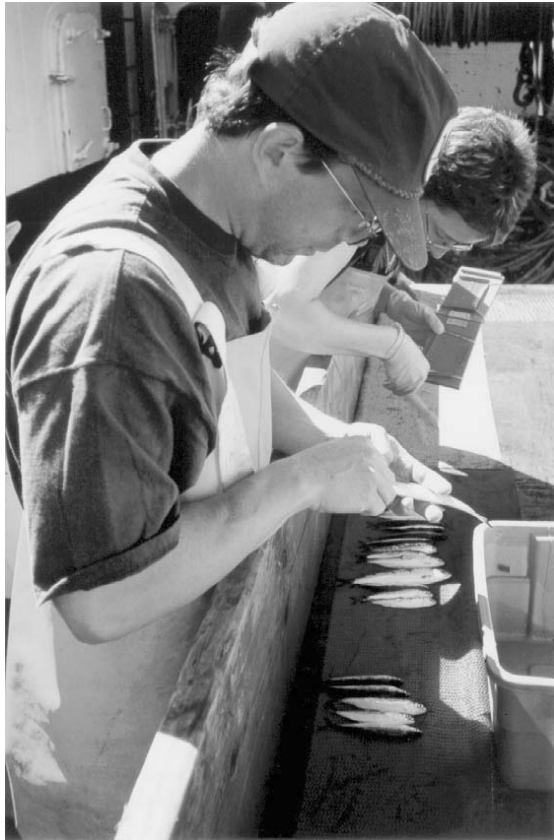
Ed Farley and Ellen Martinson processing juvenile salmon onboard the fishing vessel *Great Pacific* in the Gulf of Alaska.

eries. In striking contrast, only 1% of the chum salmon collected in Shelikof Strait were marked.

Over 70% of the juvenile chum salmon from Southeast Alaska hatcheries that we collected were caught east of PWS. One hundred forty-four chum salmon reared at the Macaulay Hatchery and released at four sites in the Juneau area were caught between the first transect at Icy Point and Gore Point on the southern end of the Kenai Peninsula. A smaller number of fish from the Hidden Falls Hatchery release groups were recovered within a smaller geographic distribution; 58 chum salmon were caught east of PWS between Icy Point and Cape St. Elias. At the Icy Point transect, a survey by biologists from the ABL Southeast Coastal Monitoring Program (SECM) 11 days after the OCC/GLOBEC survey recovered thermally marked chum

salmon. The majority of these thermally marked fish were from the Hidden Falls Hatchery as occurred in the OCC/GLOBEC survey. All of the remaining 171 thermally marked chum salmon caught west of PWS between Cape Cleare and the northern Shelikof Strait transect originated from the Wally Noerenberg Hatchery.

Genetic stock identification

The Pacific Rim chum salmon genetic baseline has been used to address salmon fisheries management issues, high-seas salmon interception questions, and Bering Sea trawl fishery bycatch. This report is the first attempt to use genetic data to identify the origin of regional groups of juvenile chum salmon populations during their migration in GOA coastal waters. Regional estimates of origin for each collection or group of collections are provided in Table 2. The numbers of chum salmon caught in the Cape Yakutaga and Cape St. Elias transects were too small for analysis of individual collections, and data were combined with the other eastern collections from Icy Point and Ocean Cape. Similarly, data from Cape Cleare and Gore Point were combined with data from the Seward Line. So few fish were recovered from Cape Chiniak and Cape Kaguyak seaward of Kodiak Island that these fish were excluded from analysis.

One analysis with all the collections combined was made with the full 356-population baseline. As expected, Asian and western Alaska regions did not contribute to the juvenile chum salmon caught in the northern GOA. Remaining analyses used a genetic baseline that excluded populations from these regions; the estimation of origin improves when noncontributing populations/regions are removed from analyses.

Chum salmon from Washington State and southern British Columbia were observed at significant levels (9.1%) in only one mixture, the Kenai Peninsula collections from Cape Cleare, Seward Line, and Gore Point, west of PWS. Other estimates of fish from the southernmost North American populations were very small and included zero in the 90% confi-

Table 2. Regional conditional maximum likelihood estimates of juvenile chum caught July and August 2001 in the Gulf of Alaska during the OCC/GLOBEC research cruise. The unmarked and marked collections at the bottom of the table were made based on the otolith analysis results. Below each point estimate is the 90% nonsymmetric bootstrap confidence interval. Estimates signifiantly greater than zero are in bold face.

| Mixture Sample | N | AK Peninsula/Kodiak Is. | Susitna | Prince William Sound | SE Alaska/N. BC | Queen Charlotte Is. | Washington/S. BC |
|---|---|---|---|---|---|---|---|
| | | | | Regional Allocation | | | |
| *Geographic Collection* | | | | | | | |
| Icy Point | 180 | **0.128** (0.049 - 0.256) | 0 (0) | 0.042 (0 - 0.084) | **0.761** (0.620 - 0.900) | 0.007 (0 - 0.014) | 0.062 (0 - 0.112) |
| Ocean Cape | 136 | **0.169** (0.015 - 0.295) | 0 (0) | **0.113** (0.026 - 0.226) | **0.63** (0.458 - 0.856) | 0.084 (0 - 0.163) | 0.004 (0 - 0.008) |
| Icy/Ocean | 316 | **0.119** (0.026 - 0.214) | 0 (0) | **0.067** (0.007 - 0.135) | **0.742** (0.619 - 0.872) | 0.041 (0 - 0.079) | 0.032 (0 - 0.57) |
| Icy/Ocean/Yakutaga/St. Elias | 380 | 0.092 (0 - 0.171) | 0 (0) | **0.056** (0.01 - 0.111) | **0.701** (0.549 - 0.804) | **0.092** (0.048 - 0.166) | 0.057 (0 - 0.097) |
| Seward Line | 144 | 0.023 (0 - 0.045) | 0 (0) | **0.689** (0.589 - 0.846) | **0.24** (0.164 - 0.425) | 0.006 (0 - 0.011) | 0.043 (0 - 0.063) |
| Cleare/Seward/Gore Pt | 279 | 0 (0) | 0 (0) | **0.606** (0.483 - 0.695) | **0.293** (0.265 - 0.465) | 0.011 (0 - 0.021) | **0.091** (0.004 - 0.133) |
| Nukshak | 317 | **0.416** (0.363 - 0.561) | **0.407** (0.352 - 0.473) | 0.019 (0 - 0.037) | **0.141** (0.029 - 0.201) | 0 (0) | 0.014 (0 - 0.028) |
| Kekurnoi | 87 | **0.67** (0.55 - 0.904) | 0 (0) | 0 (0) | 0.201 (0 - 0.331) | **0.112** (0.001 - 0.211) | 0.017 (0 - 0.035) |
| Nukshak/Kekurnoi | 404 | **0.455** (0.380 - 0.574) | **0.316** (0.260 - 0.364) | 0.016 (0 - 0.032) | **0.179** (0.089 - 0.273) | 0.026 (0 - 0.052) | 0.004 (0 - 0.009) |
| *Marked/Unmarked Collection* | | | | | | | |
| Unmarked | 690 | **0.214** (0.065 - 0.257) | **0.196** (0.168 - 0.238) | **0.06** (0.020 - 0.103) | **0.427** (0.347 - 0.568) | **0.08** (0.038 - 0.142) | 0.021 (0 - 0.037) |
| Thermal Marked | 377 | 0.005 (0 - 0.008) | 0 (0) | **0.401** (0.312 - 0.482) | **0.486** (0.440 - 0.662) | 0.013 (0 - 0.026) | **0.096** (0.036 - 0.144) |

dence intervals. Chum salmon from the Washington/southern British Columbia region are readily detected in heterogenous mixtures, thus it is likely that fish from this region were uncommon in the GOA in late July-early August.

Populations from the Queen Charlotte Island (QCI) region are genetically distinct from other nearby populations in southern Southeast Alaska and northern British Columbia. Significant contribution from this region was observed in the collections east of PWS (9.2%) and in the Kekurnoi transect in southern Shelikof Strait (11.2%). Several observations can be made: 1) the QCI chum salmon were estimated at 8.4% of the Ocean Cape sample but were not significantly detected until data from this mixture was combined with other collections east of PWS (Icy Point, Cape Yakutaga, and Cape St. Elias); and 2) though the Kekurnoi collection was very small (n= 87), the presence of QCI chum salmon was significant. QCI fish were not detected in the nearby northern Shelikof Strait sample, even given the much larger sample size (n= 317). If the estimate of QCI chum salmon in the southern Shelikof Strait is correct, it appears that some fish maintain tight formation during their coastal migration, and their migration route includes passage through Shelikof Strait rather than seaward of Kodiak Island. Body size provided additional evidence for the differences between fish caught at the northern and southern end of Shelikof Strait. The chum salmon in the Kekurnoi transect at the southern entrance of Shelikof Strait were larger than those in the Nukshak transect at the northern entrance (average 143 mm vs. 119 mm).

Chum salmon from Southeast Alaska/northern British Columbia were found at every transect, however their presence in the Kekurnoi collection was statistically insignificant. Southeast Alaska chum salmon have some genetic similarity to PWS and Alaska Peninsula populations, and this is reflected in the larger confidence interval (which includes zero) for the Southeast Alaska estimate than that for the QCI esti-

mate in the Kekurnoi collection, even though twice as many fish were estimated to be from Southeast Alaska. Southeast Alaska/northern British Columbia chum salmon comprised the majority (> 70%) of fish collected to the east of PWS; contribution from this region tapered off toward the west, representing about 30% of the Kenai Peninsula collections and 14% of the Nukshak collection in northern Shelikof Strait.

PWS is represented by only five populations in the genetic baseline, including the Wally Noerenberg Hatchery, which produced 75 million chum salmon fry in 2001. Chum salmon from this region were detected in the genetic analysis in low frequency (5.6%) east of PWS; however, thermally marked fish from the Wally Noerenberg Hatchery were found only west of PWS. An easterly migration of fish from PWS toward Southeast Alaska may be possible, but would appear improbable given the overall counter-clockwise direction of current flow in the northern GOA and the working model of juvenile salmon migration in North America. It is more likely that the small contribution from PWS in the genetic analysis is due to misallocation of Southeast Alaska chum salmon. Most of the PWS fish were found to the west, making up nearly 70% of fish in the Seward Line collection and 60% of the overall Kenai Peninsula collections (Cape Cleare, Seward, Gore Pt.).

The Susitna River and Yentna Lake/Creek systems in northern Cook Inlet are genetically very distinct (99% correct allocation in baseline simulations). Although this region is represented by only two rivers, over 40% of the chum salmon in the northern Shelikof Strait collection below the mouth of Cook Inlet were estimated to be from this region. Fish from the Susitna region were not observed in any other collection, including the Kekurnoi collection in southern Shelikof Strait, 120 km to the southwest. It appears that chum salmon from Cook Inlet migrate through Shelikof Strait rather than south of Kodiak Island.

Chum salmon from the Alaska Peninsula/Kodiak Island region were collected in

Shelikof Strait, but were not found to the east along the Kenai Peninsula. Although significant presence was detected in the Icy Point (12.8%) and Ocean Cape (16.9%) collections, contribution from this region was statistically insignificant when all the collections east of PWS were combined. Some misallocation between the Southeast Alaska and Alaska Peninsula/Kodiak Island regions is not unexpected given the level of genetic similarity between populations of the two regions. A recently developed Bayesian model of stock estimation for mixtures supports our contention that the presence of Alaska Peninsula fish in the easternmost collections is simply misallocation of Southeast Alaska fish: in a preliminary examination of the Icy Point collection, less than 1% (median) of the fish were estimated to be from the Alaska Peninsula region.

As observed in previous surveys (1996-98), juvenile chum salmon preferentially migrated through Shelikof Strait rather than south of Kodiak Island in the Alaskan Stream. Fish from every region except Washington/southern British Columbia were detected in Shelikof Strait from either genetic or thermal mark information. The 2001 OCC/GLOBEC project in the GOA sampled juvenile salmon in late July and early August and caught fish primarily at or just beyond the exit corridors from inshore habitat. Although several thermally marked Wally Noerenberg Hatchery fish were recovered from the north entrance to Shelikof Strait,



*Great Pacific* crewmember Chris Wood and biologist Mary Auburn-Cook examine a large catch of juvenile salmon during the OCC/GLOBEC summer surveys 2001.

and few juvenile chum were caught in stations south of Kodiak Island, most of the fish from PWS and regions farther east were caught early in their coastal oceanic migration, and it is unknown whether fish from these regions enter oceanic water before reaching Kodiak Island or migrate north through Shelikof Strait. Perhaps sampling the GOA in mid-to-late August/early September would answer this question.

In two of the three years that surveys were made in the GOA prior to 2001, thermally marked hatchery chum salmon from the Nitnat River Hatchery on southwestern Vancouver Island were recovered from transects along Southeast Alaska and as far west as northern Shelikof Strait. Although fish from this hatchery could not be distinguished from the Macaulay Hatchery chum salmon in 2001, these previous surveys support the concept that at least some of the more southern populations of chum salmon migrate to sea early in the summer, mix with later migrating northern populations, and extensively migrate around the coastal continental shelf corridor to the northern GOA by mid-to-late summer.

Genetic and thermal mark comparison

The large presence of thermally marked fish allowed us to investigate the ability of the genetic stock identification analysis to properly identify the origin of marked fish (Table 3). It should be kept in mind that given the nature of genetic variation among chum salmon populations, this technique provides

Table 3. Comparison of the genetic stock identification and otolith analysis results for each transect. Baseline populations were categorized as unmarked (wild and unmarked hatchery), Wally Noerenberg Hatchery or Macaulay/Hidden Falls Hatcheries. The unmarked and marked collections at the bottom of the table were made based on the otolith analysis results. Below each maximum likelihood estimate from the genetic analysis is the 90% nonsymmetric bootstrap confidence interval. Estimates significantly greater than zero are in bold face.

| Mixture Sample | Unmarked | | Wally Noerenberg Hatchery | | Macaulay/Hidden Falls Hatcheries | |
| --- | --- | --- | --- | --- | --- | --- |
| | Genetic | Otolith | Genetic | Otolith | Genetic | Otolith |
| *Geographic Collection* | | | | | | |
| Icy Point | **0.934** (0.868 - 1) | 0.647 | 0 (0) | 0 | 0.066 (0 - 0.132) | 0.353 |
| Ocean Cape | **1** (1) | 0.630 | 0 (0) | 0 | 0 (0) | 0.370 |
| Icy/Ocean | **0.978** (0.955 - 1) | 0.639 | 0 (0) | 0 | 0.023 (0 - 0.045) | 0.361 |
| Icy/Ocean/Yakutaga/St. Elias | **0.945** (0.891 - 1) | 0.602 | 0 (0) | 0 | 0.052 (0 - 0.104) | 0.398 |
| Seward Line | **0.57** (0.186 - 0.662) | 0.196 | **0.43** (0.339 - 0.814) | 0.643 | 0 (0) | 0.161 |
| Cleare/Seward/Gore Pt | **0.727** (0.508 - 0.858) | 0.189 | **0.274** (0.144 - 0.492) | 0.604 | 0 (0) | 0.207 |
| Nukshak | **0.997** (0.994 - 1) | 0.983 | 0 (0) | 0.017 | 0 (0) | 0 |
| Kekurnoi | **1** (1) | 1.000 | 0 (0) | 0 | 0 (0) | 0 |
| Nukshak/Kekurnoi | **0.998** (0.995 - 1) | 0.987 | 0 (0) | 0.013 | 0 (0) | 0 |
| *Marked/Unmarked Collection* | | | | | | |
| Unmarked | **0.997** (0.994 - 1) | | 0 (0) | | 0 (0) | |
| Thermal Marked | **0.739** (0.541 - 0.852) | | **0.261** (0.214 - 0.480) | | 0 (0) | |
| *Total (all collections combined)* | **0.908** (0.830 - 0.969) | 0.640 | **0.09** (0.058 - 0.173) | 0.165 | 0 (0) | 0.195 |

regional estimates of origin rather than specific stock estimates. Virtually 100% of the unmarked fish were properly allocated to the category of unmarked fish (all the baseline populations except Wally Noerenberg, Hidden Falls, and Macaulay Hatcheries). However, the genetic analysis underestimates the hatchery contribution–overall, 74% of the known marked fish were allocated to the unmarked category. The bias was particularly severe for the Kenai Peninsula collections, where 81% of the fish were marked and the genetic analysis estimated a marked contribution of only 27%. Of the marked fish properly allocated to hatchery populations, all were estimated to be from the Wally Noerenberg Hatchery, when in fact over 50% of the marked fish were from the Macaulay and Hidden Falls Hatcheries (Table 1). The 90% confidence intervals for the Wally Noerenberg Hatchery contribution to all collections combined (5.8% - 17.3%) includes the value of 16.5% observed from the otolith analysis. In contrast, the genetic analysis did not detect the 19.5% Southeast Alaska hatchery marked fish found by the otolith analysis.

Inspection of the genetic data for the marked fish revealed the presence of eight alleles that were not observed in the baseline collections for the Macaulay and Wally Noerenberg Hatchery populations. When fish with these alleles were deleted from the marked mixture, the estimation improved (64% unmarked, 27% Wally Noerenberg, 9% Macaulay/Hidden Falls), but the hatchery allocation remained severely under-represented. Although the genetic analysis underestimated hatchery contribution, nearly 90% of the thermally marked fish were properly allocated to the PWS and Southeast Alaska/northern British Columbia regions, if not to the exact hatchery populations within these two regions (Table 2).

The estimate of approximately 10% contribution from Washington/southern British Columbia to the marked mixture may explain their presence in the Kenai Peninsula collections (Table 2). Most of the fish from these collections were thermally marked and this suggests that the significant, but small contribution from the Washington/southern British Columbia region, estimated by the genetic analysis may be correct, given the indistinguishable otolith mark pattern between Macaulay and Nitinat River Hatcheries.

The next step is to use the Bayesian model to analyze all of the collections. It is computationally intensive, but better accommodates the problem of rare alleles undetected in baseline populations and should provide better regional estimates of origin. The current genetic baseline for chum salmon contains information for 20 genetic characters. Future efforts by fishery agencies to expand the baseline to incorporate additional genetic characters may increase the resolution of stock estimation, particularly for the southern Alaska regions. Other types of genetic information such as microsatellite loci in genomic DNA or mtDNA haplotypes may also reveal further population structure, however a comprehensive baseline for these characters has not yet been developed. The results of our stock identification analysis will eventually be used in conjunction with oceanographic information and growth and diet data to more fully understand the factors that affect the distribution, abundance, and survival of chum salmon in the GOA.