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Shunpei Sato¹, Shogo Moriya², Tomonori Azumaya³,
Hiroyuki Nagoya¹, Syuiti Abe⁴, and Shigehiko Urawa^{1,5}

¹National Salmon Resources Center, Fisheries Research Agency,
2-2 Nakanoshima, Toyohira-ku, Sapporo 062-0922, Japan

²Business Development Division, Nisshinbo Industries, Inc.,
1-2-3 Onodai, Midori-ku, Chiba 267-0056, Japan

³Hokkaido National Research Institute, Fisheries Research Agency,
116 Katsurakoi, Kushiro 085-0802, Japan

⁴Graduate School of Fisheries Science, Hokkaido University,
3-1-1 Minato-cho, Hakodate 041-8611, Japan

⁵Present address: North Pacific Anadromous Fish Commission,
502-889-West Pender Street, Vancouver, BC, V6C 3B2 Canada

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Abstract

Stock origins of chum salmon caught in Bering Sea and North Pacific Ocean during the summer and fall of 2002-2004 were estimated by mitochondrial DNA marker. The mixture samples of chum salmon were more than 97% immature fish in the fall of 2002 and 2003 and 80-88% in the summer of 2003 and 2004. Our genetic stock estimates and genetic-estimated CPUE suggested that immature fish were mostly of Asian (Japanese and Russian) origins, and were widely distributed in the surveyed areas of the Bering Sea during summer and fall. The stock abundance of North America was lower than those of Asian stocks in the survey areas. In the central Bering Sea, the Japanese stock was predominant compared to the other areas during summer and fall of 2002-2004. The present results suggest that the ocean distribution pattern of Japanese chum salmon showed no inter-annual variation within the survey years, and it was not significantly related with the limited sea surface temperature range (6.6-11.9°C).

Introduction

Chum salmon (*Oncorhynchus keta*) is the most widely distributed salmon species in the Pacific Rim and an important commercial fisheries resource. Estimation of ocean distribution and stock origins of chum salmon is important to clarify the stock assessment and the pattern of ocean migration. Since 1992, Japanese scientists have been conducted salmon survey cruises and collected biological data of Pacific salmon and oceanographic data of the Bering Sea and North Pacific Ocean in summer, fall, winter, and spring (Nagasawa et al. 1994; Ueno et al. 1996; Ishida et al. 1998; Azumaya et al. 2003, 2005; Fukuwaka et al. 2006; Morita et al. 2006, 2007, 2008).

Chum salmon is mainly distributed in the Bering Sea during summer and fall (Salo 1991).

Genetic stock identification (GSI) results using allozyme and mtDNA marker showed that Japanese and Russian chum salmon stocks are predominant in the central Bering Sea during summer and fall (Urawa et al. 2004, 2005; Moriya et al. 2007). However, it is still unclear whether the marine distribution of particular stock shows inter-annual changes or not. Furthermore, sea temperature may be an important factor to affect the ocean distribution of chum salmon (Urawa et al. 2000), but their relationships are also unclear.

The objectives of this document were to determine the stock origins of chum salmon caught on the 2003 and 2004 summer cruise in the Bering Sea and North Pacific Ocean using mtDNA marker, in comparison with the stock composition estimated in September 2002 and 2003 (Moriya et al. 2007). Furthermore, the relationships between distribution pattern of specific stocks and sea surface temperature (SST) were examined by randomization test.

Materials and Methods

Fish samples and DNA extraction

Samples of chum salmon were collected from the Bering Sea and North Pacific Ocean during Bering/Aleutian Salmon International Survey (BASIS) research cruises of R/V *Kaiyo maru* between June 30 and July 18 in 2003 and between June 24 and July 8 in 2004. One-hour trawl operation was made in the surface layer (from surface to 50m in depth) with 5 knot towing speed at 23 stations in the Bering Sea and North Pacific Ocean (49°50' to 58°24'N, 174°44'E to 164°42'W) in 2003 (Fig.1 and Table 1) and at 18 stations in the Bering Sea and North Pacific Ocean (50°38' to 57°58'N, 175°14'E to 170°00'W) in 2004 (Fig.1 and Table 2). A total of 1,537 and 2,149 individuals of chum salmon were collected in 2003 and 2004, respectively. Whole blood samples were collected from the caudal vasculature or gill and frozen at -40 °C. DNA was isolated from the whole blood samples from 1,063 individuals in 2003 and 1,248 individuals in 2004 by a Puregene™ DNA Purification kit (QIAGEN Inc., Valencia, CA) following a manufacturer's instructions. DNA extraction was accomplished during the research cruise of R/V *Kaiyo maru* in 2003. On the other hand, DNA was extracted at the laboratory of National Salmon Resources Center, Fisheries Research Agency.

MtDNA analysis and GSI estimation of chum salmon

Thirty mtDNA haplotypes of chum salmon which was collected from the Bering Sea and North Pacific Ocean were detected by DNA microarray (Moriya et al. 2004) and assigned them to the population origins (Japanese, Russian or North American stocks) using the mtDNA data sets of 96 chum salmon populations in the Pacific Rim (Yoon et al. 2008). These data sets were used as a baseline with recruitment of 48 additional populations to those obtained from the previously analyzed 48 populations by Sato et al. (2004). This baseline was created using more than 4,200 individuals from 96 populations of chum salmon in the Pacific Rim.

Stock contributions of the mixed samples were estimated via a conditional maximum likelihood (Pella and Milner 1987; Masuda et al. 1991). A conjugate-gradient searching algorithm using a square root transformation was employed, because it provides good performance with large baselines and small stock differences (Pella et al. 1996). Standard deviations were estimated by 1,000 bootstrap resamplings of the baseline and mixture samples. Estimates were made to individual stock and then pooled to regional stock groups: Japan, Russia, and North America. These regional stock groups were categorized based on previous genetic

analysis for the baseline data set of 96 populations of chum salmon in the Pacific Rim (Yoon et al. 2008). Computations were performed with the Statistics Programs for Analyzing Mixtures (SPAM version 3.7b, ADFG 2005). The previously reported stock composition in the fall Bering Sea and North Pacific Ocean in 2002 and 2003 (Moriya et al. 2007) were re-estimated using new mtDNA baseline.

Randomization test

The randomization test of cumulative frequency was used for the difference in distribution between each regional stock group and SST (Perry and Smith 1994). In this test, the Cramer-von Mises test statistics and 999 permutations of random combination of 2 variants were used for the significance (Syrjara 1996). Relationships between the distribution of each regional stock and SST were tested by the randomization test for cumulative functions of CPUE and stations over SST in each year. The randomization test was calculated using handmade EXCEL macro, which was made by Fukuwaka and Suzuki (1998).

Results

MtDNA baseline of chum salmon and baseline evaluation

Yoon et al. (2008) demonstrated that a total of 22 variable nucleotide sites, including two new and 20 previous polymorphic sites (Sato et al. 2004), defined 32 haplotypes among 4,245 individuals in the combined 96 population samples (detail shown in Yoon et al. 2008). The performance of the maximum likelihood model for chum salmon was investigated through simulation studies of three regional stock groups, Japan, Russia, and North America. In simulation studies where the true regional contributions were 100%, the average of maximum likelihood estimates was more than 80% accuracy. Estimates for the Japanese and North American regions reached more than 90% accuracy (91.6% Japan and 94.5% North America), whereas the estimate for the Russian region was 80.2% accuracy (Table 3), given essentially similar performance to that of the previous baseline with 48 populations (Moriya et al. 2007).

Distribution and maturity

A total of 1,537 and 2,149 individuals of chum salmon were collected in summer 2003 and 2004, respectively (Tables 1 and 2). Chum salmon was more abundant in the Bering Sea than in the North Pacific Ocean in summer 2003 and 2004, but their distribution patterns in the Bering Sea were different between those two years (Fig. 2). In 2003, chum salmon was widely distributed in the survey areas of the Bering Sea, but 2004, about 30% of chum salmon were caught in the one station (H18, see Fig. 2 and Table 2). The mixture samples of chum salmon were less than 90% immature fish in the summer of 2003 and 2004 (80.2% in 2003 and 88.1% in 2004). On the other hand, the occurrence of immature fish was more than 97% in the fall of 2002 and 2003 (Moriya et al. 2007).

Genetic stock identification

The mixed stock composition of chum salmon in the Bering Sea and North Pacific Ocean in the summer of 2003 was estimated (Fig. 3, Table 4). The stock composition in the central Bering Sea (A08-A10, A17, and A19) was estimated 47.0-68.2% Japanese, 20.5-42.3% Russian, and 9.4-20.5% North American stocks. The estimated stock composition of chum salmon in the southern Bering Sea (A12, A14, A21, and A23) was composed of 19.3-57.9% Japanese,

27.6-64.1% Russian, and 12.5-16.5% North American chum salmon. In the eastern Bering Sea (A26-A28), the percentages of Asian stocks (48.1-59.7% Japanese and 27.7-37.2% Russian) were larger than those of North American stock (7.5-24.2%). The estimated stock composition in the western Bering Sea (A01-A04) was 29.0-40.8% Japanese, 28.5-49.5% Russian, and 16.6-30.7% North American stocks. In the eastern North Pacific Ocean (A25, A30, A32, A33, A35, and A37), the stock composition was estimated 4.9-25.9% Japanese, 20.1-59.3% Russian, and 30.4-57.1% North American chum salmon (Fig. 3, Table 4).

The mixed stock composition of chum salmon in the Bering Sea and North Pacific Ocean in the summer of 2004 was estimated (Fig. 4, Table 5). The stock composition in the central Bering Sea (H07, H09, H20, and H21) was 59.6-67.4% Japanese, 19.1-36.1% Russian, and 4.3-21.0% North American stocks. The estimated stock composition of chum salmon in the southern Bering Sea (H11 and H18) was composed of 33.3-47.5% Japanese, 36.7-58.1% Russian, and 8.7-15.8% North American chum salmon. Chum salmon in the eastern Bering Sea (H04-06) were estimated 47.0-65.5% Japanese, 15.7-47.4% Russian, and 5.6-30.9% North American stocks. The stock composition in the western Bering Sea (H22-H25) was 14.3-19.0% Japanese, 13.8-54.2% Russian, and 26.8-70.3% North American stocks. In the eastern North Pacific Ocean (H01-H03, and H13), the stock composition was estimated 41.2-49.8% Japanese, 19.8-41.6% Russian, and 17.3-30.4% North American chum salmon (Fig. 4, Table 5).

Re-estimation of the previously reported stock composition in the Bering Sea and North Pacific Ocean in the fall of 2002 and 2003 using new mtDNA baseline provided essentially the same ocean distribution profile of chum salmon as that estimated previously (Tables 6 and 7, Moriya et al. 2007).

Stock distribution

GSI-estimated CPUE of chum salmon by stock origin in the Bering Sea and North Pacific Ocean was calculated by five areas (central, southern, eastern, and western Bering Sea and eastern North Pacific Ocean) in each survey period (Fig. 5, Tables 8-11). Asian (Japanese and Russian) stocks were widely distributed in the survey areas, and relatively abundant in the central and southern Bering Sea. The abundance of North American stocks was lower than those of Asian stocks in the Bering Sea (Fig. 5, Tables 8-11).

Relationship between distribution of each stock and SST

Associations between cumulative frequencies of genetic-estimated CPUE for three regional stocks and cumulative frequency of SST in each survey period were estimated based on stock abundance and SST data in each survey station (Tables 8-11). All regional stocks were distributed in proportion to the available SST (6.6-11.9°C) in each survey period (Fig. 6A to 5D), and the all test values for statistical significance indicated negative values ($P > 0.05$). SST anomalies in the Bering Sea in the summer of 2003 and 2004 showed plus 0-1 degrees, while SST anomalies in the Bering Sea in the fall of 2002 and 2003 indicated plus 1-2 degrees. In the North Pacific Ocean in the summer and fall of 2003 showed minus 0.5-plus 1 degree. These SST anomalies data are collected from HP of Japan Meteorological Agency (<http://www.data.kishou.go.jp/kaiyou/db/kaikyo/dbindex.html>).

Discussion

We used a new mtDNA baseline collected from 96 chum salmon populations around the

Pacific Rim (Yoon et al. 2008). In simulation studies where the true regional contributions were 100%, estimations for the Japanese and North American regions reached more than 90%, while estimate for Russian region was 80.2% accurate. This simulation result is similar to the previous result (Moriya et al. 2007), however, the present assignment performance for Japan and Russia was lowered to some extent than the previous result (Wilmot et al. 1998; Seeb and Crane 1999). Particularly, the accuracy of Russian region is low. It may be related that Russian and North American populations share some clade B haplotypes (Sato et al. 2004) and these two regional populations, especially Russian and Northwest Alaskan populations, were not clearly separated by present mtDNA markers (Yoon et al. 2008).

More than 600 individuals of chum salmon were collected at the one station of the Bering Sea in 2004. It is unknown why a CPUE bias was indicated in the Bering Sea in 2004 only. In summer of 2007, we surveyed in the Bering Sea and 117 individuals of chum salmon were collected from the same station (Morita et al. 2007). A continuous salmon research cruise in the summer Bering Sea is requested to clarify the distribution of chum salmon.

Our genetic stock estimates and GSI-estimated CPUE indicated that immature chum salmon were mostly of Asian (Japanese and Russian) origins, and were widely distributed in the surveyed areas of the Bering Sea during summer 2003 and 2004 and fall of 2002 and 2003. Particularly, the Japanese stock was predominant in the central Bering Sea during the summer and fall of 2002 and 2004. Allozyme analyses also indicated that Japanese stock was most abundant in the central Bering Sea during the summer and fall of 2002 and 2003 (Urawa et al. 2004, 2005). The randomization test showed non-significant correlation between the stock distribution and SST within the limited range (6.6-11.9°C). These results suggest that the ocean distribution pattern of Japanese chum salmon may be non-random in the summer and fall and it may not be related with SST. The ocean distribution and migration patterns of salmon may be affected by abundance of food organisms, interactions within or between species, ocean conditions, timing and location of spawning as well as winter habitat (Urawa et al. 2005). In future studies, we should clarify factors influencing the migration and distribution of chum salmon in the ocean.

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Table. 1. A list of chum salmon samples caught in the Bering Sea and North Pacific Ocean during June-July research cruise R/V *Kaiyo maru* in 2003.

Station	Latitude	Longitude	Date	Number of catches	Number of genetic samples
A04	53°05'N	174°44'E	2003/6/30	34	57
A03	53°50'N	174°59'E	2003/6/30	27	23
A02	55°00'N	174°41'E	2003/7/1	127	54
A01	56°00'N	175°00'E	2003/7/1	72	57
A08	58°24'N	179°44'E	2003/7/2	69	55
A09	57°23'N	179°42'E	2003/7/3	60	59
A10	56°24'N	179°42'E	2003/7/3	106	58
A12	55°40'N	179°58'W	2003/7/4	131	59
A14	52°35'N	179°44'E	2003/7/5	134	57
A16	50°35'N	179°43'W	2003/7/6	39	38
A25	49°50'N	175°05'W	2003/7/7	38	36
A23	52°33'N	175°05'W	2003/7/8	49	49
A21	53°49'N	174°59'W	2003/7/9	34	34
A19	55°49'N	175°00'W	2003/7/10	110	57
A17	57°49'N	175°00'W	2003/7/11	118	60
A26	56°00'N	170°03'W	2003/7/12	67	60
A27	55°08'N	170°08'W	2003/7/13	109	59
A28	54°02'N	170°34'W	2003/7/13	122	57
A30	52°09'N	169°56'W	2003/7/14	13	13
A32	49°52'N	170°14'W	2003/7/15	25	24
A37	50°03'N	165°14'W	2003/7/16	30	30
A35	51°55'N	164°46'W	2003/7/17	24	24
A33	53°26'N	164°42'W	2003/7/18	40	40
Total				1,578	1,063

Table 2. A list of chum salmon samples caught in the Bering Sea and North Pacific Ocean during June-July research cruise R/V *Kaiyo maru* in 2004.

Station	Latitude	Longitude	Date	Number of catches	Number of genetic samples
H01	50°53'N	170°10'W	2004/6/26	70	70
H02	51°49'N	170°00'W	2004/6/26	148	94
H03	53°05'N	170°22'W	2004/6/27	71	64
H04	53°56'N	170°01'W	2004/6/27	49	43
H05	55°04'N	170°01'W	2004/6/28	46	40
H06	55°40'N	170°05'W	2004/6/28	56	52
H07	57°58'N	174°42'W	2004/6/29	100	93
H09	56°01'N	174°42'W	2004/6/30	173	101
H11	54°10'N	175°02'W	2004/7/1	160	98
H13	51°40'N	175°06'W	2004/7/2	75	61
H14	50°38'N	180°00'	2004/7/3	16	14
H18	54°35'N	179°46'E	2004/7/5	633	100
H20	56°21'N	179°52'W	2004/7/6	144	101
H21	57°20'N	179°53'W	2004/7/6	75	72
H22	55°57'N	175°17'E	2004/7/7	101	95
H23	55°05'N	175°14'E	2004/7/7	179	100
H24	53°57'N	175°16'E	2004/7/8	35	34
H25	52°58'N	175°16'E	2004/7/8	18	16
Total				2,149	1,248

Table 3. Mean estimated contribution for 1,000 bootstrap resampling where each region composes 100% of the mixtures (N=500 each). Bold italic cells denote correct regional allocations.

Regional allocation	Region		
	Japan	Russia	North America
Japan	<i>0.916 (0.054)</i>	0.058 (0.053)	0.025 (0.030)
Russia	0.019 (0.019)	<i>0.802 (0.129)</i>	0.179 (0.129)
North America	0.000 (0.000)	0.055 (0.045)	<i>0.945 (0.045)</i>

Table 4. Estimated regional proportions of chum salmon in the Bering Sea and North Pacific Ocean in 2003 summer. Standard deviations (SD) were calculated from 1,000 bootstrap resamplings of the mixture and baseline samples.

Station	Japan		Russia		North America	
	Estimate	SD	Estimate	SD	Estimate	SD
A04	0.290	0.141	0.495	0.207	0.215	0.172
A03	0.388	0.135	0.447	0.219	0.166	0.182
A02	0.408	0.112	0.285	0.172	0.307	0.148
A01	0.371	0.150	0.362	0.202	0.267	0.151
A08	0.589	0.137	0.205	0.168	0.205	0.133
A09	0.630	0.120	0.276	0.152	0.094	0.115
A10	0.470	0.150	0.423	0.181	0.108	0.111
A12	0.579	0.140	0.276	0.177	0.145	0.125
A14	0.287	0.112	0.584	0.195	0.129	0.157
A16	0.221	0.119	0.609	0.223	0.171	0.184
A25	0.259	0.108	0.330	0.202	0.412	0.178
A23	0.319	0.151	0.556	0.207	0.125	0.131
A21	0.193	0.164	0.641	0.223	0.165	0.132
A19	0.615	0.125	0.245	0.147	0.140	0.100
A17	0.682	0.143	0.222	0.146	0.096	0.083
A26	0.547	0.128	0.372	0.16	0.080	0.101
A27	0.597	0.136	0.329	0.155	0.075	0.086
A28	0.481	0.123	0.277	0.177	0.242	0.151
A30	0.104	0.103	0.593	0.315	0.304	0.307
A32	0.133	0.098	0.499	0.273	0.369	0.253
A37	0.049	0.062	0.476	0.250	0.475	0.230
A35	0.197	0.121	0.351	0.215	0.452	0.178
A33	0.228	0.086	0.201	0.146	0.571	0.146

Table 5. Estimated regional proportions of chum salmon in the Bering Sea and North Pacific Ocean in 2004 summer. Standard deviations (SD) were calculated from 1,000 bootstrap resamplings of the mixture and baseline samples.

Station	Japan		Russia		North America	
	Estimate	SD	Estimate	SD	Estimate	SD
H01	0.498	0.156	0.198	0.213	0.304	0.195
H02	0.450	0.137	0.327	0.207	0.223	0.181
H03	0.257	0.144	0.607	0.203	0.136	0.168
H04	0.470	0.174	0.474	0.203	0.056	0.109
H05	0.535	0.148	0.157	0.208	0.309	0.208
H06	0.655	0.163	0.177	0.184	0.168	0.154
H07	0.674	0.125	0.196	0.157	0.130	0.135
H09	0.613	0.122	0.243	0.160	0.143	0.135
H11	0.333	0.147	0.581	0.193	0.087	0.138
H13	0.412	0.118	0.416	0.223	0.173	0.194
H14	0.282	0.143	0.018	0.045	0.700	0.153
H18	0.475	0.141	0.367	0.206	0.158	0.173
H20	0.599	0.129	0.191	0.175	0.210	0.172
H21	0.596	0.148	0.361	0.166	0.043	0.088
H22	0.177	0.127	0.522	0.265	0.300	0.254
H23	0.190	0.124	0.542	0.295	0.268	0.284
H24	0.143	0.114	0.367	0.367	0.490	0.348
H25	0.160	0.110	0.138	0.165	0.703	0.191

Table 6. Re-estimated regional proportions of chum salmon in the Bering Sea September 2002. The previously estimated proportions using 48 baseline populations are shown in parenthesis (Moriya et al. 2007).

Station	Japan		Russia		North America	
	Estimate	SD	Estimate	SD	Estimate	SD
D46	0.433 (0.485)	0.110 (0.108)	0.370 (0.316)	0.203 (0.188)	0.197 (0.199)	0.176 (0.168)
D38	0.321 (0.378)	0.140 (0.163)	0.562 (0.522)	0.247 (0.243)	0.118 (0.100)	0.195 (0.176)
D39	0.278 (0.339)	0.104 (0.113)	0.395 (0.311)	0.230 (0.209)	0.328 (0.349)	0.211 (0.183)
D31	0.231 (0.317)	0.108 (0.121)	0.619 (0.544)	0.210 (0.215)	0.150 (0.139)	0.180 (0.168)
D30	0.425 (0.494)	0.189 (0.216)	0.441 (0.399)	0.278 (0.273)	0.134 (0.107)	0.222 (0.202)
D66	0.526 (0.571)	0.126 (0.134)	0.386 (0.354)	0.179 (0.176)	0.088 (0.075)	0.134 (0.122)
D29	0.690 (0.770)	0.136 (0.135)	0.287 (0.188)	0.142 (0.145)	0.022 (0.042)	0.050 (0.076)
D18	0.511 (0.691)	0.170 (0.140)	0.424 (0.241)	0.189 (0.160)	0.066 (0.069)	0.094 (0.103)
D20	0.708 (0.771)	0.126 (0.114)	0.129 (0.030)	0.124 (0.076)	0.163 (0.200)	0.102 (0.120)
D22	0.405 (0.487)	0.134 (0.123)	0.324 (0.330)	0.215 (0.208)	0.271 (0.183)	0.180 (0.178)
D24	0.404 (0.461)	0.113 (0.122)	0.428 (0.384)	0.202 (0.194)	0.169 (0.155)	0.176 (0.167)
D27	0.247 (0.314)	0.144 (0.179)	0.533 (0.507)	0.323 (0.312)	0.220 (0.180)	0.295 (0.268)
D12	0.110 (0.221)	0.117 (0.138)	0.506 (0.399)	0.313 (0.288)	0.384 (0.380)	0.295 (0.278)
D10	0.370 (0.451)	0.172 (0.203)	0.444 (0.398)	0.289 (0.283)	0.186 (0.151)	0.258 (0.236)
D04	0.256 (0.319)	0.118 (0.140)	0.571 (0.522)	0.246 (0.251)	0.173 (0.159)	0.214 (0.199)
D03	0.380 (0.443)	0.134 (0.145)	0.515 (0.462)	0.204 (0.208)	0.106 (0.095)	0.158 (0.146)
D06	0.226 (0.340)	0.135 (0.141)	0.618 (0.523)	0.227 (0.232)	0.157 (0.135)	0.189 (0.177)
D01	0.367 (0.436)	0.147 (0.166)	0.477 (0.438)	0.265 (0.256)	0.156 (0.126)	0.221 (0.201)

Standard deviations (SD) were calculated from 1,000 bootstrap resamplings of the mixture and baseline samples.

Table 7. Re-estimated regional proportions of chum salmon in the Bering Sea and North Pacific Ocean September 2003. The previously estimated proportions using 48 baseline populations are shown in parenthesis (Moriya et al. 2007).

Station	Japan		Russia		North America	
	Estimate	SD	Estimate	SD	Estimate	SD
C33	0.124 (0.160)	0.060 (0.057)	0.083 (0.015)	0.137 (0.068)	0.793 (0.825)	0.125 (0.084)
C35	0.040 (0.082)	0.042 (0.060)	0.118 (0.048)	0.127 (0.121)	0.843 (0.870)	0.127 (0.126)
C37	0.000 (0.027)	0.000 (0.028)	0.168 (0.082)	0.165 (0.142)	0.832 (0.891)	0.165 (0.141)
C32	0.055 (0.105)	0.052 (0.064)	0.224 (0.096)	0.157 (0.152)	0.721 (0.799)	0.148 (0.152)
C30	0.276 (0.363)	0.112 (0.110)	0.349 (0.258)	0.201 (0.233)	0.375 (0.380)	0.166 (0.201)
C28	0.235 (0.328)	0.105 (0.114)	0.481 (0.384)	0.184 (0.214)	0.284 (0.288)	0.159 (0.189)
C27	0.262 (0.373)	0.126 (0.134)	0.512 (0.440)	0.215 (0.246)	0.226 (0.187)	0.180 (0.193)
C26	0.110 (0.171)	0.071 (0.084)	0.344 (0.251)	0.240 (0.232)	0.545 (0.579)	0.230 (0.221)
C17	0.473 (0.592)	0.132 (0.150)	0.375 (0.228)	0.179 (0.192)	0.152 (0.181)	0.129 (0.154)
C19	0.420 (0.496)	0.122 (0.126)	0.332 (0.285)	0.177 (0.194)	0.248 (0.219)	0.134 (0.156)
C21	0.475 (0.525)	0.108 (0.108)	0.360 (0.327)	0.171 (0.176)	0.165 (0.149)	0.141 (0.152)
C23	0.459 (0.519)	0.114 (0.010)	0.242 (0.154)	0.174 (0.154)	0.299 (0.327)	0.145 (0.145)
C25	0.266 (0.346)	0.104 (0.113)	0.368 (0.256)	0.203 (0.197)	0.366 (0.398)	0.186 (0.185)
C16	0.318 (0.393)	0.105 (0.105)	0.402 (0.309)	0.201 (0.222)	0.280 (0.298)	0.174 (0.203)
C14	0.366 (0.481)	0.139 (0.145)	0.283 (0.142)	0.162 (0.173)	0.351 (0.377)	0.119 (0.166)
C12	0.433 (0.567)	0.138 (0.128)	0.322 (0.126)	0.182 (0.153)	0.245 (0.307)	0.141 (0.149)
C10	0.496 (0.587)	0.123 (0.144)	0.273 (0.150)	0.155 (0.161)	0.231 (0.264)	0.121 (0.150)
C09	0.550 (0.676)	0.123 (0.143)	0.312 (0.151)	0.164 (0.161)	0.138 (0.172)	0.118 (0.152)
C01	0.340 (0.403)	0.098 (0.110)	0.387 (0.306)	0.213 (0.235)	0.273 (0.291)	0.195 (0.220)
C02	0.231 (0.380)	0.121 (0.142)	0.634 (0.454)	0.172 (0.212)	0.135 (0.166)	0.128 (0.161)
C03	0.239 (0.298)	0.094 (0.090)	0.517 (0.446)	0.222 (0.249)	0.245 (0.257)	0.194 (0.230)
C04	0.071 (0.136)	0.085 (0.123)	0.436 (0.340)	0.208 (0.227)	0.493 (0.524)	0.186 (0.198)
C07	0.042 (0.165)	0.068 (0.139)	0.832 (0.712)	0.185 (0.233)	0.126 (0.122)	0.167 (0.184)

Standard deviations (SD) were calculated from 1,000 bootstrap resamplings of the mixture and baseline samples.

Table 8. Genetic-estimated CPUE of chum salmon by stock origin in each survey station and each pooled area in the Bering Sea in the fall of 2002. CPUE means number of catch per 1-h trawl.

Station/Area	SST	CPUE	Japan	Russia	North America
D46	9.8	343	148.5	126.9	67.6
D38	10.0	429	137.7	241.1	50.6
D39	9.0	126	35.0	49.8	41.3
D31	9.5	143	33.0	88.5	21.5
D30	9.0	120	51.0	52.9	16.1
D66	10.5	152	80.0	58.7	13.4
D29	10.5	173	119.4	49.7	3.8
D18	10.1	115	58.8	48.8	7.6
D20	9.8	39	27.6	5.0	6.4
D22	9.6	208	84.2	67.4	56.4
D24	9.0	75	30.3	32.1	12.7
D12	11.5	28	3.1	14.2	10.8
D10	9.7	38	27.0	32.4	13.6
D04	9.7	73	52.2	116.5	35.3
D03	9.8	204	42.2	57.2	11.8
D06	8.7	111	7.0	19.2	4.9
D01	9.8	31	72.3	94.0	30.7
CBS		479	291.2	161.9	25.9
SBS		1001	344.3	510.5	147.1
WBS		485	162.5	248.8	73.7

CBS: central Bering Sea, SBS: southern Bering Sea, WBS: western Bering Sea.

Table 9. Genetic-estimated CPUE of chum salmon by stock origin in each survey station and each pooled area in the Bering Sea and North Pacific Ocean in the summer of 2003. CPUE means number of catch per 1-h trawl.

Station/Area	SST	CPUE	Japan	Russia	North America
A04	8.0	34	9.9	16.8	7.3
A03	7.1	27	10.5	12.1	4.5
A02	6.9	127	51.8	36.2	39.0
A01	7.2	72	26.7	26.1	19.2
A08	7.9	69	40.6	14.1	14.1
A09	7.9	60	37.8	16.6	5.6
A10	7.5	106	49.8	44.8	11.4
A12	7.2	131	75.8	36.2	19.0
A14	7.2	134	38.5	78.3	17.3
A25	7.9	38	9.8	12.5	15.7
A23	8.3	49	15.6	27.2	6.1
A21	8.2	34	6.6	21.8	5.6
A19	8.4	110	67.7	27.0	15.4
A17	8.4	118	80.5	26.2	11.3
A26	8.9	67	36.6	24.9	5.4
A27	9.1	109	65.1	35.9	8.2
A28	9.3	122	58.7	33.8	29.5
A30	10.1	13	1.4	7.7	4.0
A32	9.9	25	3.3	12.5	9.2
A37	9.4	30	1.5	14.3	14.3
A35	11.0	24	4.7	8.4	10.8
A33	10.1	40	9.1	8.0	22.8
CBS		463	278.7	131.5	53.2
SBS		348	186.5	119.0	42.8
WBS		260	101.7	112.8	45.5
EBS		298	167.2	102.8	28.3
ENPO		170	35.0	70.2	64.8

CBS: central Bering Sea, SBS: southern Bering Sea, WBS: western Bering Sea, EBS: eastern Bering Sea, ENPO: eastern North Pacific Ocean.

Table 10. Genetic-estimated CPUE of chum salmon by stock origin in each survey station and each pooled area in the Bering Sea and North Pacific Ocean in the fall of 2003. CPUE means number of catch per 1-h trawl.

Station/Area	SST	CPUE	Japan	Russia	North America
C33	11.3	100	12.4	8.3	79.3
C35	11.8	37	1.5	4.4	31.2
C37	11.9	125	0.0	21.0	104.0
C32	11.8	138	7.6	30.9	99.5
C30	11.7	158	43.6	55.1	59.3
C28	10.4	263	61.8	126.5	74.7
C27	10.8	130	34.1	66.6	29.4
C26	10.9	45	5.0	15.5	24.5
C17	11.4	57	27.0	21.4	8.7
C19	10.4	205	86.1	68.1	50.8
C21	10.5	183	86.9	65.9	30.2
C23	8.4	255	117.0	61.7	76.2
C25	11.6	59	15.7	21.7	21.6
C14	7.2	93	34.0	26.3	32.6
C12	11.0	324	140.3	104.3	79.4
C10	10.3	199	98.7	54.3	46.0
C09	11.1	224	123.2	69.9	30.9
C01	10.8	195	66.3	75.5	53.2
C02	10.4	77	17.8	48.8	10.4
C03	10.3	205	49.0	106.0	50.2
C04	9.0	24	1.7	10.5	11.8
CBS		685	358.9	233.6	92.5
SBS		855	419.0	254.8	182.1
WBS		501	145.3	259.0	96.2
EBS		438	104.7	201.5	131.8
ENPO		617	106.7	127.7	382.5

CBS: central Bering Sea, SBS: southern Bering Sea, WBS: western Bering Sea, EBS: eastern Bering Sea, NPO: eastern North Pacific Ocean.

Table 11. Genetic-estimated CPUE of chum salmon by stock origin in each survey station and each pooled area in the Bering Sea and North Pacific Ocean in the summer of 2004. CPUE means number of catch per 1-h trawl.

Station/Area	SST	CPUE	Japan	Russia	North America
H01	8.8	70	26.8	4.3	39.0
H02	8.6	148	64.4	50.8	32.9
H03	7.6	71	18.2	43.1	9.7
H04	7.2	49	22.5	23.5	3.0
H05	8.5	46	24.6	7.2	14.2
H06	9.1	56	38.3	8.7	9.0
H07	8.7	100	67.6	18.9	13.5
H09	8.2	173	106.0	42.0	24.7
H11	7.9	160	53.3	93.0	13.9
H13	8.3	75	30.9	31.2	13.0
H18	7.7	633	300.7	232.3	100.0
H20	8.3	144	86.0	19.7	38.3
H21	8.4	75	45.4	24.0	5.6
H22	8.8	101	15.4	56.6	27.0
H23	7.9	179	33.7	102.6	42.8
H24	8.1	35	5.0	12.8	17.2
H25	7.2	18	2.9	2.5	12.7
CBS		492	318.3	116.1	57.6
SBS		793	308.5	387.0	97.5
WBS		333	51.9	192.1	88.9
EBS		151	83.5	49.2	18.3
ENPO		364	148.1	152.9	63.0

CBS: central Bering Sea, SBS: southern Bering Sea, WBS: western Bering Sea, EBS: eastern Bering Sea, NPO: eastern North Pacific Ocean.

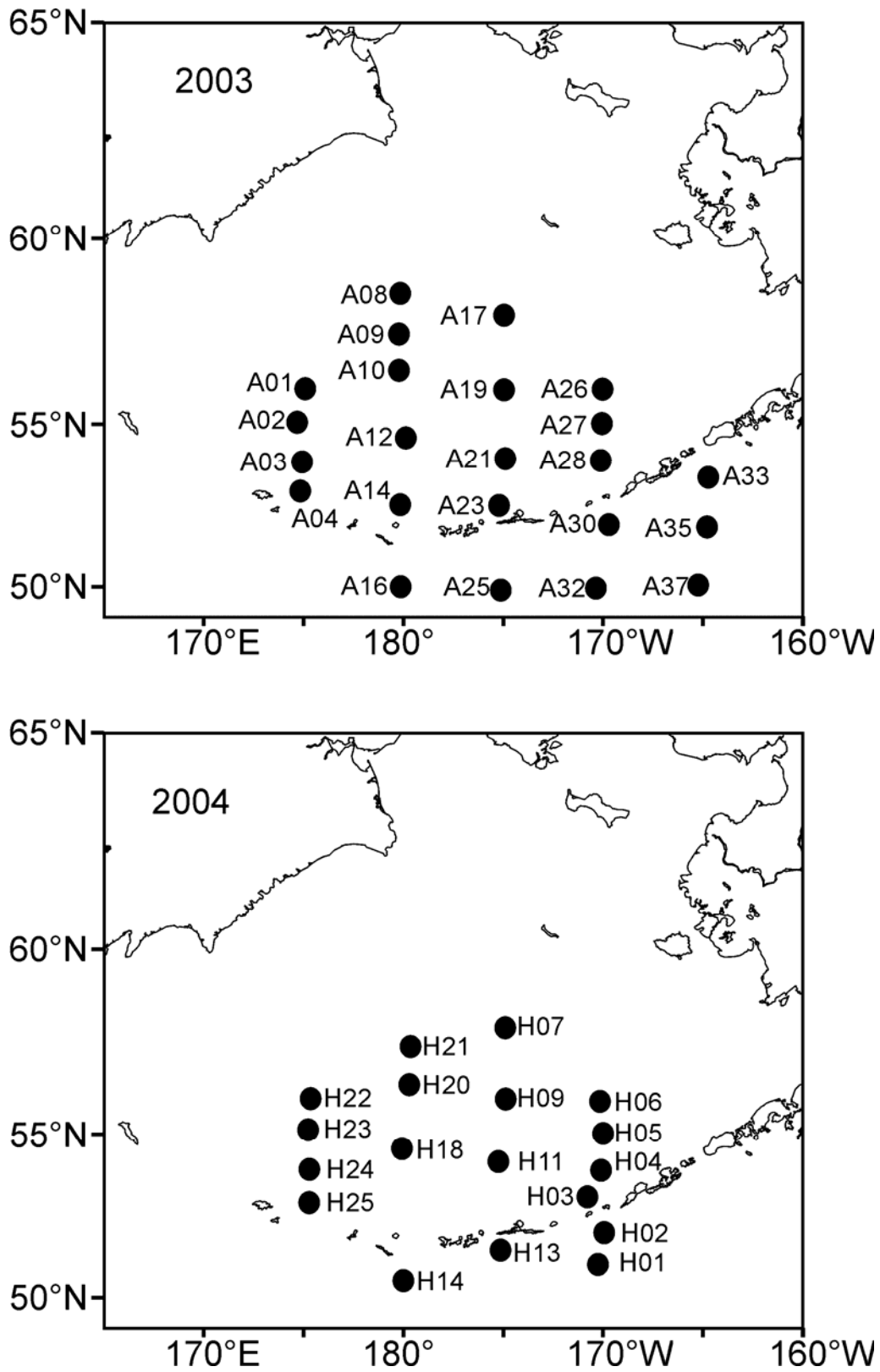


Fig. 1. Sampling locations of chum salmon in the Bering Sea and North Pacific Ocean in summer of 2003 and 2004.

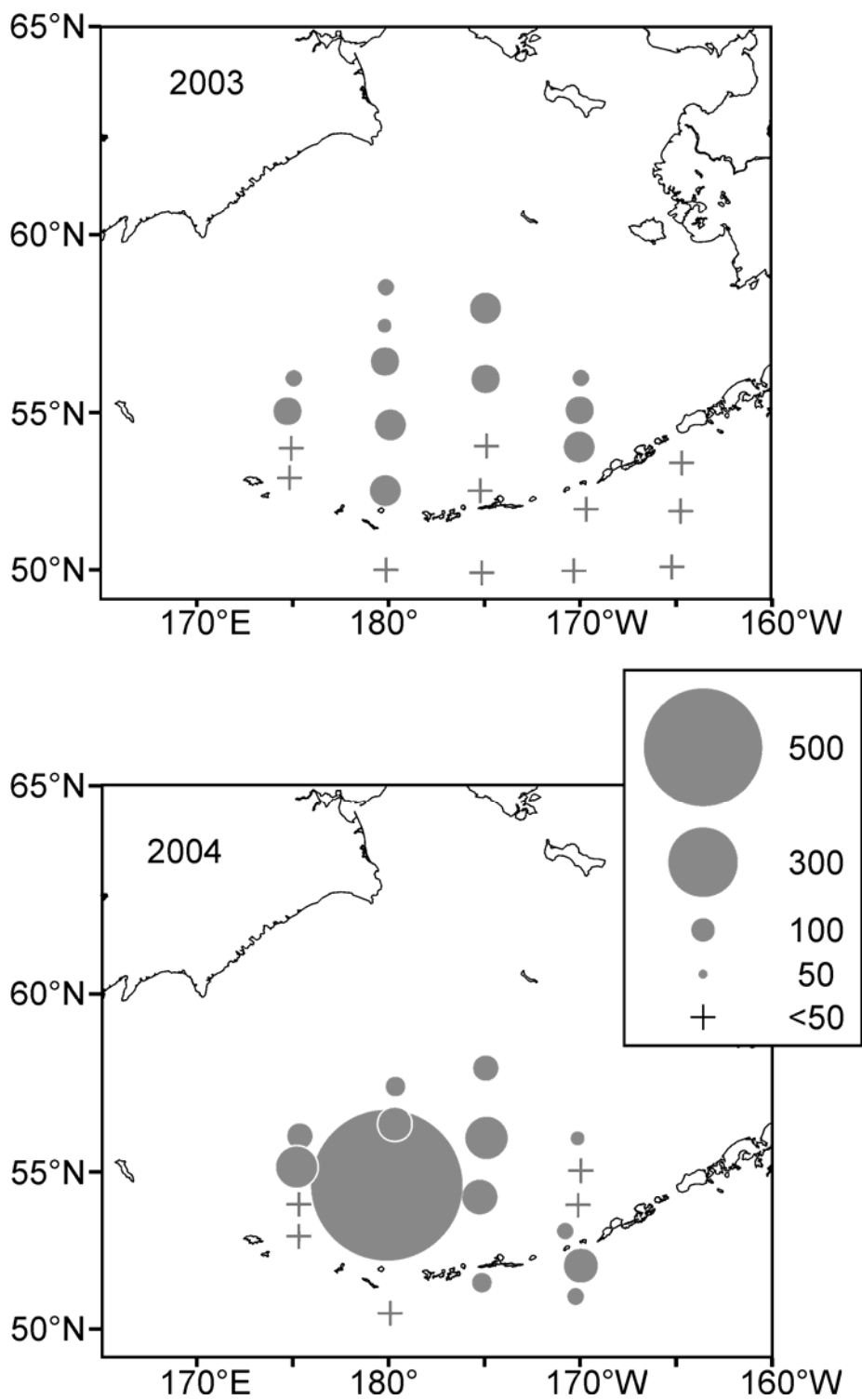


Fig. 2. Number of chum salmon caught by 1-h trawl (CPUE) in the Bering Sea and North Pacific Ocean in summer of 2003 and 2004.

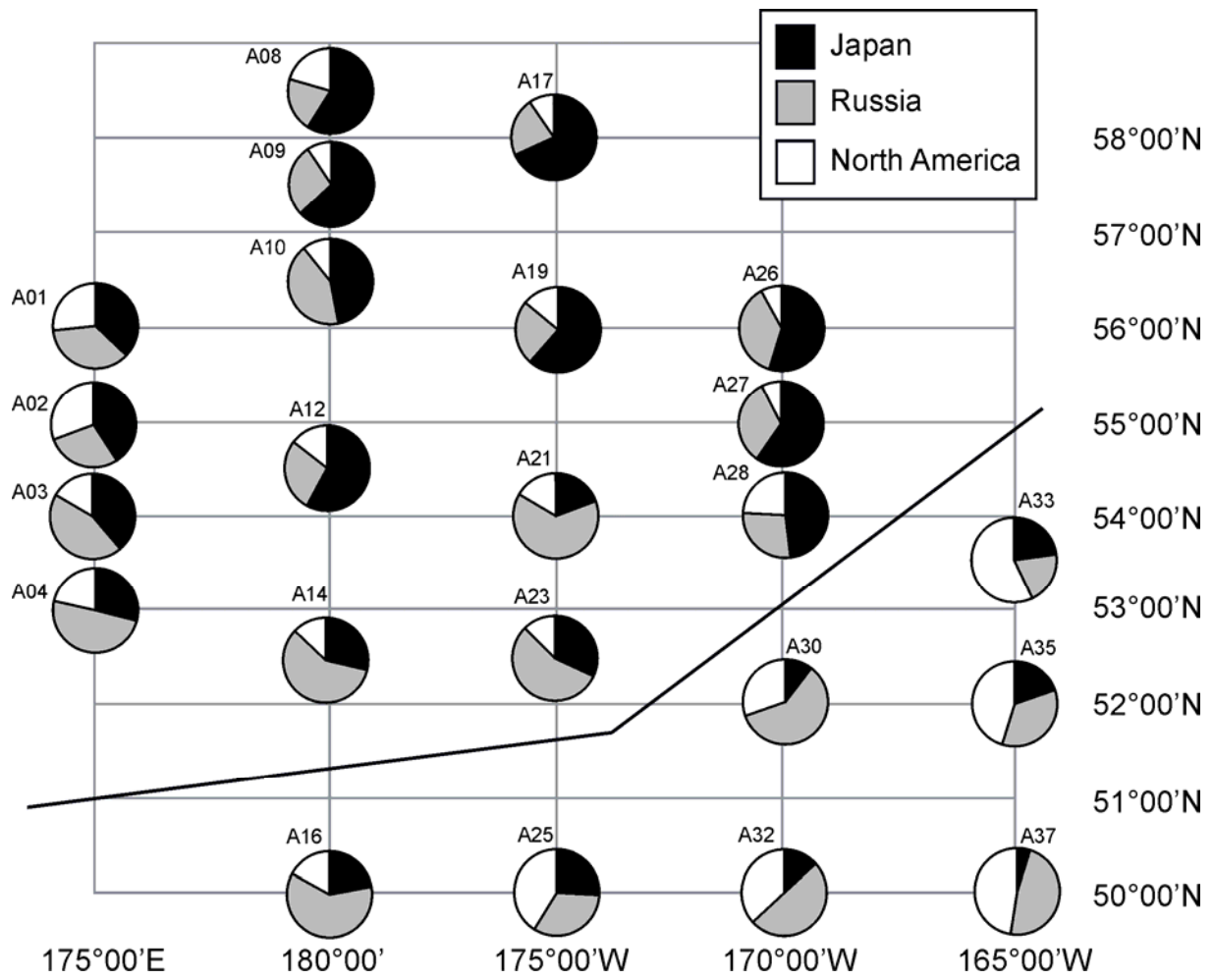


Fig. 3. Genetic-estimated stock composition (%) of chum salmon caught in the Bering Sea and North Pacific Ocean in summer of 2003.

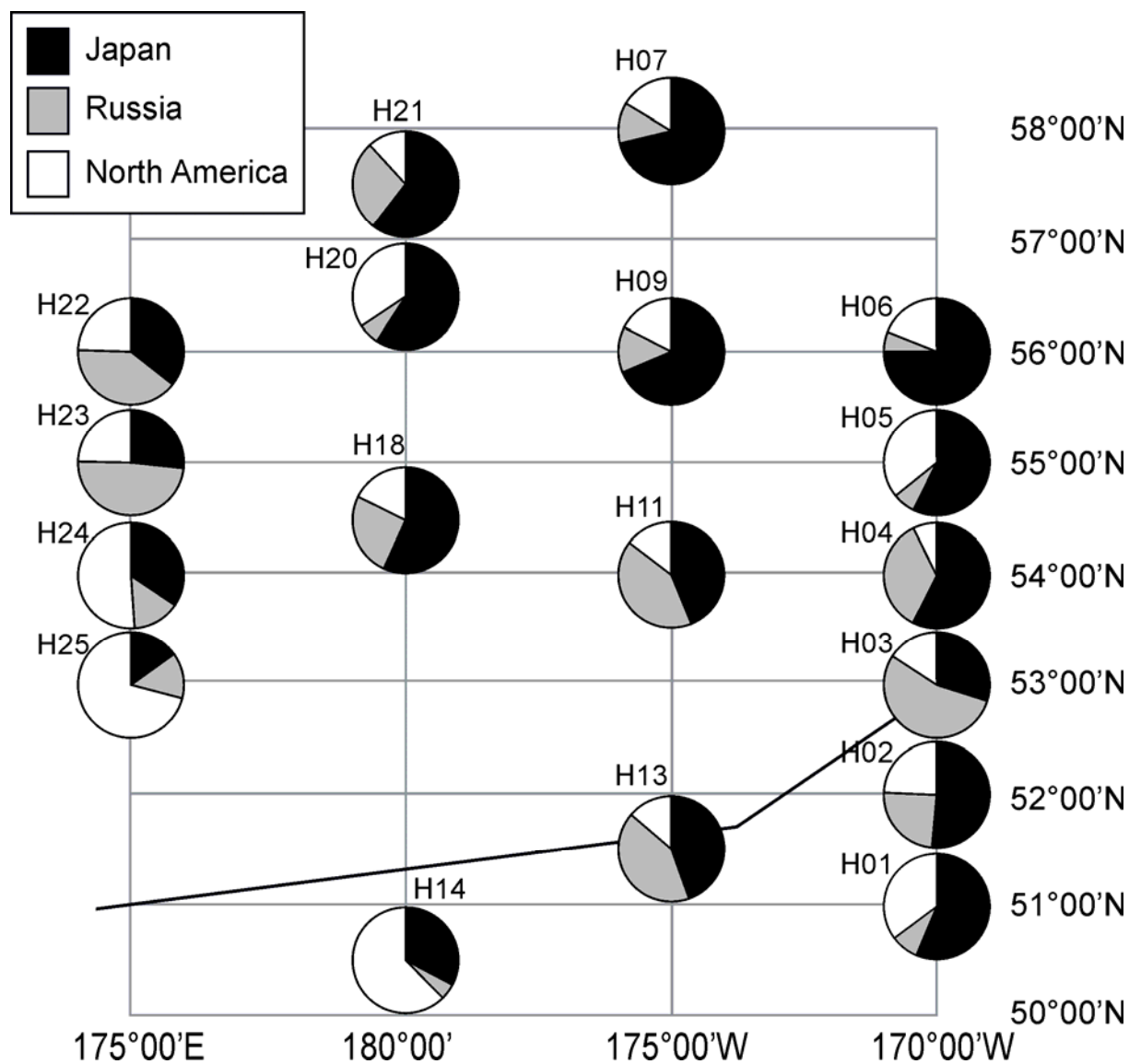


Fig. 4. Genetic-estimated stock composition (%) of chum salmon caught in the Bering Sea and North Pacific Ocean in summer of 2004.

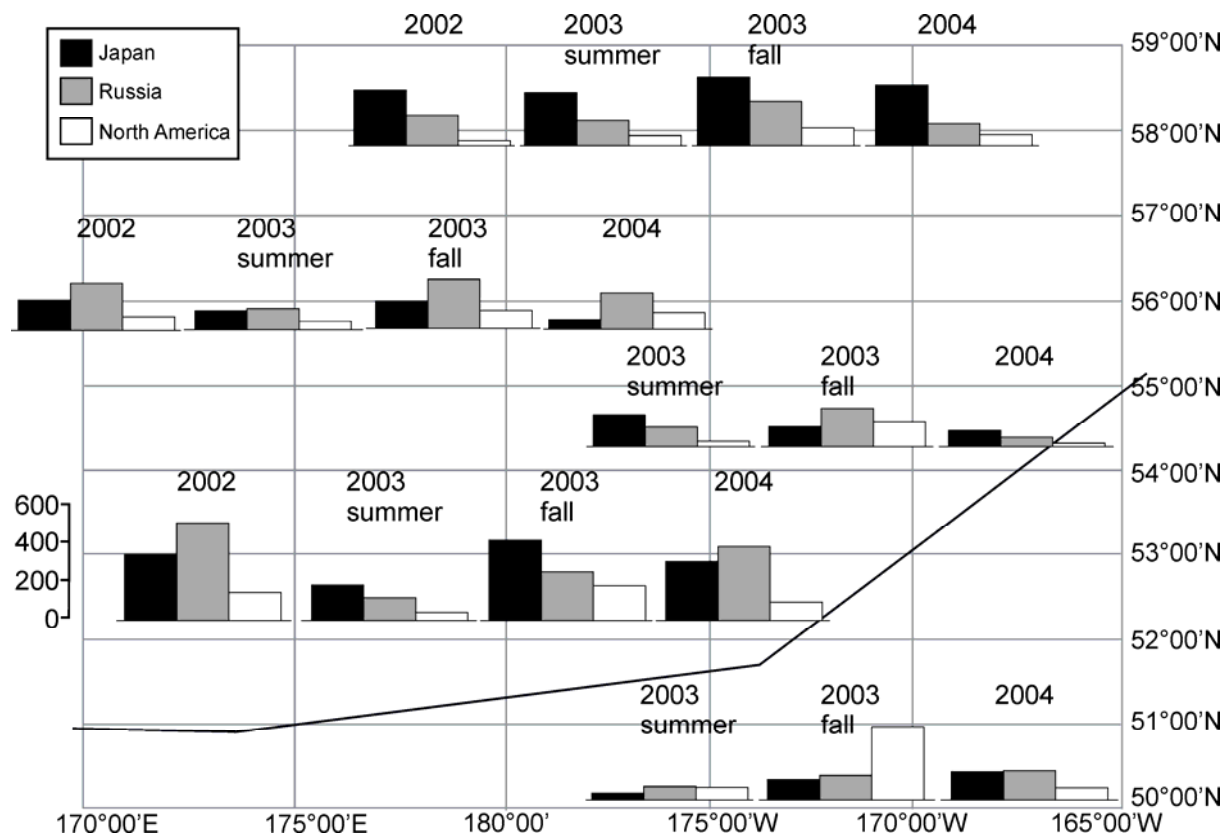


Fig. 5. GSI-estimated CPUE of immature chum salmon by stock origin in the Bering Sea and North Pacific Ocean during 2002-2004. CPUE means number of catch per 1-h trawl.

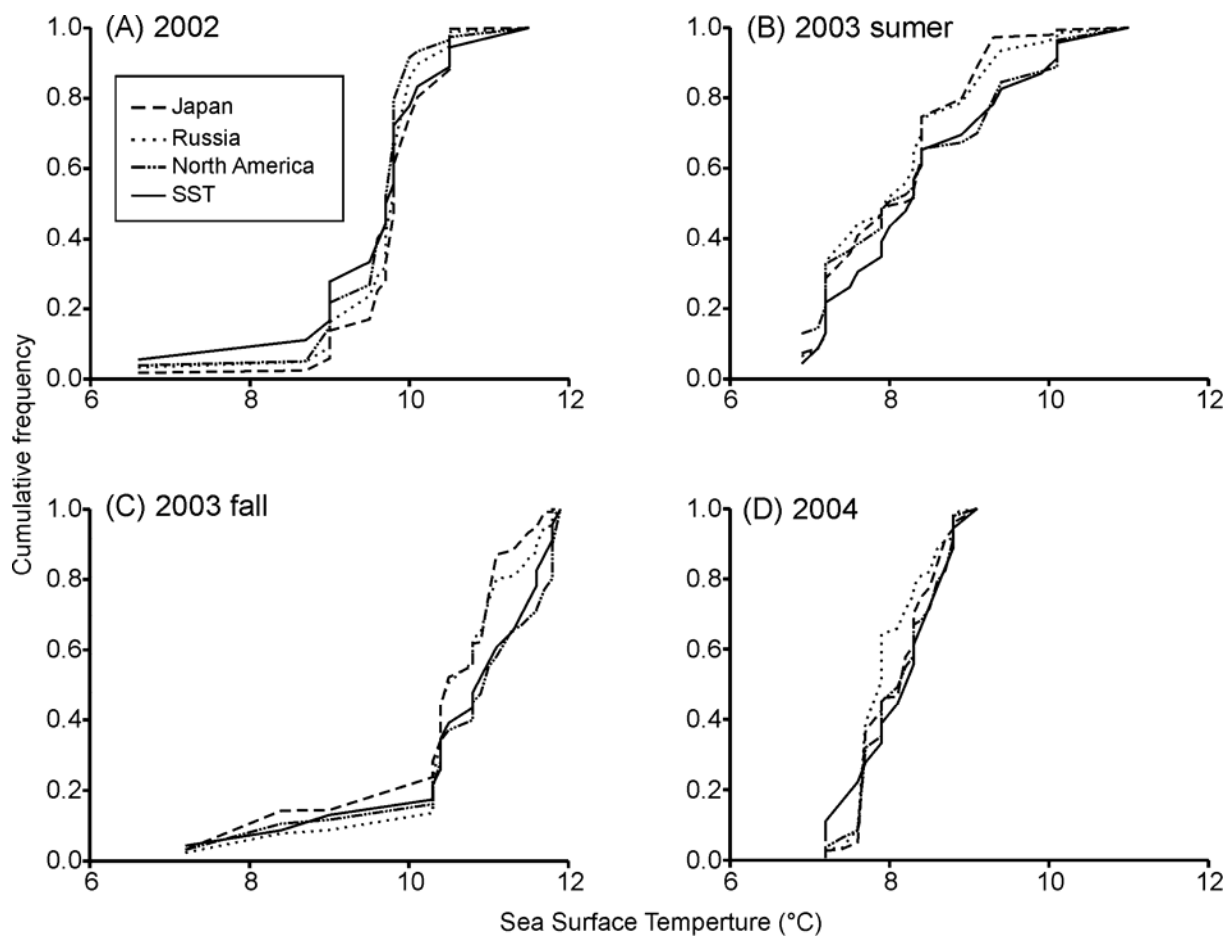


Fig.6. Relationships between cumulative frequencies of chum salmon CPUE for three regional stocks (Japan, Russia, and North America) and sea surface temperature.