Origins and Distribution of Chum Salmon in the Central Bering Sea

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The Bering Sea provides major feeding habitats for various salmon stocks originating from Asia and North America. A better understanding of salmon community structure will clarify the mechanisms of salmon population response to recent environmental changes. Chum salmon (*Oncorhynchus keta*) is a dominant pelagic fish in the Bering Sea during summer and fall especially after pink salmon (*O. gorbuscha*) have moved to coastal areas for spawning.

Genetic stock identification (GSI) techniques using allozyme variation have been established for estimating stock compositions of high-seas chum salmon (Seeb et al. 1995, 2004; Urawa et al. 1997, 1998; Wilmot et al. 1998; Winans et al. 1998; Seeb and Crane 1999a, 1999b). The present study was conducted to determine stock origin of chum salmon caught in the central Bering Sea by allozyme analysis.

Japanese BASIS troll surveys were conducted at 36 stations in the Bering Sea by the research vessel *Kaiyo maru* between August 21 and September 18, 2002 (Azumaya et al. 2003). We caught approximately 7,700 chum salmon, most of which were immature fish. For the genetic stock identification (GSI), tissue samples (liver, heart and muscle) were collected from 2,136 chum salmon, and immediately deep frozen until the analysis.

Selected samples were examined for protein electrophoretic variation on horizontal starch gels using standard procedures described by Aebersold et al. (1987). Standard nomenclature for loci and alleles was used as outlined in Shaklee et al. (1990). Alleles were compared and standardized for 20 polymorphic loci (ALAT*, mAAT-1*, sAAT-1,2*, mAH-3*, ESTD*, G3PDH-2*, GPI-A*, GPIB-1,2, mIDHP-1*, sIDHP-2*, LDH-A1*, LDHB-2*, sMDHA-1*, sMDHB-1,2*, mMEP-2*, sMEP-1*, MPI*, PEPA*, PEPB-1*, and PGDH*).

We used the simplified baseline data set (124 stock groups/20 loci) formulated in Seeb et al. (1997) with additional data from Japan. Estimates of stock contributions were made with a conditional maximum likelihood algorithm (Pella and Milner 1987) by using the Statistical Package for Analyzing Mixtures (SPAM version 3.5) developed by Debevec et al. (2000). Standard deviations of estimates were estimated by 1,000 bootstrap resamplings of the baseline and mixture samples. Based on genetic similarity and 100% simulation analysis among baseline stocks, 12 reporting regions were selected. These are five regions in Asia, 1) Japan, 2) Sakhalin, 3) Premorye, 4) Amur, 5) Northern Russia; and seven regions in North America, 6) NW Alaska summer, 7) Fall Yukon, 8) Alaska Peninsula/Kodiak Island, 9) Susitna, 10) Prince William Sound, 11) Southeast Alaska/North BC, 12) South BC/Washington. Estimates were made to individual stocks and than pooled to regional stock groups. Simulation studies indicated that most reporting regions showed greater than 90% accurate when true group contributions were 100%.

Chum salmon were widely distributed in the Bering Sea north of 52°N, and they were relatively abundant in the eastern waters off the continental shelf (Fig. 1). The mixture chum samples were 97% immature fish (Fig. 2), and the age composition was 29% ocean age .1, 54% ocean age .2, and 13% ocean age .3 fish (Fig. 3).

The estimated stock composition for all maturing chum salmon was 70% Japanese, 10% Russian, and 20% North American stocks, and 54% Japanese, 33% Russian, and 13% North American stocks for immature fish. The stock estimates of immature chum salmon were similar among three age groups (0.1, 0.2 and 0.3). Asian chum salmon were dominant in all 11 estimates, while North American stock contribution was 5–28% (Fig. 4). Asian chum salmon were widely distributed in the survey areas, being relatively abundant in eastern waters (Fig. 5). North American stocks were mainly distributed in eastern water. Regional stock composition estimates of immature chum salmon biomass in the whole survey areas were 47% Japanese, 34% Russian, and 19% North American stocks.

The previous genetic studies suggested that Japanese and Russian stocks are predominant in chum salmon mixtures caught in the central Bering Sea (Urawa et al. 1997, 1998; Winans et al. 1998). However, these study areas were limited to the international water. The present genetic estimates confirmed that Asian chum salmon are

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Fig. 1. CPUE distribution of chum salmon in the Bering Sea, August/September 2002. CPUE = number of catches per 1 h trawl by R/V *Kaiyo maru*.

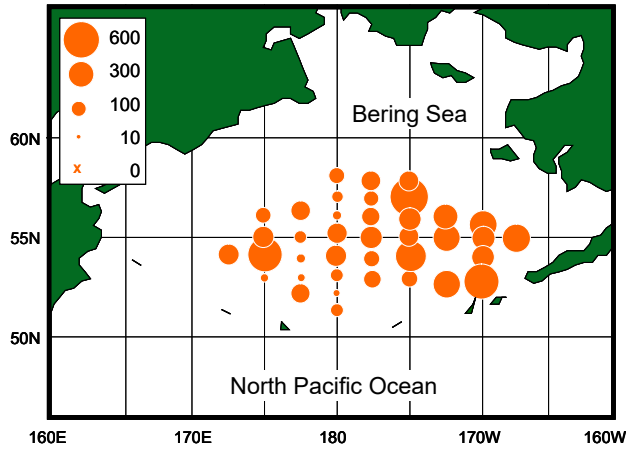


Fig. 2. Percent composition of maturing and immature chum salmon mixtures caught in the Bering Sea, August/September 2002.

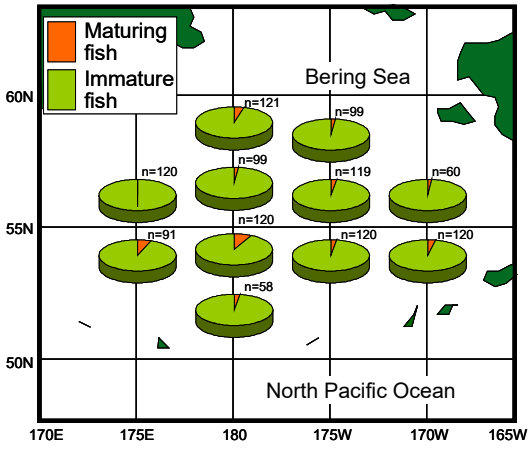


Fig. 3. Percent composition of ocean age in chum salmon mixtures caught in the Bering Sea, August/September 2002.

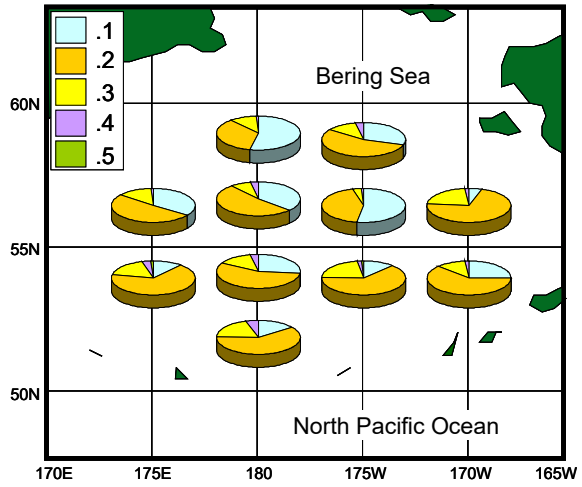
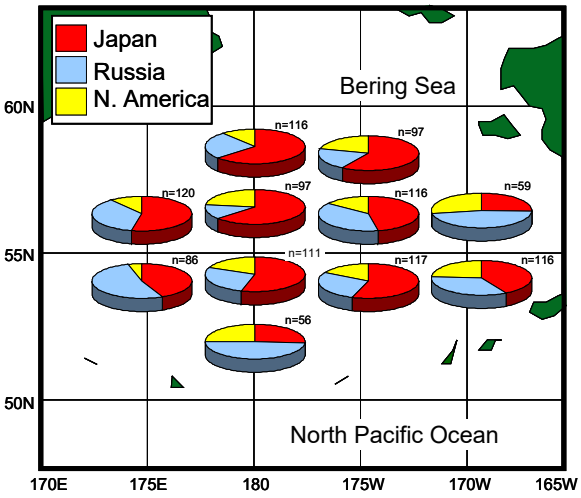


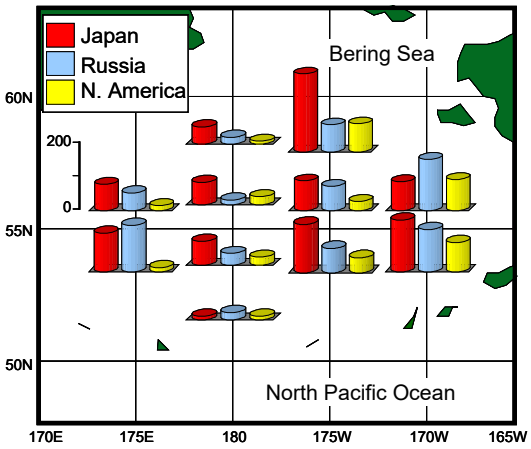
Fig. 4. GSI-estimated stock composition of immature chum salmon mixtures caught in the Bering Sea, August/September 2002.



abundant in wide areas of the Bering Sea. Wilmot et al. (1998) conducted genetic stock identification for chum salmon caught incidentally in the eastern Bering Sea trawl fisheries during the late summer and fall of 1994. Their estimates indicated 40% Japanese, 26% Russian, and 44% North American stocks in areas 521/541 west of 170°W, and 23% Japanese, 19% Russian and 58% North American stocks in areas 509/513/517 east of 170°W. Our results showed similar estimates in the former areas.

It is an important question why Asian chum salmon migrate so far to the eastern water. One reason may be related with their overwintering habitats. Urawa (2000) indicated that Japanese chum salmon spend the first winter in the western North Pacific and the following winters in the Gulf of Alaska. During the overwinter period, chum salmon prefer water with low temperatures between 4 and 6°C. The habitat in this temperature range was more widely available in the eastern North Pacific

Fig. 5. GSI-estimated CPUE of immature chum salmon by stocks in the Bering Sea, August/September 2002. CPUE = number of catches per 1 h trawl.



than the western North Pacific Ocean. For Japanese chum salmon in the eastern North Pacific, the shortest homing migration route is through the Bering Sea. Thus maturing fish as well as immature fish migrate from the eastern North Pacific to the Bering Sea in early summer, and immature fish may remain in the Bering Sea for further feeding. The Bering Sea is one of most productive ecosystems in the world, and provides favorite feeding habitats for salmon during summer and fall.

It is an interesting result that the contribution of chum salmon from the northwest Alaska including the Yukon River was extremely low (0.5% among immature fish), although these areas are geographically close to the Bering Sea. Urawa et al. (2000) made a GSI estimation that Northwest Alaskan chum salmon occupied 15% among immature chum salmon caught in the western and central Gulf of Alaska during summer. It is possible that juvenile chum salmon migrate from the northwest Alaska coast to the Gulf of Alaska for the first winter, and remain there until maturing.

The present study suggests that the oceanic migration and distribution pattern of chum salmon are apparently different among stocks. Further studies are requested to clarify factors affecting the migration and distribution of salmon in the ocean.

REFERENCES

Aebersold, P.B., G.A. Winans, D.J. Teel, G.B. Milner, and F.M. Utter. 1987. Manual for starch gel electrophoresis: a method for the detection of genetic variation. NOAA Tech. Rep. NMFS No. 61: 19p.

Azumaya, T., S. Urawa, O. Yamamura, M. Fukuwaka, A. Kusaka, T. Nagasawa, T. Nomura, S. Moriya, and A. Urano. 2003. Results of the survey by Kaiyo maru in the Bering Sea, 2002. (NPAFC Doc. 717). 12p. Hokkaido National Fisheries Research Institute, Fisheries Research Agency, 116 Katsurakoi, Kushiro 085-0802, Japan.

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. J. Hered. 91: 509–511.

Pella, J.J., and G.B. Milner. 1987. Use of genetic marks in stock composition analysis. *In* Population genetics and fishery management. *Edited by* N. Ryman and F. Utter. University of Washington Press, Seattle, WA. pp. 247–276.

Seeb, L.W., and P.A. Crane. 1999a. High genetic heterogenecity in chum salmon in western Alaska, the contact zone between northern and southern lineages. Trans. Am. Fish. Soc. 128: 58–87.

Seeb, L.W., and P.A. Crane. 1999b. Allozymes and mitochondrial DNA discriminate Asian and North American populations of chum salmon in mixed-stock fisheries along the south coast of the Alaska Peninsula. Trans. Am. Fish. Soc. 128: 88–103.

Seeb, L.W., P.A. Crane, and R.B. Gates. 1995. Progress report of genetic studies of Pacific rim chum salmon and preliminary analysis of the 1993 and 1994 south Unimak June fisheries. Regional Information Report No. 5J95-07, Alaska Department of Fish and Game, Division of Commercial Fisheries Management and Development, Anchorage, AK, USA.

Seeb, L.W., P.A. Crane, and E.M. Debevec. 1997. Supplementary appendices: genetic analysis of chum salmon harvested in the South Unimak and Shumagin Islands June Fisheries, 1993–1996. Regional Information Report No. 5J97-18, Alaska Department of Fish and Game, Anchorage, AK.

Seeb, L.W., P.A. Crane, C.M. Kondzela, R.L. Wilmot, S. Urawa, N.V. Varnavskaya, and J.E. Seeb. 2004. Migration of Pacific Rim chum salmon on the high seas: insights from genetic data. Environ. Biol. Fish. 69: 21–36.

Shaklee, J.B., F.W. Allendorf, D.C. Morizot, and G.S. Whitt. 1990. Gene nomenclature for protein-coding loci in fish. Trans. Am. Fish. Soc. 119: 2–15.

Urawa, S. 2000. Ocean migration route of Japanese chum salmon with a reference to future salmon research. National Salmon Resources Center Newsletter 5: 3–9. (In Japanese.)

Urawa, S., Y. Ishida, Y. Ueno, S. Takagi, G. Winans, and N. Davis. 1997. Genetic stock identification of chum salmon in the North Pacific Ocean and Bering Sea during the winter and summer of 1996. (NPAFC Doc. 259). 11p. National Salmon Resources Center, Fisheries Agency of Japan, Toyohira-ku, Sapporo 062-0922, Japan.

Urawa, S., Y. Ueno, Y. Ishida, S. Takagi, G. Winans, and N. Davis. 1998. Genetic stock identification of young chum salmon in the North Pacific Ocean and adjacent seas. (NPAFC Doc. 336). 9p. National Salmon Resources Center, Fisheries Agency of Japan, Toyohira-ku, Sapporo 062-0922, Japan.

Urawa, S., M. Kawana, G. Anma, Y. Kamei, T. Shoji, M. Fukuwaka, K. Munk, K.W. Myers, and E.V. Farley, Jr. 2000. Geographical origin of high-seas chum salmon determined by genetic and thermal otolith markers. N. Pac. Anadr. Fish Comm. Bull. 2: 283–290.

Wilmot, R.L., C.M. Kondzela, C.M. Guthrie, and M.S. Masuda. 1998. Genetic stock identification of chum salmon harvested incidentally in the 1994 and 1995 Bering Sea trawl fishery. N. Pac. Anadr. Fish Comm. Bull. 1: 285–299.

Winans, G.A., P.B. Aebersold, Y. Ishida, and S. Urawa. 1998. Genetic stock identification of chum salmon in highseas test fisheries in the western North Pacific Ocean and Bering Sea. N. Pac. Anadr. Fish Comm. Bull. 1: 220–226.