

## Stock Identification Studies of High Seas Salmon in Japan: A Review and Future Plan

Shigehiko Urawa

National Salmon Resources Center,  
2-2 Nakanoshima, Toyohira-ku, Sapporo 062-0922, Japan



Keywords: Genetic stock identification, chum salmon, Japan

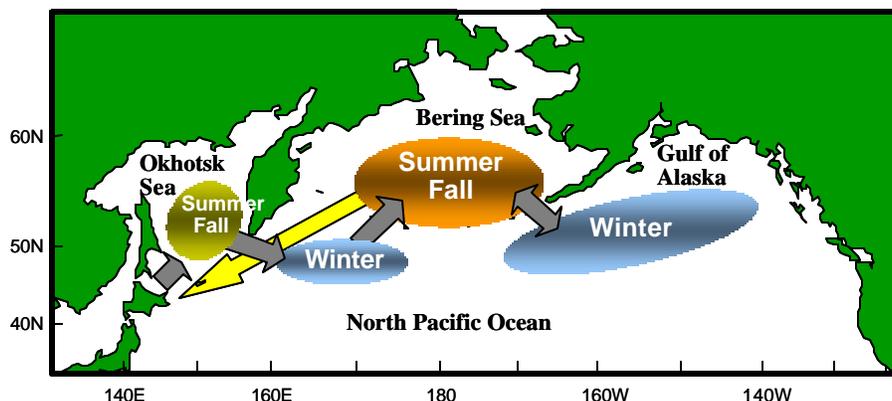
To manage salmon internationally, stock identification is indispensable to determine ocean distributions and abundance. In Japan, tag release, scale pattern, parasites, genetic variation, and otolith mark are mainly used to estimate the geographical origin of salmon in the ocean. In collaboration with the North Pacific Rim countries, intensive salmon tagging experiments have been conducted on the high seas since 1956. Recovery information indicated ocean migration routes of major stocks of maturing sockeye, chum, pink, and coho salmon (Ogura 1994). However, the tagging information was insufficient to clarify the distribution and abundance of major salmon stocks throughout the entire ocean life including juvenile and overwintering periods.

The migration route of Japanese chum salmon was estimated using recent information on fish abundance and genetic stock identification (GSI) of mixtures ( $n = 6,400$ ) sampled on the high seas in 1993–99 (Urawa 2000). A genetic baseline of 20 allozyme loci from major stocks throughout the North Pacific Rim was employed. The GSI results showed that Japanese chum salmon globally shift their marine distribution depending on the life stage and season (Fig. 1). Juveniles are distributed in the Okhotsk Sea during summer and fall, but are confined to a narrow band (SST 4–6°C) of the western North Pacific during the first winter. Young salmon enter the Bering Sea by the next summer. In the late fall, immature chum salmon move southeast to the Gulf of Alaska for the second wintering. They migrate between summer feeding grounds in the Bering Sea and winter habitat in the Gulf of Alaska until they return to spawn through the Bering Sea and western North Pacific.

Nucleotide sequence analyses suggested that variation in the mitochondrial (mt) DNA control region of chum salmon will be useful for future stock identification (Sato et al. 2001; Abe et al. 2002). An oligonucleotide microarray hybridization method has been developed for rapid and accurate detection of 30 haplotypes in the mt DNA control region (Moriya et al. in press). In addition to GSI, an otolith mark program started in 1998. Approximately 45 million chum salmon fry with thermal marks were released from five hatcheries in northern Japan in the spring of 2002, and 14 marked juveniles were captured in the Okhotsk Sea in the following fall (Urawa et al. 2004). The number of otolith mark releases will increase year by year, with over 100 millions in 2004. Thus otolith marking is expected to be a practical tool for various salmon studies in Japan.

Future Japanese research plans include the long-term monitoring of salmon stocks in the major feeding habitats (the Okhotsk Sea and Bering Sea) to estimate their distribution and abundance during summer and fall. The stock identification of mixture samples will be conducted by allozyme, mt DNA, and otolith mark analyses. These identification methods should contribute to sustainable salmon fishery management.

Fig. 1. A seasonal migration model of Japanese chum salmon estimated by genetic stock identification.



**REFERENCES**

- Abe, S., S. Sato, H. Kojima, J. Ando, H. Ando, R.L. Wilmot, L. W. Seeb, V. Efremov, L. LeClair, W. Buchholtz, D.-H. Jin, S. Urawa, M. Kaeriyama, and A. Urano. 2002. Development of molecular markers for genetic stock identification of chum salmon. *Fish. Sci.* 68 (Suppl): 353–356.
- Moriya, S., S. Urawa, O. Suzuki, A. Urano, and S. Abe. In press. DNA microarray for rapid detection of mitochondrial DNA haplotypes of chum salmon. *Marine Biotechnology*.
- Ogura, M. 1994. Migratory behavior of Pacific salmon (*Oncorhynchus* spp.) in the open sea. *Bull. Nat. Res.Inst. Far Seas Fish.* 31: 1–139. (In Japanese with English summary.)
- Sato, S., J. Ando, H. Ando, S. Urawa, A. Urano, and S. Abe. 2001. Genetic variation among Japanese populations of chum salmon inferred from the nucleotide sequences of the mitochondrial DNA control region. *Zool. Sci.* 18: 99–106.
- 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., J. Seki, M. Kawana, P.A. Crane, L. Seeb, and M. Fukuwaka. 2004. Juvenile chum salmon in the Okhotsk Sea: their origins estimated by genetic and otolith marks. *N. Pac. Anadr. Fish Comm. Tech. Rep.* 5: 87–88.