

Origins of Young Chum Salmon in the North Pacific Ocean during the Winter: Rapid Estimates by SNP Markers

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Information upon the marine distribution of chum salmon during the winter has been limited. In 1996 and 1998, Japanese scientists conducted winter salmon surveys and determined the stock origins of chum salmon caught in the North Pacific Ocean by allozyme analysis (Urawa and Ueno 1997, 1999; Urawa et al. 1997, 1998). In 2006 after a long gap, the research vessel *Kaiyo maru* winter cruise was conducted to examine the spatial distribution and biological status of salmon in the North Pacific Ocean (Fukuwaka et al. 2007).

DNA techniques provide significant advantage in sampling, sample handling, and the potential for improved resolution for stock identification of salmon. Of the various DNA markers, single nucleotide polymorphisms (SNPs) may be particularly appropriate for stock identification of chum salmon (Seeb et al. 2005). The objectives of the present study were to estimate the stock origins of chum salmon in the western North Pacific Ocean during the winter of 2006 using SNP and mitochondrial (mt) DNA microarray techniques, and to compare the accuracies of estimates by both methods.

We created a SNP baseline by 86 population samples collected throughout the range of chum salmon in Asia and North America. These populations represent most of the major lineages detected in the larger allozyme baseline used in previous NPAFC studies (Kondzela et al. 2002). Individuals were assayed for 30 nuclear SNPs and 6 mitochondrial SNPs using the 5' nuclease reaction previously reported by the US and Japan (Seeb et al. 2005; Smith et al. 2005).

One hour trawl operation was made in the surface layer (from the surface to about 50 m in depth) with 5 knots towing speed at 14 stations in the western North Pacific Ocean during January and February 2006 (Fig. 1). The pectoral fins were collected from young chum salmon (age 0.1; n = 174) and fixed in the 100% ethanol on the board. DNA was isolated from the fixed pectoral fins. The extracted DNA samples were assayed genetic variation for 36 SNPs and assigned to population of origin. For a comparison, we also analyzed the same samples using the mtDNA microarray technique (Moriya et al. 2004) and assigned them to population of origin using previously reported mtDNA baseline (Sato et al. 2004). We compared these results to allozyme-estimated stock compositions of young chum salmon caught in similar waters in 1996 and 1998 winters (Urawa and Ueno 1997, 1999).

Most young chum salmon were collected from a few stations along 165° E line in the western North Pacific Ocean (Fig. 1)(Fukuwaka et al. 2007). The stock composition of young chum salmon estimated by SNP analysis was 25.0% Japanese, 60.3% Russian, and 14.7% North American (mostly Alaskan) fish (Fig. 2). The mtDNA microarray analysis provided a similar estimate: 17.1% Japanese, 66.8% Russian, and 16.1% North American origins. The variation (90% confidence interval) of SNP estimate was low, compared with that of mtDNA estimate (Fig. 2). The

Fig. 1. CPUE distribution of young chum salmon (age 0.1) in the western North Pacific Ocean during the winter of 2006. CPUE means the number of catches per one hour trawl at 5 knots.

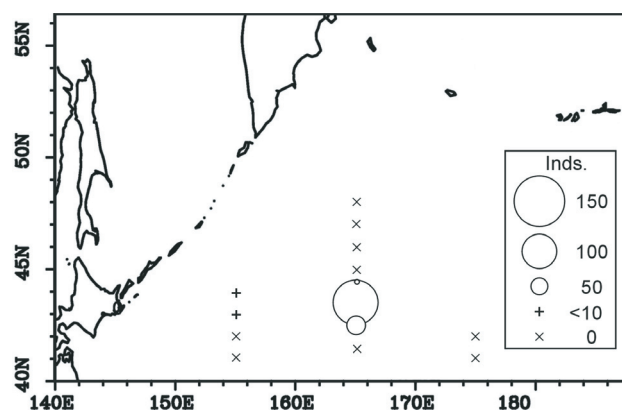


Fig. 2. Stock composition estimates of young chum salmon (age 0.1) caught in the western North Pacific Ocean during the winter of 2006 using SNP and mtDNA microarray techniques. Bars indicate 90% confidence of estimates.

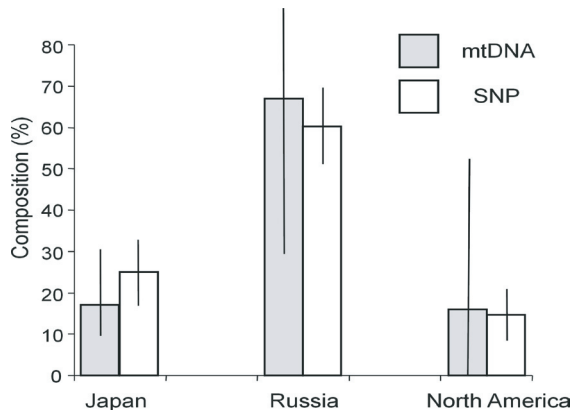
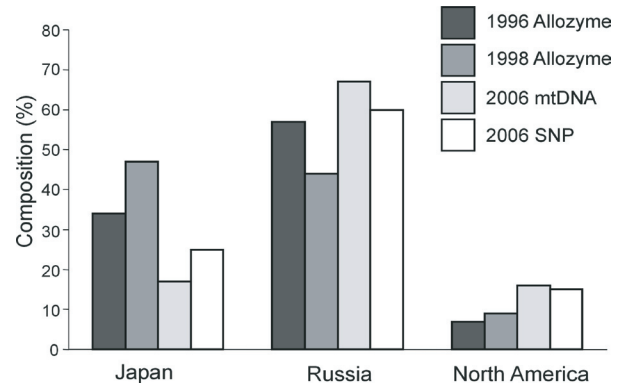


Fig. 3. A comparison of stock composition estimates of young chum salmon (age 0.1) caught in the western North Pacific Ocean during the winter of 1996, 1998, and 2006. The allozyme estimates in January 1996 and February 1998 were cited from Urawa and Ueno (1997, 1999).



SNP analysis used 30 nuclear loci and one mtDNA combined haplotype, while the mtDNA analysis used only one combined haplotype. It might be a reason for differences in variation of estimates by both methods. The stock composition estimates in 2006 winter were slightly different from those in January 1996 and February 1998: the proportion of Japanese stock was higher in 1996 and 1998 than 2006 (Fig. 3). It was impossible to estimate stock-specific biomass of chum salmon in the western North Pacific Ocean, because the survey area was limited by severe weather condition during the winter.

REFERENCES

- Fukuwaka, M., S. Sato, S. Takahashi, T. Onuma, O. Sakai, N. Tanimata, K. Makino, N. Davis, A. Volkov, K.B. Seong, and J. Moss. 2007. Distribution of chum salmon during the first winter of ocean life in the western North Pacific. *N. Pac. Anadr. Fish Comm. Tech. Rep.* 7: 29–30.
- Kondzela, C.M., P.A. Crane, S. Urawa, J.B. Burger, N.V. Varnavskaya, V.V. Efremov, X. Luan, W.B. Templin, K. Hayashizaki, R.L. Wilmot, and L.W. Seeb. 2002. Development of a comprehensive allozyme baseline for Pacific Rim chum salmon. *NPAFC Doc.* 629. 23 pp. (Available at <http://www.npafc.org>).
- Moriya, S., S. Urawa, O. Suzuki, A. Urano, and S. Abe. 2004. DNA microarray for rapid detection of mitochondrial DNA haplotypes of chum salmon. *Mar. Biotechnol.* 6: 430–434.
- Sato, S., H. Kojima, J. Ando, H. Ando, R.L. Wilmot, L.W. Seeb, V. Efremov, L. LeClair, W. Buchholz, D.-H. Jin, S. Urawa, M. Kaeriyama, A. Urano, and S. Abe. 2004. Genetic population structure of chum salmon in the Pacific Rim inferred from mitochondrial DNA sequence variation. *Environ. Biol. Fish.* 69: 37–50.
- Seeb, L.W., W.D. Templin, C.T. Smith, C. Elfstrom, S. Urawa, R.L. Wilmot, S. Abe, and J.E. Seeb. 2005. SNPs provide an easily-standardized baseline for NPAFC studies of chum salmon. *NPAFC Doc.* 907. 12 pp. (Available at <http://www.npafc.org>).
- Smith, C.T., J. Baker, L. Park, L.W. Seeb, C. Elfstrom, S. Abe, and J.E. Seeb. 2005. Characterization of 13 single nucleotide polymorphism markers for chum salmon. *Mol. Ecol. Notes* 5: 259–262.
- Urawa, S., and Y. Ueno. 1997. Genetic stock identification of chum salmon (*Oncorhynchus keta*) in the North Pacific Ocean in the winter 1996. *Salmon Rep. Ser.* 43: 97–104. (Available from the National Salmon Resources Center, Toyohira-ku, Sapporo 062-0922, Japan).
- Urawa, S., and Y. Ueno. 1999. The geographical origin of chum salmon (*Oncorhynchus keta*) caught in the western and central North Pacific Ocean in the winter of 1998. *Salmon Rep. Ser.* 48: 52–58. (Available from the National Salmon Resources Center, Toyohira-ku, Sapporo 062-0922, Japan).
- 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. 11 pp. (Available at <http://www.npafc.org>).
- 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. 9 pp. (Available at <http://www.npafc.org>).