

Migration Patterns of Sockeye Salmon in the Bering Sea Discerned from Stock Composition Estimates of Fish Captured during BASIS Studies

Christopher Habicht¹, Natalia V. Varnavskaya², Tomonori Azumaya³, Shigehiko Urawa⁴,
Richard L. Wilmot⁵, Charles M. Guthrie III⁵, and James E. Seeb¹

¹Gene Conservation Laboratory, Commercial Fisheries Division, Alaska Department of Fish and Game,
333 Raspberry Road, Anchorage, Alaska 99418, U.S.A.

²Kamchatka Research Institute of Fisheries and Oceanography (KamchatNIRO),
18, Naberezhnaya Street, Petropavlovsk-Kamchatsky 683602, Russia

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

⁴National Salmon Resources Center, 2-2 Nakanoshima, Toyohira-ku, Sapporo 062-0922, Japan

⁵U.S. Department of Commerce, NOAA, NMFS, Alaska Fisheries Science Center, Auke Bay Laboratory,
11305 Glacier Highway, Juneau, Alaska 99801, USA



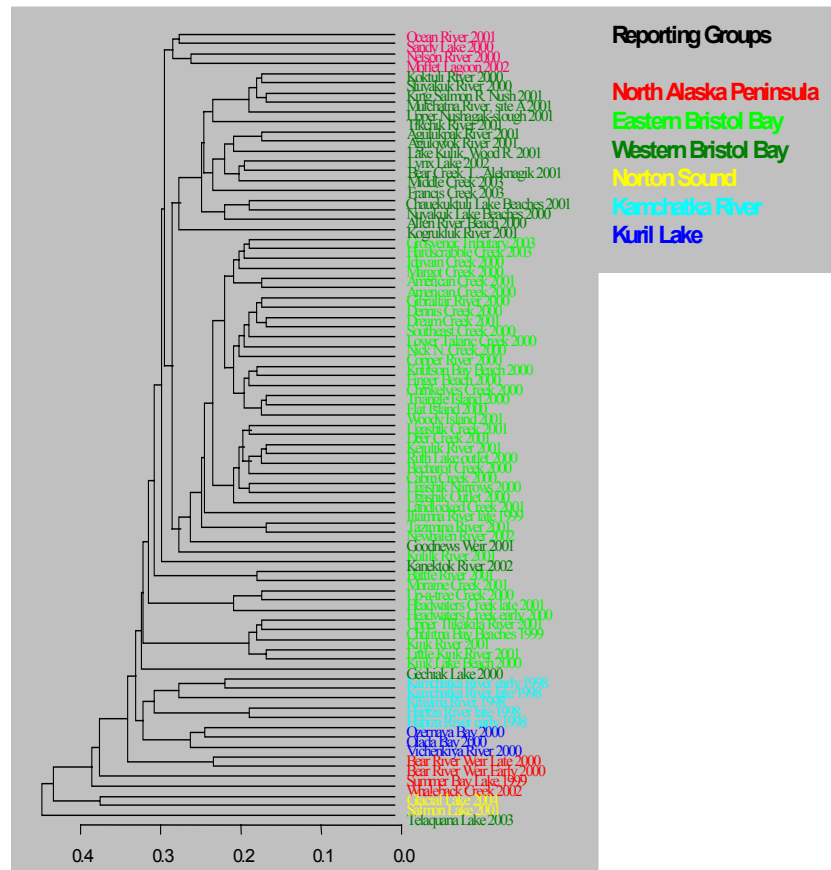
Keywords: Sockeye, salmon, Bering Sea, microsatellite, single nucleotide polymorphism, migration, genetic stock identification, BASIS

The Bering Sea provides major feeding habitats for sockeye salmon stocks originating from Asia and North America. Little is known about the migratory patterns of specific stocks throughout the Bering Sea. A better understanding of these patterns may clarify the mechanisms of salmon population response to recent environmental changes.

We developed a DNA baseline for 13 microsatellite and two single nucleotide polymorphism (SNP) markers from collections of approximately 96 sockeye salmon each from 80 spawning locations draining into the Bering Sea and southeastern Sea of Okhotsk. Data from the same set of markers was collected from 2,300 sockeye salmon captured by the RV *TINRO*, RV *Kaiyo maru*, FV *Great Pacific* and FV *Sea Storm* during the summers of 2002 and 2003. Allocation of these mixture samples to stock of origin enabled a better understanding of the relative distribution of Alaskan and Russian stocks during these months.

The DNA baseline provided the power to resolve 15 reporting groups and was particularly powerful at distinguishing among populations from six reporting groups: Kuril Lake, Kamchatka River, North Alaska

Fig. 1. UPGMA tree using Cavalli-Sforza and Edward distances based on 13 microsatellites and 2 SNPs for collections of sockeye salmon spawning in tributaries to the Bering Sea. Baseline stocks were pooled into six reporting groups and are symbolized with colored letters.



Peninsula, eastern Bristol Bay, western Bristol Bay and Norton Sound (Fig. 1). Mixture samples were grouped by geographic location (using features of the ocean floor including: the northeastern continental shelf, the Bowers Ridge north of the Aleutian Islands and the Shirshov Ridge in the west; Fig. 2), seasonal timing (August, September and October) and age (one ocean and two-plus ocean) and subjected to mixed-stock analyses.

The most comprehensive data available throughout the Bering Sea were for August. Stock distributions in August show the highest proportions of western-originating stocks on the western side of the Bering Sea and the highest proportions of eastern-originating stocks on the eastern side (Fig. 3). When all samples are taken in combination, the eastern Bristol Bay stock is the most abundant reporting group. The next most common reporting group is composed of western Bristol Bay stocks. These results are consistent with expectations based on the proportions of sockeye salmon produced within the five regions (Bugaev 2004; Alaska Department of Fish and Game unpublished data). Although Russian sockeye salmon stocks contribute less than half of the stock mixtures in every sample except the most southwesterly sample, their presence in samples from the central Bering Sea basin and Aleutian Islands indicates that they migrate eastward at least half way across the Bering Sea. Alaskan sockeye appear to migrate throughout the Bering Sea and make up, almost exclusively, the stock proportions on the northeastern Continental Shelf including the western side near Russia.

Stock distributions divided into ages one and two-plus ocean fish showed generally higher proportions of Russian stocks in the two-plus ocean mixtures than in the one ocean mixtures (Figs. 4 and 5). This pattern may indicate that larger proportions of two-plus ocean fish from Alaska migrate south into the North Pacific relative to stocks originating from Russia or that Russian one ocean fish are in the North Pacific and migrate north as two-plus ocean age. Of the immature fish captured on the northeastern continental shelf, 89% were one ocean fish, so stock compositions could only be calculated on this age group (these were again almost exclusively Alaska-origin stocks). This pattern may indicate that one ocean fish favor different environmental variables than two-plus ocean fish and that Russian one ocean fish generally do not utilize the northeastern continental shelf.

Fig. 2. Geographic features of the ocean floor in the Bering Sea used to divide samples of immature sockeye salmon captured during the BASIS cruises in 2002 and 2003 for mixed-stock analysis using genetic markers.



Fig. 3. Stock proportions of immature sockeye salmon sampled from throughout the Bering Sea during August of 2002 and 2003. Baseline stocks were pooled into six reporting groups and are symbolized with colored ovals. Pale ovals under the pies represent the general area where stock mixtures were captured and pie colors correspond to reporting group colors.

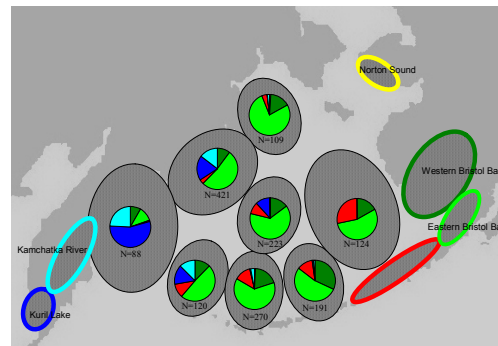


Fig. 4. Stock proportions of 1-ocean immature sockeye salmon sampled from throughout the Bering Sea during August, September and October of 2002 and 2003. "NS" indicates insufficient samples to estimate mixture composition.

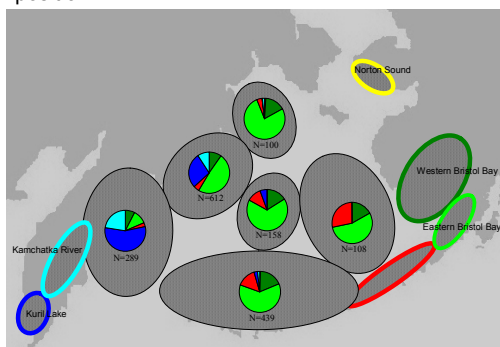
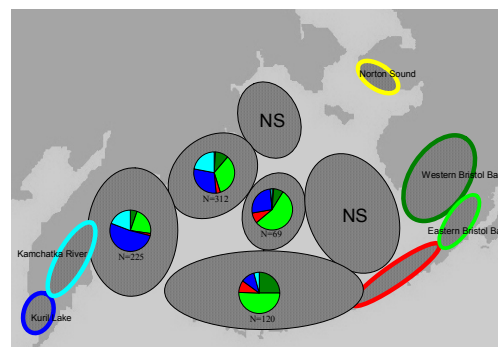


Fig. 5. Stock proportions of two-plus ocean immature sockeye salmon sampled from throughout the Bering Sea during August of 2002 and 2003. "NS" indicates insufficient samples to estimate mixture composition.



Stock distributions over time within locations off the Russian coast showed fairly stable compositions from August through October (Fig. 6). These data only represent $\frac{1}{4}$ of the year, and stock distributions may vary substantially within location over time if more samples were taken throughout the year. The consistent stock distribution over time does not necessarily indicate a lack of migration because co-migrating stocks might have little effect on stock distributions. Adding abundance information to the stock composition information could provide additional insight into migration patterns.

This project relied on the cooperation of BASIS partners from the United States, Russia and Japan to collect and share tissue samples for genetic analysis and specifically we would like to acknowledge the contributions from: T. Walker, K. Meyers, E. Farley, J. Murphy, L. Low, O. Temnykh, V. Sviridov, N. Klovatch, I. Glebov, N. Starovoytov, S. Urawa, and S. Abe. Genetic analysis was funded in part by the North Pacific Research Board grants R0205 and R0303.

REFERENCES

- Bugaev, A.V. 2004. Scale pattern analysis estimates of the age and stock composition of sockeye salmon *Oncorhynchus nerka* in R/V *TINRO* trawl catches in the western Bering Sea and northwest Pacific Ocean in September–October 2002 (NPAFC Doc. 763). 25p. KamchatNIRO, Kamchatka Fisheries and Oceanography Inst., Fisheries State Commit. of Russia, Naberezhnaya Street 18, Petropavlovsk-Kamchatski, Russia.

Fig. 6. Stock proportions of immature sockeye salmon sampled from western Bering Sea during August, September, and October of 2002 and 2003.

