

Microsatellite Identification of Sockeye Salmon Rearing in the Bering Sea 2011

by

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submitted to the

North Pacific Anadromous Fish Commission

by

Canada

October 2012

THIS PAPER MAY BE CITED IN THE FOLLOWING MANNER:

Beacham, T. D, J.C. Candy, S. Sato, and S. Urawa. 2012. Microsatellite identification of sockeye salmon rearing in the Bering Sea 2011. NPAFC Doc. 1389. 9 pp. Fisheries and Oceans Canada, Nanaimo, BC. (Available at <http://www.npafc.org>).

Abstract

Stock composition of sockeye salmon (*Oncorhynchus nerka*) caught in the southern central Bering Sea during a Japanese research cruise in the summer of 2011 was estimated through an analysis of microsatellite variation. Variation at 14 microsatellites was analyzed for 177 immature sockeye salmon, and a 387-population baseline spanning Japan, Russia, Alaska, Canada, and Washington State was used to determine the stock composition of the fish sampled. Alaskan-origin sockeye salmon were the most abundant in the catch, comprising 86.1% of all sockeye salmon caught (United States total 86.7%), with the catch dominated by sockeye salmon of Bristol Bay origin. Russian-origin salmon accounted for 12.1% of the catch, while Canadian-origin sockeye salmon accounted for 1.2% of the catch.

Introduction

The application of DNA-based genetic markers to salmon stock identification studies has provided greater resolution of stock composition relative to other biological markers (Beacham et al. 2005) such as scale pattern analysis (Ishida 1989), parasites (Bennett et al. 1998), and otolith characters (Sohn et al. 2005). High resolution stock composition of sockeye salmon mixed-stock samples to lake or river of origin is crucial to our understanding of their population-specific responses to recent climatic regime shifts in the north Pacific Ocean (Welch et al. 2000; Mueter et al. 2002). DNA markers provide a natural tag with which the origin of all individual fish within a sample can be determined if required (Beacham et al. 2005). This is in marked contrast to physical tags, where recovery rate of individually marked juvenile salmon fish is typically well under 1% (Hartt and Dell 1986; Trudel et al. 2009). By employing DNA-based genetic markers for stock identification, larger scale sampling of juvenile salmon in the ocean can be undertaken in order to determine migration routes and areas of marine residence.

The initial application of DNA-based genetic markers to estimation of sockeye salmon stock composition in the Bering Sea was reported by Habicht et al. (2010). By applying a set of 45 single nucleotide polymorphisms (SNPs) to identify population structure in a Pacific Rim distribution of populations, Habicht et al. (2010) defined eight regional stocks of sockeye salmon in the baseline, with a single eastern Gulf of Alaska (EGOA) stock comprised of sockeye salmon from southeast Alaska, British Columbia, and Washington. This EGOA stock, which comprised a mixture of Canadian and American populations, was reported to comprise up to 10% of immature sockeye salmon sampled in the south central Bering Sea during September of 2002 and 2003. Beacham et al. (2011) reported that stock composition of juvenile sockeye salmon captured between 15 July to 9 August 2009 during a research cruise conducted with the Japanese research vessel *Hokko-maru* in the central and northern Bering Sea was 86% Alaskan origin, 10% Russian origin, and 4% Canadian origin. In the current study, we evaluate the stock composition of immature sockeye salmon caught during a Japanese research cruise in the south central Bering Sea in 2011.

Methods and Materials

Sample collection and analysis

Juvenile sockeye salmon were captured between 26 July to 3 August 2011 during a research cruise conducted with the Japanese research vessel *Hokko-maru* in the central and southern Bering Sea. The cruise was designed to conduct the annual survey of Japanese stocks of chum salmon (*O. keta*) in the southern Bering Sea, with cruise track and details of the cruise outlined by Morita et al. (2011). Details of the trawl nets and sampling regime were also outlined by Morita et al. (2011). Juvenile sockeye salmon captured were weighed to the nearest 10 g, fork length measured (nearest mm), a tissue sample collected for subsequent analysis of genetic variation. Fish age was determined from scales by staff of the Hokkaido National Fisheries Research Institute, Fisheries Research Agency, Japan. Age reporting followed the method outlined by Koo (1962). An individual designated as x.1 spent 1-3 winters rearing in fresh water (x years), and one winter in the ocean, having been sampled during the summer in their second ocean year. Similarly, individuals identified as x.2 reared for two winters in the ocean, with subsequent capture and sampling during their third summer of ocean rearing. Individuals identified as x.3 were in their fourth summer of ocean rearing. Tissue samples were preserved in 95% ethanol, and sent to the Molecular Genetics Laboratory at the Pacific Biological Station of Fisheries and Oceans Canada in Nanaimo. Fourteen microsatellites (Beacham et al. 2005) were surveyed with an ABI 3730 capillary DNA sequencer, and genotypes were scored by GeneMapper software 3.0 (Applied Biosystems, Foster City, CA) using an internal lane sizing standard as outlined by Beacham et al. (2005).

Baseline populations

The baseline used for estimation of stock composition consisted of a survey of about 67,000 sockeye salmon from 387 populations from Japan, Russia, Alaska, Canada, and Washington as outlined by Beacham et al. (2011). Baseline populations were organized into 46 reporting groups as outlined by Beacham et al. (2011).

Estimation of stock composition in mixed-stock samples

Stock compositions of mixture samples were estimated with the genetic stock identification software ONCOR (Kalinowski et al. 2007) that incorporated the likelihood model of Rannala and Mountain (1997). Allocations were made to 387 individual populations, and these were summed to provide estimates to 46 regional stock groups. Regional stock groups were not listed in Table 1 if estimated stock composition of the reporting group was zero. Precision of the stock composition estimates were calculated through 100 bootstrap simulations of both the baseline and mixture data.

Results

Location, size, and age of catch

The 177 sockeye salmon analyzed were captured between 52°59' N and 58°31' N and 174°51' E and 174°55' W in the central Bering Sea, with 60 fish caught at 56°N and 175°W (Figure 1). Ocean age x.1 individuals were well separated from ocean age x.2 and x.3 individuals in fork length, with a bimodal distribution observed in observed fork length (Figure 2). Age x.1 individuals were typically less than 400 mm, with a mean fork length of 349 mm and standard deviation of 24 mm. Mean length of age x.2 individuals

was 468 mm (SD=27 mm), and that of x.3 individuals was 540 mm (SD=53 mm). Body weight distributions were similarly well defined between age x.1 and x.2 individuals, with x.1 individuals typically less than 800 g in weight, reflective of the bimodal distribution of body weight (Figure 3). Mean weight of age x.1 individuals was 510 g (SD=114 g), that of age x.2 individuals was 1270 g (SD=230 g), and that of age x.3 individuals was 2060 g (SD=730 g).

Stock composition of Bering Sea samples

Alaskan-origin sockeye salmon were the most abundant in the catch of 177 immature individuals in the central Bering Sea, comprising 86.1% of all sockeye salmon caught. Russian-origin salmon accounted for 12.1% of the catch, while Canadian-origin sockeye salmon accounted for 1.2% of the catch. Sockeye salmon from Bristol Bay dominated the catch of Alaskan-origin salmon, with those from the Naknek River drainage the largest contributor to the catch, with 23.5% of individuals estimated to be of Naknek River origin (Table 1). Age composition of the Naknek River immature sockeye salmon was 25.0% age 1.1, 38.6% age 1.2, 27.3% age 2.1, and 9.1% age 2.2. Sockeye salmon from the Kvichak River drainage were estimated to be the next most important contributor to the catch, comprising 13.7% of the salmon sampled. Sockeye salmon from the Nushagak River drainage were estimated to comprise 10.4% of the sample. Sockeye salmon from the Ugashik River drainage and Wood River drainage were also identified as important contributors to the catch. One age 1.2 individual was estimated to have originated from Lake Washington in Washington State.

Russian-origin sockeye salmon caught in the central Bering Sea in 2011 were estimated to originate primarily from Kuril Lake (5.3%), Karaginsky Bay (2.2%), and Kamchatka River (2.0%) (Table 1). Age composition of the Kuril Lake individuals was primarily age 1.2, with one individual estimated as age 1.1 and one individual as age 2.2.

Canadian-origin salmon were estimated to originate from the Skeena River (0.6%, one age 1.1 individual) and the Stikine River (0.6%, one age 1.1 individual) (Table 1).

Discussion

Bering Sea analysis

Size distributions of the immature sockeye salmon sampled during the research cruise in 2011 were quite similar to those sampled in 2009. For example, the mean fork length of ocean age x.1 individuals was 349 mm in 2011 and 348 mm in 2009. Mean fork length of ocean age x.2 individuals was 468 mm in 2011 and 476 mm in 2009 (Beacham et al. 2011). Mean weight of ocean age x.1 individuals was 510 g in 2011 and 490 g in 2009, while that of the x.2 individuals was 1,270 g in 2011 and 1,300 g in 2009 (Beacham et al. 2011).

Analysis of stock composition indicated that the catch was dominated by stocks of Bristol Bay origin, similar to results of tagging experiments (Myers et al. 1996), scale pattern analysis (Bugaev and Myers 2009), and previous analyses of genetic stock composition (Habicht et al. 2010; Beacham et al. 2011). Juvenile sockeye salmon catches in the eastern Bering Sea were also reported to be dominated by salmon of Bristol Bay origin (Seeb et al. 2011). Based upon geography and relative abundance, sockeye salmon of Bristol Bay origin should be expected to dominate catches of immature sockeye salmon rearing in the Bering Sea, with sockeye salmon originating from Russia the next

most abundant stock. These were precisely the results observed from our analysis of immature sockeye salmon rearing in the central Bering Sea in July and August of 2011. Our analysis, along with the results of Habicht et al. (2010) and Beacham et al. (2011), indicated that some small portion of Canadian sockeye salmon rear in the Bering Sea during summer, with perhaps some trace contribution by sockeye salmon from Washington State. Recent genetic and otolith mark analyses indicated that Canadian chum salmon (*O. keta*) were also distributed in the Bering Sea (Urawa et al. 2009). As outlined by Habicht et al. (2010), it is uncertain whether rearing of Canadian-origin salmon in the Bering Sea is something new, perhaps brought on by changes in climate, or is in fact typical of a normal rearing pattern of summer movement in the Bering Sea and winter rearing in the Gulf of Alaska.

Improved information of location and timing of specific stocks of sockeye salmon in the Bering Sea and North Pacific Ocean can be obtained through the application of DNA technology to salmon stock identification problems. The major limitation at the present time to refine knowledge on stock-specific areas of ocean residence and timing of migration movement is the difficulty and cost associated with obtaining the appropriate samples from ocean rearing areas and migration routes.

Acknowledgments

We thank the captain and crew of the R/V *Hokko-maru* for sample collection in the Bering Sea. Brenda McIntosh conducted the laboratory analysis of microsatellite variation for the sockeye salmon sampled from the Bering Sea. Funding for the study was provided by Fisheries and Oceans Canada.

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Table 1. Estimated stock compositions (% , 95% confidence limits in parentheses) of mixed-stock samples of sockeye salmon (N=177) from the central Bering Sea, 2011. Estimated stock compositions were derived from applying a 387-population baseline for each sample, with a Pacific Rim distribution of the baseline ranging from Japan, Russia, Alaska, British Columbia, and Washington State as outlined by Beacham et al. (2011). Reporting regions with no estimated stock composition (27 of 46 reporting regions) are not listed.

Major region		Estimate	95% CI
Washington State	Washington	0.6	(0.0, 1.7)
British Columbia	Skeena River	0.6	(0.0, 2.2)
	Stikine River	0.6	(0.0, 3.2)
Southeast Alaska	SE Alaska	1.8	(0.0, 3.9)
Central Alaska	Cook Inlet	3.5	(1.1, 7.9)
	Kodiak Island	3.7	(0.0, 5.6)
Bristol Bay	Ugashik River	8.9	(0.0, 11.3)
	Egegik River	4.1	(1.1, 15.9)
	Naknek River	23.5	(10.0, 26.5)
	Alagnak River	7.3	(3.3, 12.0)
	Kvichak River	13.7	(5.0, 22.9)
	Nushagak River	10.4	(2.8, 14.7)
	Wood River	6.3	(2.6, 12.8)
	Igushik River	2.9	(0.0, 6.9)
Russia	Chukotka	1.3	(0.0, 4.3)
	Karaginsky Bay	2.2	(0.0, 6.8)
	Kamchatka River	2.0	(0.0, 3.0)
	Kuril Lake	5.3	(1.0, 8.2)
	Bolshaya River	1.3	(0.0, 4.7)

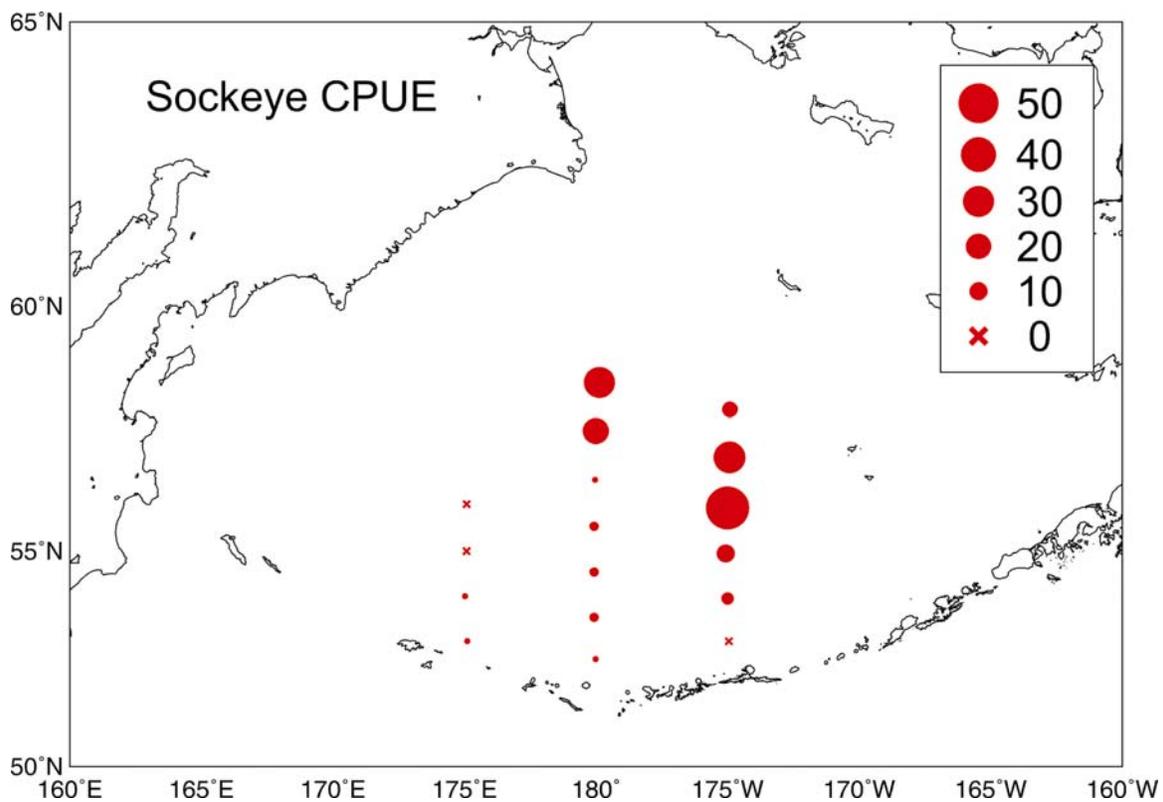


Figure 1. Catch locations of immature sockeye salmon during the 2011 research cruise of the *Hokko-maru* in the central Bering Sea, with catch abundance outlined by size of the symbol.

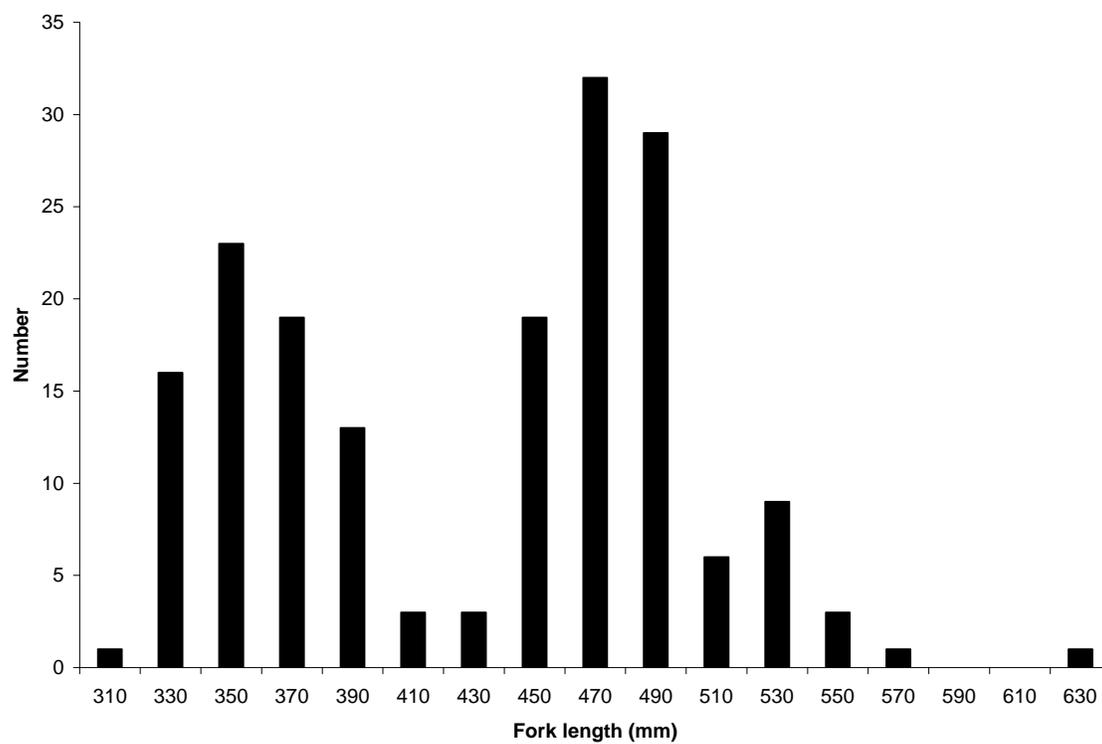


Figure 2. Frequency histogram based upon fork length of immature sockeye salmon caught during the 2011 research cruise of the *Hokko-maru* in the central Bering Sea.

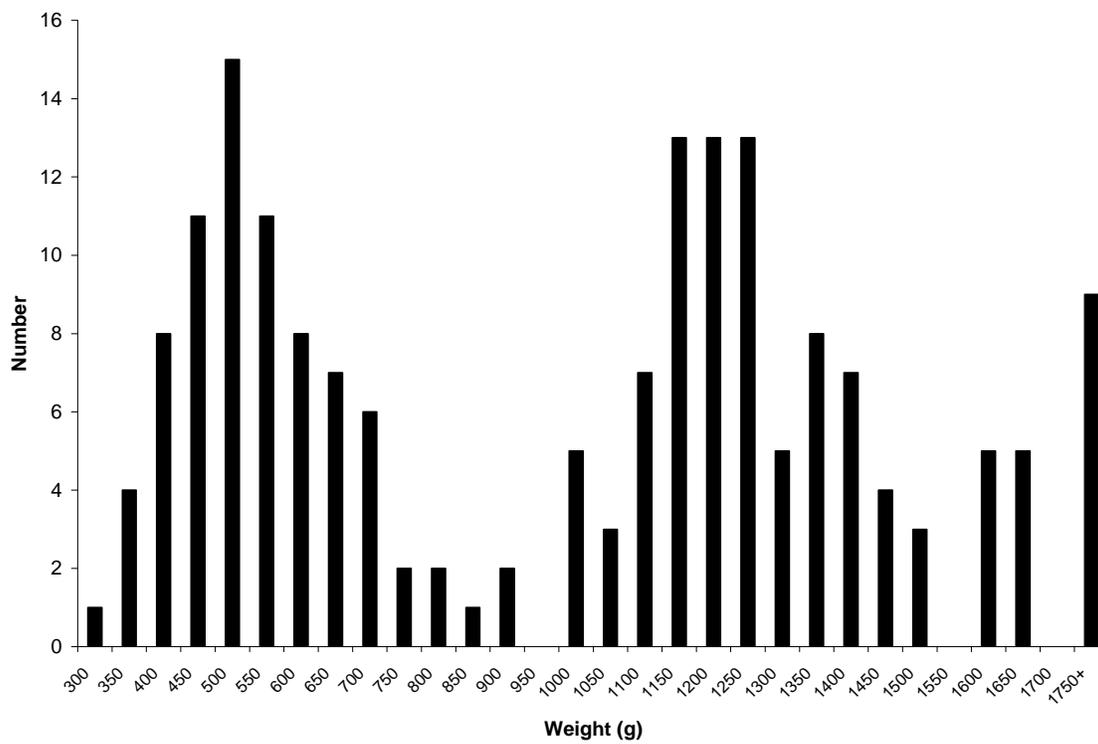


Figure 3. Frequency histogram based upon weight (grams) of immature sockeye salmon caught during the 2011 research cruise of the *Hokko-maru* in the central Bering Sea.