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Salmon International Survey**

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Abstract

Habitat-specific patterns in the genetic stock composition of chum salmon (*Oncorhynchus keta*) provide insight into migratory behavior in the eastern Bering Sea. Based upon 11 microsatellites assayed on 1625 samples collected from Bering-Aleutian International Salmon Surveys during summer and fall of 2006 and 2007, substantial differences were found in the origin of chum salmon from different ocean habitats in the northern and eastern Bering Sea. Overall, Asian stocks were dominant and stock composition was not different between collection years for continental slope and northern continental shelf habitats, but the southern continental shelf collections in the eastern Bering Sea were different between years and were dominated by North American stocks. This supports previous studies and provides evidence that stock composition of chum salmon is both nonrandom in some areas and dynamic in others.

Introduction

Chum salmon (*Oncorhynchus keta*) are the most widely distributed Pacific salmon and are an important resource to the peoples of Asia and North America. An understanding of the stock-specific ocean distribution patterns of chum salmon is critical to fisheries management and conservation. Several studies that have used various types of genetic markers and baselines have shown that adult chum salmon are distributed non-randomly in the Bering Sea, with Russian stocks predominant in the western Bering Sea, Japanese stocks widely distributed throughout the northern and central Bering Sea, and North American stocks occupying the eastern Bering Sea (Moriya et al. 2007; Moriya et al. 2009; Sato et al. 2004; Sato et al. 2008; Urawa et al. 1997; Urawa et al. 2005; Urawa et al. 2009; Yoon et al. 2009). Studies have also shown that chum salmon stock composition is dynamic on the continental shelf habitat of the Southeastern Bering Sea (Wilmot et al. 1998; Seeb et al. 2004), although it is important to recognize that some samples for those studies were obtained from the incidental bycatch of the U.S. Bering Sea groundfish trawl fishery. Understanding whether the stock composition of chum salmon in the Bering Sea is nonrandom or dynamic is essential to fisheries management and conservation due to growing concerns of the incidental bycatch taken in the U.S. groundfish trawl fishery. Our study extends the previous research to describe the stock composition of chum salmon collected from the U.S. Bering-Aleutian Salmon International Survey (BASIS) during summer and fall of 2006 and 2007 (Figure 1, 2).

Materials and methods

Fish samples

One thousand and seventy-five chum salmon were collected in the Bering Sea aboard the fishing vessel (F/V) *Sea Storm* and F/V *Northwest Explorer* from 16-August to 14-September 2006 (Figure 1; NPAFC Doc. 941). Five hundred and fifty BASIS chum salmon samples were collected aboard the F/V *Sea Storm* and the NOAA ship *Oscar Dyson* from 15-August to 8-

October 2007 (Figure 2; NPAFC Doc. 1024). Chum salmon were measured and tissue was excised and stored in 95% ethanol. Genomic DNA was extracted with a Qiagen[®] DNeasy 96 Blood & Tissue Kit¹ (Germantown, Maryland, USA) by following the manufacturer's instructions.

Microsatellite analysis

Genetic variation was assayed at 11 microsatellite markers (Oki100, Omm1070, Omy1011, One101, One102, One104, One114, Ots103, Ots3, Ots68, and Ssa419) as employed previously (Beacham et al. 2009a) by using a Qiagen[®] Multiplex PCR Kit and following the manufacturer's protocols. PCR was performed on a GeneAmp[®] PCR System 9700 (Applied Biosystems, Foster City, California, USA) and loci were separated by fluorescent dyes and sizes on an ABI 3130xl Genetic Analyzer. Multilocus genotypes were scored and independently verified using GeneMapper[®] software (Applied Biosystems).

Baseline population allele frequencies were downloaded from the Fisheries and Oceans Canada web page (<http://www.pac.dfo-mpo.gc.ca/science/facilities-installations/pbs-sbp/mgl-lgm/data-donnees/index-eng.htm>). The 381 baseline populations (Beacham et al. 2009b) were conservatively clustered into six groups based upon geography, genetic similarity, and 100% simulation studies conducted with the computer program SPAM 3.7 (Alaska Department of Fish and Game 2003). Stocks from Japan, South Korea, China, and the Primorye region of Russia formed the East Asia group ($n=31$), Chinese and Russian stocks comprised the North Asia group ($n=31$), Alaskan stocks were partitioned into the Western Alaska ($n=37$), Southwest Alaska ($n=17$), and Upper/Middle Yukon ($n=23$; including Yukon Territory, Canada) groups, and stocks from Southeast Alaska, British Columbia and Washington formed the Pacific Northwest group ($n=242$) See Gray et al. (2010) for further details.

The number of samples collected at individual stations ranged from $n=1$ to $n=55$ and were not sufficient for mixture analysis, so samples from stations were pooled to describe the stock composition of chum salmon occupying different ocean habitats in the eastern and northern Bering Sea (Figure 1, Figure 2). All stations north of 60° N latitude formed the north shelf group, samples collected from the continental shelf south of 60° N latitude formed the south shelf group, and stations along the continental slope formed the slope group. Stock compositions of the mixtures were estimated with the computer program BAYES (Pella and Masuda 2001) by using six independent chains for each mixture and 5,000 iterations each of burn-in and MCMC length. MCMC simulations were started with 95% allocation to a single region and the remaining 5% was divided equally among the five other regions. Convergence of the independent chains to a single posterior distribution was assessed using Gelman and Rubin (1992) shrink factors.

Results

Sample quality

Of the 1625 chum salmon analyzed, 176 individuals were missing a single genotype, 43 fish were missing two genotypes, and three genotypes were missing from 108 individuals. Approximately 3% of the microsatellite genotypes were missing from the final dataset due to PCR failure and removal of ambiguous alleles. Missing data was not symptomatic of particular loci, collections, or mixture groups.

¹REFERENCE TO TRADE NAMES DOES NOT IMPLY ENDORSEMENT BY THE NATIONAL MARINE FISHERIES SERVICE, NOAA.

Genetic stock identification with microsatellites

Average baseline reassignment accuracy for the six groups as estimated by the maximum likelihood method in SPAM 3.7 was 91%, with 89% of East Asia, 85% of North Asia, 96% of Western Alaska, 93% of Upper/Middle Yukon, 82% of Southwest Alaska, and 98% of Pacific Northwest simulated mixtures correctly reallocating back to their respective groups.

Overall, Asian stocks were dominant in the 2006 and 2007 BASIS collections, with 17-59% of the mixtures estimated as originating from East Asia and 24-46% from North Asia (Table 1). Each North American regional stock contributed relatively less to the mixtures, with 2-15% originating from Western Alaska, 1-9% from Upper/Middle Yukon, 0-13% from Southwest Alaska, and 6-33% from Pacific Northwest (Table 1). Gelman and Rubin (1992) shrink factors were all less than 1.2 which indicated strong convergence to a single posterior distribution for each Bayesian estimate of stock composition.

Discussion

It is remarkable that the stock compositions from 2006 and 2007 were not significantly different for each of the north shelf and slope habitats, and provides evidence that the habitat-specific distribution of chum salmon in the Bering Sea is nonrandom (Figures 3, 5). In contrast, the marked differences between the 2006 and 2007 mixtures from the south shelf habitat suggest inter-annual variability in stock composition (Figure 4). As previously reported by others (Wilmot et al. 1998; Seeb et al. 2004), the southern shelf habitat also appears to support the highest proportion of North American stocks, with 46% of the estimated mixture originating from North America in 2006, and 56% in 2007. Of special concern is the presence of Western Alaska and Upper/Middle Yukon stocks in these mixtures (11-24%) because salmon in that region have experienced declines in recent years which have led to disaster declarations by state and federal management agencies. Furthermore, the variability exhibited in the chum salmon stock composition of the southern shelf habitat raises conservation and management concerns because this is the area where a portion of the incidental take of chum salmon occurs in the Bering Sea trawl fishery (Stram and Ianelli 2009). Continued work that addresses the inter-annual variability in stock composition of the south shelf habitat is essential to effective management and conservation of this important resource.

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Table 1. Sample sizes, average fork lengths in millimeters, and regional stock compositions of chum salmon collected during the 2006 and 2007 U.S. Bering-Aleutian Salmon International Survey. Standard deviations of estimates are given in parentheses.

Mixture	<i>n</i>	Fork Length	East Asia	North Asia	Western Alaska	Upper/Mid Yukon	Southwest Alaska	Pacific Northwest
2006								
North Shelf	191	576 (59.0)	0.59 (0.04)	0.25 (0.04)	0.05 (0.02)	0.04 (0.02)	0.00 (0.00)	0.07 (0.02)
South Shelf	459	550 (79.7)	0.30 (0.02)	0.24 (0.02)	0.07 (0.02)	0.04 (0.01)	0.02 (0.01)	0.33 (0.02)
Slope	425	473 (70.0)	0.44 (0.03)	0.41 (0.03)	0.02 (0.01)	0.01 (0.01)	0.01 (0.01)	0.11 (0.02)
2007								
North Shelf	132	616 (61.3)	0.46 (0.05)	0.34 (0.05)	0.06 (0.02)	0.07 (0.03)	0.00 (0.00)	0.06 (0.02)
South Shelf	225	570 (106.8)	0.17 (0.03)	0.27 (0.04)	0.15 (0.03)	0.09 (0.02)	0.13 (0.03)	0.19 (0.03)
Slope	193	483 (65.2)	0.30 (0.04)	0.46 (0.05)	0.10 (0.03)	0.01 (0.01)	0.01 (0.01)	0.13 (0.03)

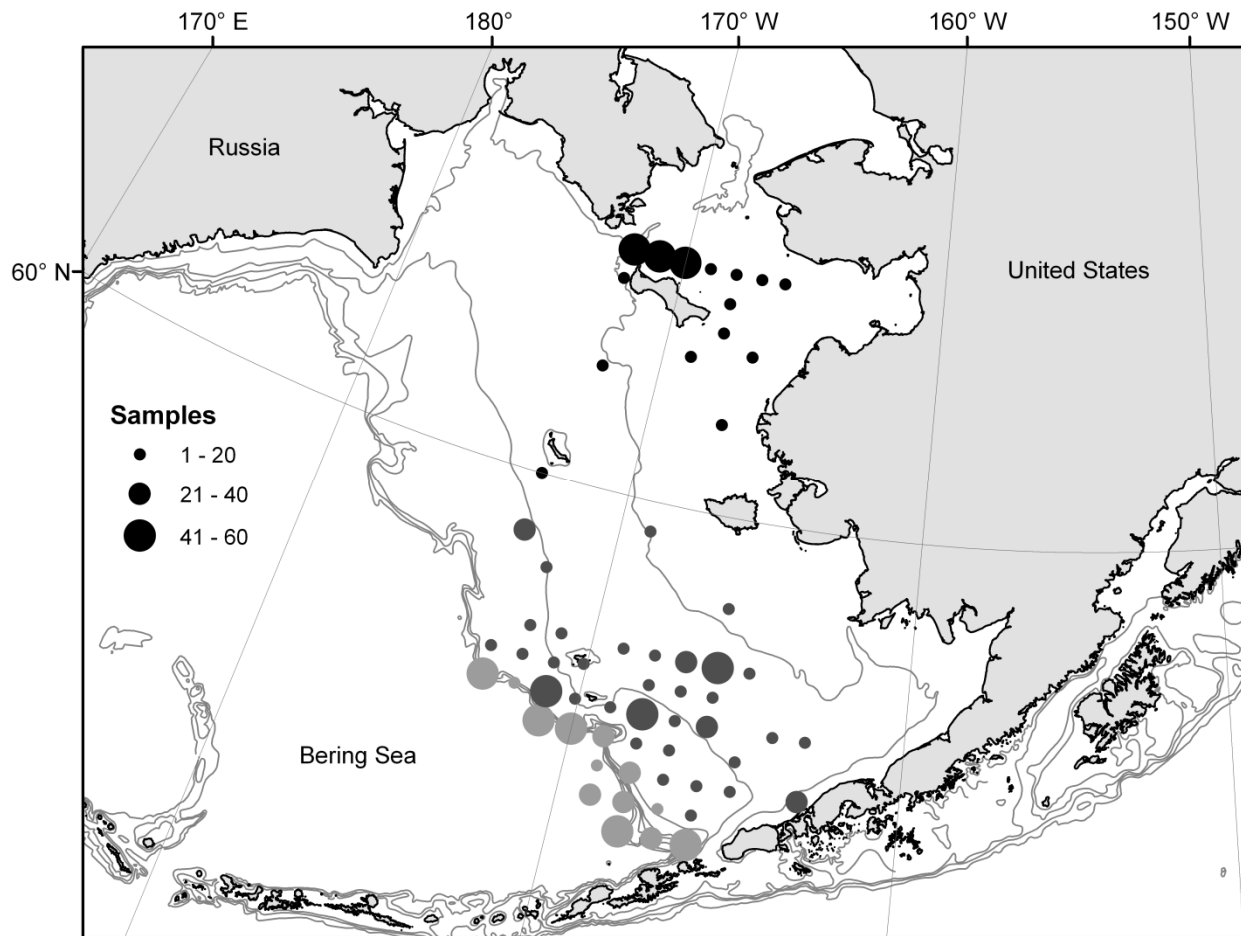


Figure 1. Locations in the Bering Sea where chum salmon were collected during BASIS, summer 2006. North shelf, south shelf, and slope collections are marked with black, dark grey and light grey circles, respectively. Contour lines represent 50 m isobaths.

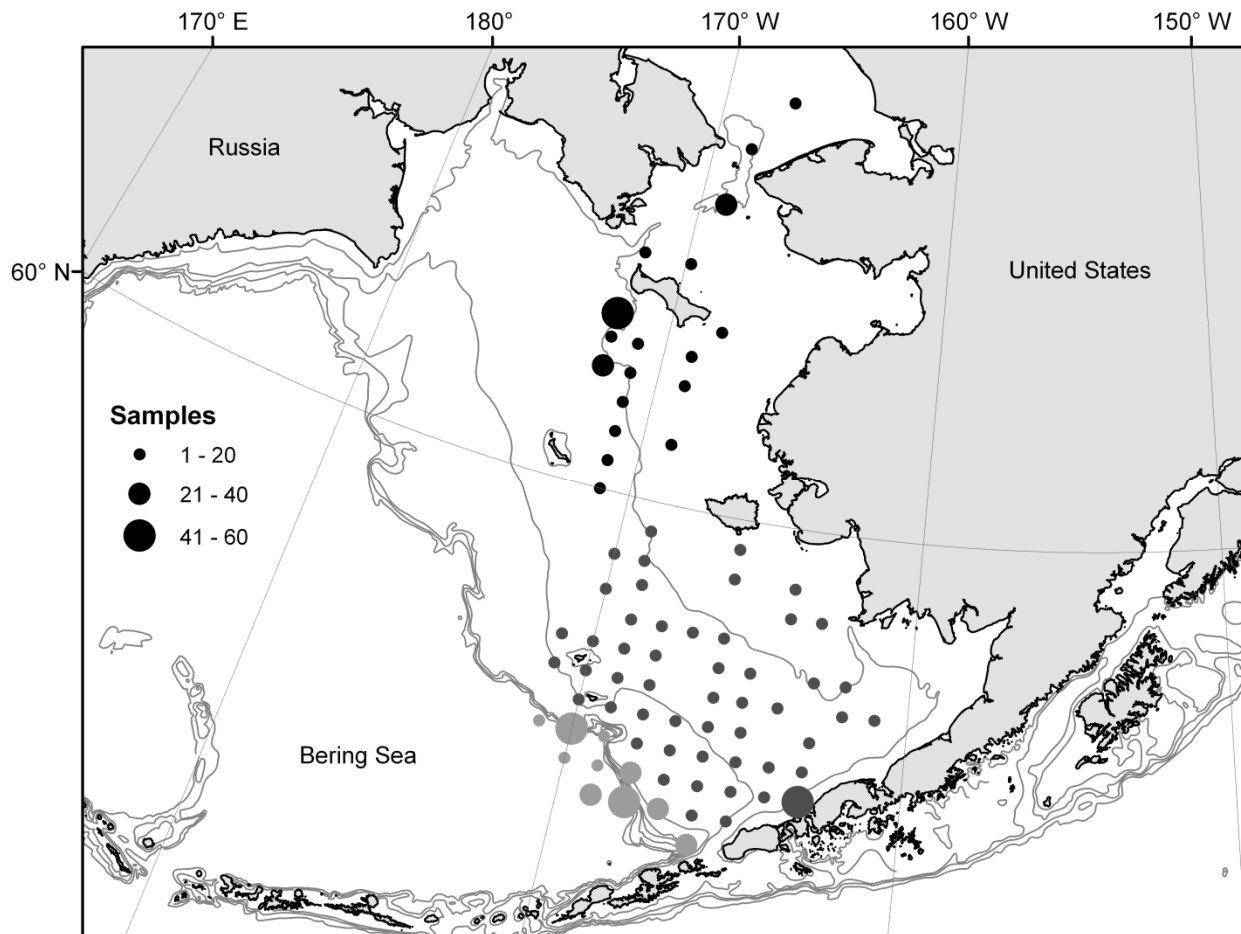


Figure 2. Locations in the Bering Sea where chum salmon were collected during BASIS, summer and fall 2007. North shelf, south shelf, and slope collections are marked with black, dark grey and light grey circles, respectively. Contour lines represent 50 m isobaths.

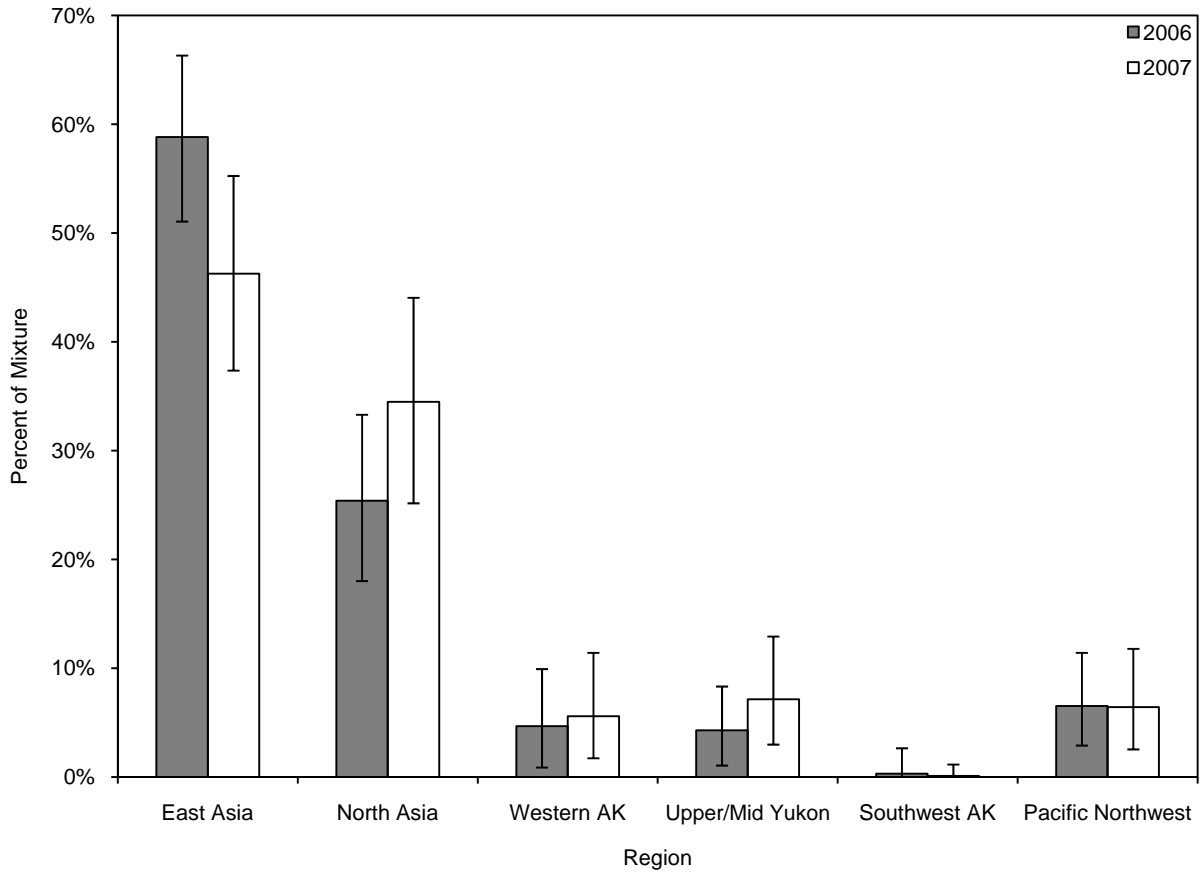


Figure 3. Stock composition of chum salmon in the north shelf habitat of the Bering Sea from 2006-2007, as estimated with microsatellites. Error bars indicate 95% credible intervals.

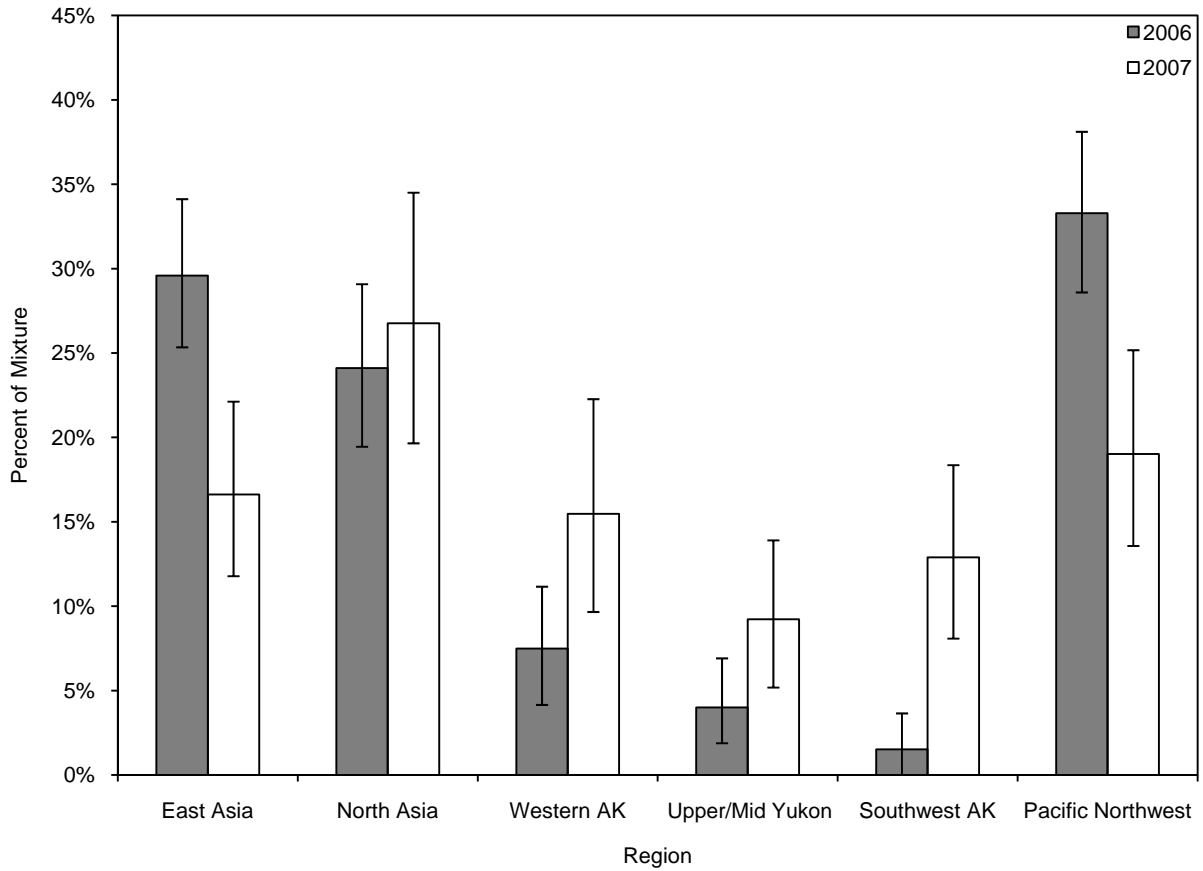


Figure 4. Stock composition of chum salmon in the south shelf habitat of the eastern Bering Sea from 2006-2007, as estimated with microsatellites. Error bars indicate 95% credible intervals.

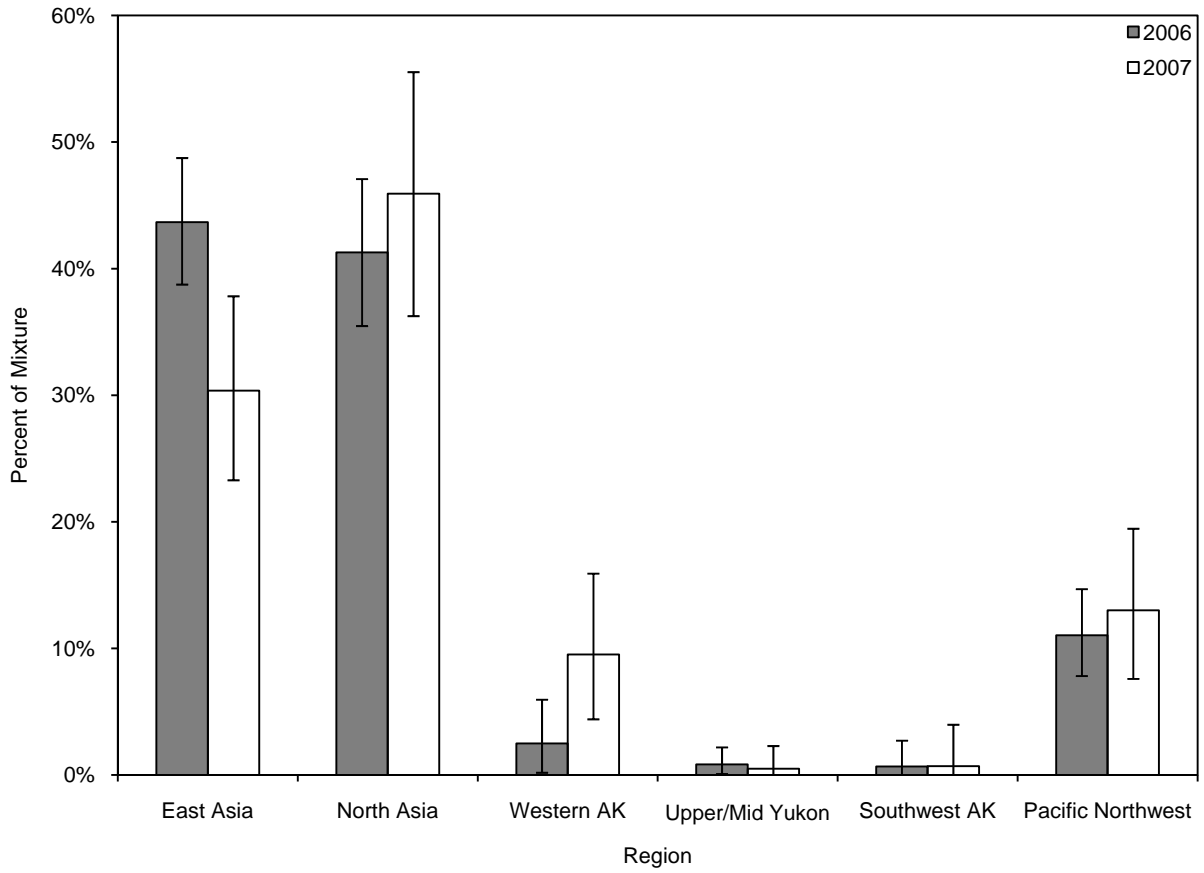


Figure 5. Stock composition of chum salmon in the slope habitat of the eastern Bering Sea from 2006-2007, as estimated with microsatellites. Error bars indicate 95% credible intervals.