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Stock Estimates of Juvenile Chum Salmon Captured on the 2013 Bering Sea and Chukchi Sea Research Survey

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Abstract

Juvenile chum salmon (*Oncorhynchus keta*) were collected during late-summer/fall in the northern Bering and southeastern Chukchi seas as part of the 2013 U.S. BASIS/Arctic Ecosystem Integrated Survey (Arctic Eis) cruises. A small number of genetic samples were collected, most from the Chukchi Sea, and genotyped for 11 microsatellite markers to determine freshwater origin. All of the juvenile chum salmon samples were from western Alaska populations: about half from the Yukon River, one-quarter from Kotzebue Sound, and the remainder from Norton Sound and Kuskokwim/northeastern Bristol Bay. About two-thirds of the fish that originated from the Yukon River were from fall-run populations in the middle and upper reaches of the river. This study adds to a growing body of information about the early marine distribution of juvenile chum salmon from western Alaska.

Introduction

Chum salmon (*Oncorhynchus keta*) are an important resource throughout the North Pacific region. Over the last couple of decades, the abundance of chum salmon returns in some western Alaska drainages has fluctuated widely (JTC 2014), the causes of which remain unknown. There is some speculation that a significant source of mortality exists during the transition when juvenile salmon migrate out of fresh water as fry and smolts into salt water (Healey 1982). Understanding the migration dynamics of juvenile salmon stocks and their relative abundance at sea may help determine the stresses that salmon undergo during this transition and could possibly lead to future models of estimating adult returns.

Since 2002, juvenile chum salmon have been collected during annual U.S. BASIS cruises in the eastern Bering Sea. In 2012, juvenile chum salmon were also collected in the northern Bering and Chukchi seas during the first Arctic Ecosystem Integrated Survey (Arctic Eis) survey (Andrews 2012). Genetic stock identification of juvenile chum salmon from these surveys is providing insight into their migration routes during the first summer in the marine environment (Farley et al. 2004; Kondzela et al. accepted; Kondzela et al. 2014, 2009). Juvenile chum salmon collected in the eastern Bering Sea in an area west of the Kuskokwim and Yukon rivers were

from coastal western Alaska and fall-run Yukon River stocks. Northern Russian stocks were present in more northerly Bering Sea stations, but samples from the Chukchi Sea were from primarily from Kotzebue and Norton sounds.

Our study reports the genetic stock composition estimates for available samples of juvenile chum salmon collected from the Bering Sea and Chukchi Sea on the 2013 U.S. BASIS/Arctic Eis research cruises (Anonymous 2014). These results add to our understanding of migration processes of juvenile salmon in western Alaska as they emigrate from freshwater to marine environments.

Materials and Methods

Sample Collection and DNA Extraction

Juvenile chum salmon samples were collected in the northern Bering Sea and southeastern Chukchi Sea as part of the 2013 U.S. BASIS/Arctic Eis surveys, following the methods described in Farley et al. (2005). DNA was extracted from the tails or opercles of the juvenile salmon with a DNeasy[®] Blood and Tissue Kit (Qiagen, Inc., Germantown, Maryland)¹ and a QIAcube HT[®] instrument as described by the manufacturer (Qiagen). Extracted DNA was stored in 96-well DNA plates at -20°C.

Genetic Baseline

Allele frequencies of the 381-population Pacific Rim chum salmon microsatellite baseline (Beacham et al. 2009) were downloaded from the Fisheries and Oceans Canada (DFO) Molecular Genetics web page (http://www-sci.pac.dfo-mpo.gc.ca/mgl/data_e.htm). Baseline files were created with Excel (Microsoft, Inc.) for 11 of the 14 markers that we routinely use in our laboratory for mixed-stock analyses (e.g., McCraney et al. 2012, Kondzela et al. accepted).

Genotyping

The juvenile chum salmon samples were assayed for 11 microsatellite loci (Beacham et al. 2009)–*Oki100*, *Omm1070*, *Omy1011*, *One101*, *One102*, *One104*, *One114*, *Ots103*, *Ots3*, *Ots68*, and *Ssa419*–with a Qiagen[®] Multiplex PCR Kit following the manufacturer’s protocols. Thermal cycling for the amplification of DNA fragments with the polymerase chain reaction (PCR) was performed on a dual 384-well GeneAmp[®] PCR System 9700 (Applied Biosystems, Foster City, California). Samples from the PCR reactions were diluted into 96-well plates for analysis on the 16- and 48-capillary, 36 cm arrays on the ABI 3130*xl* and 3730*xl* Genetic Analyzers (Applied Biosystems).

Genotypes were double-scored with GeneMapper[®] software, Version 5.0 (Applied Biosystems) and exported to Excel spreadsheets for further analysis. Quality control of sample

¹ Reference to trade names does not imply endorsement by the National Marine Fisheries Service, NOAA.

handling and genotyping was examined by comparing genotypes from the two DNA Genetic Analyzers. Microsatellite allele designations were converted to match those in the DFO chum salmon microsatellite baseline (Beacham et al. 2009) from a conversion table that was developed by genotyping samples shared between laboratories. Converted genotypes were then formatted into mixture files that were compatible with BAYES software.

Stock Composition Analysis

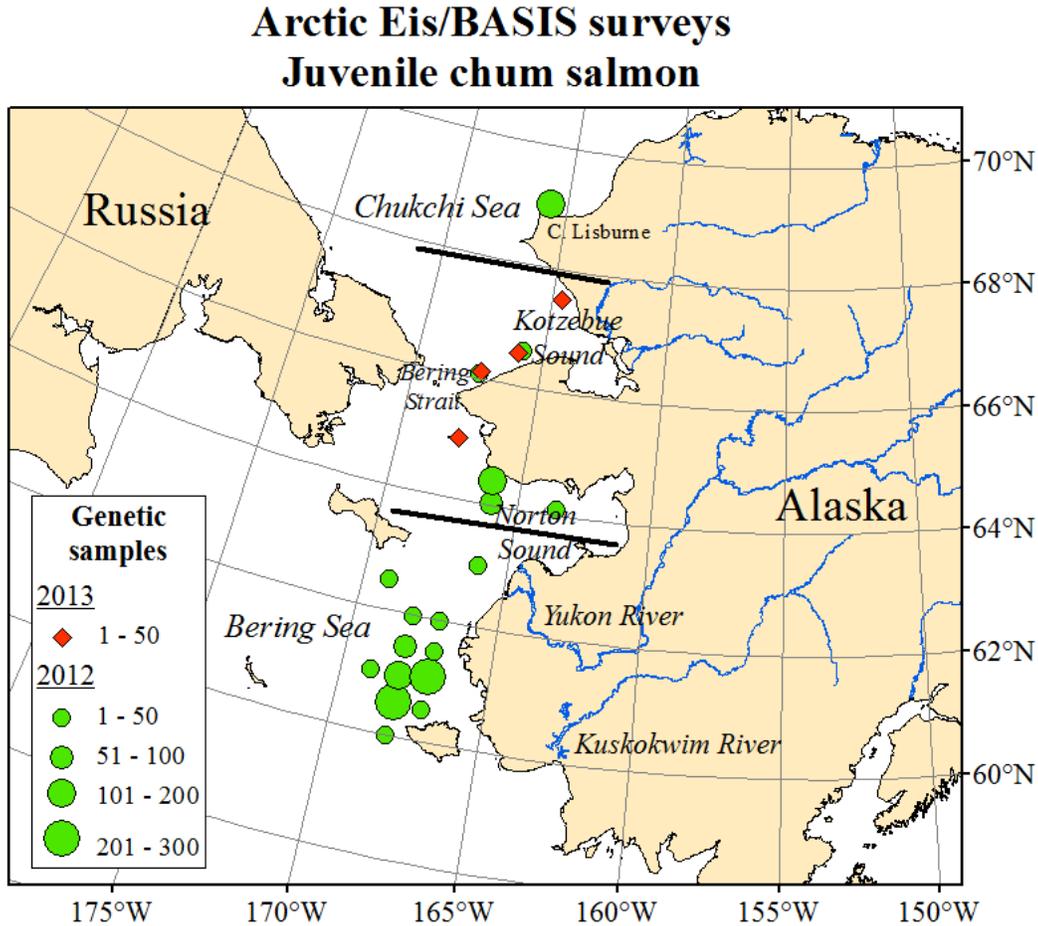
Stock composition estimates were determined with a Bayesian (BAYES; Pella and Masuda 2001) approach by comparing mixture genotypes with allele frequencies from reference baseline populations. For all estimates, the Dirichlet prior parameters for the stock proportions were defined by reporting group to be $1/(GC_g)$, where C_g is the number of baseline populations in reporting group g , and G is the number of reporting groups. For each BAYES analysis, Monte Carlo chains starting at disparate values of stock proportions for each reporting group were configured such that 95% of the stocks came from one reporting group with weights equally distributed among the stocks of that reporting group. The remaining 5% was equally distributed among remaining stocks from all other reporting groups. The stock composition analyses were completed for a chain length of 50,000 or 100,000 MCMC with the first half discarded as burn-in and convergence of the chains to posterior distributions of stock proportions was assessed with Gelman and Rubin (1992) shrink factors. As was done with the 2012 Arctic EIS juvenile chum salmon samples (Kondzela et al. 2014), stock composition analyses were run for six large regional groups with the 381-population coastwide baseline, and for five finer-scale temporal-spatial stock groups with the subset of 58 western Alaska populations.

Results

Sample collection and distribution

Between 8 August and 11 September 2013, stations along the northern Bering Sea (60-65.5°N) and Chukchi Sea shelf (65.5-72.5°N) were sampled for juvenile chum salmon. Most of the samples collected from the northern Bering Sea during 2013 were lost at sea (Mueter et al. 2014). Of the 105 available samples, 96 were successfully genotyped for 8 or more of the markers (average 10.8 markers), the sampling locations of which are shown in Figure 1. The remaining 9 samples were deleted from the project due to a low number of successfully genotyped markers in five fish, four of which were subsequently determined to be pink salmon; two samples that contained DNA from more than one individual; and two pairs of duplicates—the data from one sample from each of two pairs of duplicates were deleted. The 87 samples from the Chukchi Sea were collected during 8-11 August. Nine samples were collected southeast of the Bering Strait on 11 September, a month after the Chukchi samples were collected. Quality control testing of sample handling and genotyping indicated that the genotyping error rate was < 1%.

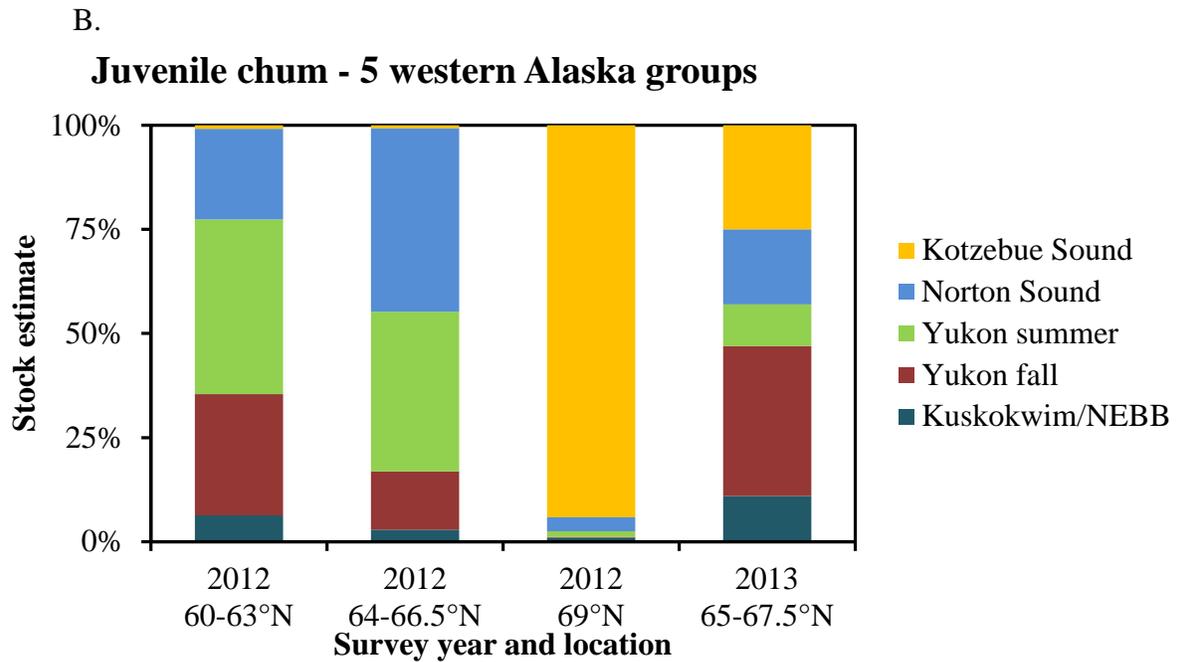
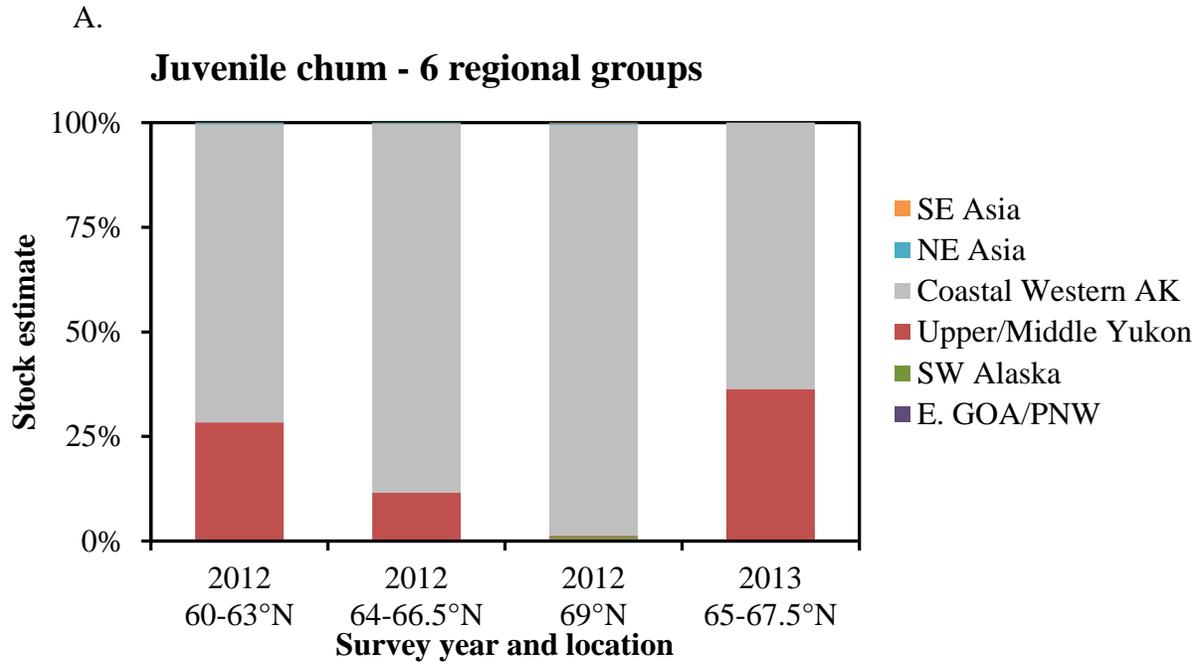
Figure 1. Sampling locations of juvenile chum salmon samples genotyped from the 2012 (green circles) and 2013 (red diamonds) U.S. BASIS/Arctic Eis research surveys. Black lines separate the three aggregated sample sets from 2012 used to estimate stock compositions. Relative sample sizes are indicated by the size of the markers.



Stock composition

When six large regional baseline stock groupings were used in the stock composition analyses, about two-thirds of the 96 juvenile chum salmon samples were estimated to be from the Coastal Western Alaska stock group and one-third from the Upper/Middle Yukon stock group (Figure 2A). Stock composition estimates made with the smaller western Alaska baseline (Figure 2B) showed that a portion of the samples were from northern Alaska stocks in Kotzebue Sound (25%) and Norton Sound (18%). Nearly half of the samples were from the Yukon River stocks, with about one-third of those from summer-run Yukon (11%) and two-thirds of those from fall-run Yukon (36%) stocks. Kuskokwim/NE Bristol Bay (10%) stocks made up the remainder.

Figure 2. Stock composition estimates for juvenile chum salmon samples from the 2013 U.S. BASIS/Arctic Eis research survey. Estimates from the 2012 survey are included for comparison. Estimates from analyses that used a coastwide baseline (panel A), and a more localized western Alaska baseline (panel B). GOA = Gulf of Alaska, PNW = Pacific Northwest, NEBB = northeastern Bristol Bay



Discussion

Juvenile chum salmon samples were collected in late-summer/fall 2013 from U.S. BASIS/Arctic Eis research cruises in the northern Bering Sea and southeastern Chukchi Sea. As in 2012, genetic stock composition analysis showed that juvenile chum salmon were from western Alaska stocks. However, with the finer-scale baseline of western Alaska populations, stock proportions differed between the two years. In 2013, a higher proportion of the juvenile chum samples were from fall-run Yukon River stocks and a lower proportion from Kotzebue Sound stocks. Because the stations in the northern Bering Sea and southeastern Chukchi Sea were sampled at nearly the same locations and dates each year, temporal variation can be ruled out. What did differ between years was the quantity and spatial distribution of the samples. First, the sample set from 2013 was very small (96 total) in comparison to the 2012 sample sets (1,222 total) (Kondzela et al. 2014) due to the loss of northern Bering Sea samples during a flooding event at sea (Mueter et al. 2014). Second, most of the 2013 samples were collected in waters between the two northernmost sample sets in 2012 (Figure 1).

Stock estimates from 2013 indicate that some portion of the juvenile chum salmon from western Alaska stocks migrate northward through the Bering Strait in the same direction as the Alaska Coastal Current (ACC), the prevailing surface current (Danielson et al. 2015). Whether juvenile chum salmon north of the Bering Strait survive or migrate southward before winter sea-ice formation in the Chukchi and Bering seas is unknown.

The distributions of marine species assemblages are influenced by atmospheric and oceanographic conditions in this region (Sigler et al. 2016). Although the same nearshore stations were trawled at virtually the same time of year during the two years of sampling, no juvenile chum salmon were caught north of Cape Lisburne in 2013. The dominant northward transport of water around the shore of northwestern Alaska via the ACC was reduced during August-September in 2013 and the westward spread of the Alaska Coastal Water mass in the northern Bering Sea increased in 2013 (Danielson et al. 2015), and we speculate that these conditions may have restricted the northern extent of juvenile chum salmon distribution in 2013.

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The findings and conclusions are those of the authors and do not necessarily represent the views of the National Marine Fisheries Service.

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