Identification of Pink Salmon Mixed-Stock Aggregations on the Basis of Mitochondrial DNA Polymorphism

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The ability to identify contributing regional stock complexes and major pink salmon populations in marine aggregations will help to increase accuracy in forecasting pink salmon abundance. Pink salmon are the most abundant species of Pacific salmon in the Russian Far East. To determine the level of population and regional genetic variation, we analyzed the Cytb/D-loop region of mtDNA polymorphism in populations contributing to mixed-stock marine aggregations. We used the following restriction enzymes our analysis: *Dde* I, *Hin*6 I, *Hinf* I, *Msp* I, *Rsa* I, *Sfr*13 I.

Variations in the frequency of composite haplotypes of pink salmon returning to spawn in even-numbered years were investigated for populations from East and West Kamchatka, Sakhalin, rivers of the northern coast of the Okhotsk Sea, Primorye, and the Amur River. Maximum likelihood was used to estimate identification accuracy in the baseline stocks. The accuracy for Kamchatka was not high and was determined to be in range of 42.9-68.8%. Identification accuracy for Sakhalin populations was lower, from 40.8% to 83.2%. Amur River pink salmon were identified with 66.1% accuracy, and stocks from Primorye and the north coast of the Okhotsk Sea were identified with 40.7–78.3% accuracy.

Simulations using a 100% composition of each stock at the five-region level indicated high accuracies at the regional level, which averaged 94.2% for Kamchatka pink salmon and 84.7% for Sakhalin pink salmon (II analysis; Table 1). Separation of West and East Kamchatka in a six-way analysis decreased accuracy to 74.7% and 68.0 %, respectively (III analysis; Table 1).

Table 1. Average percent (and standard deviation) correct and incorrect allocations (read vertically) by region for simulated mixtures based on the number of even-year pink salmon regional groups. Expected value for estimates shown in bold is 100%.

№	Region	1	2	3	4	5	6
	I analysis						
№	Region	1	2				
1	Northern populations	**93.6**$_{(6.3)}$	12.8				
2	Southern populations	6.0	**86.8**$_{(7.3)}$				
	Unknown	0.4	0.4				
	II analysis						
№	Region	1	2	3	4	5	
1	Sakhalin Island	**84.7**$_{(9.8)}$	19.3	12.0	14.2	2.3	
2	Amur River	2.2	**66.1**$_{(14.1)}$	0.1	0.4	0.1	
3	Northern shore of the Okhotsk Sea	2.8	2.3	**52.0**$_{(16.7)}$	3.7	2.6	
4	Primorye	2.7	2.4	2.8	**64.5**$_{(14.2)}$	0.4	
5	Kamchatka	7.5	8.8	32.4	16.1	**94.2**$_{(6.2)}$	
	Unknown	0.1	1.1	0.7	1.1	0.4	
	III analysis						
№	Region	1	2	3	4	5	6
1	Sakhalin Island	**84.7**$_{(9.8)}$	19.3	12.0	14.2	2.4	2.1
2	Amur River	2.2	**66.1**$_{(14.1)}$	0.1	0.4	0.0	0.1
3	Northern shore of the Okhotsk Sea	2.8	2.3	**52.0**$_{(16.7)}$	3.7	3.5	5.6
4	Primorye	2.7	2.4	2.8	**64.5**$_{(14.2)}$	0.3	0.4
5	West Kamchatka	4.9	2.5	11.5	11.6	**74.7**$_{(14.3)}$	23.6
6	East Kamchatka	2.6	6.3	20.9	4.5	18.6	**68.0**$_{(17.3)}$
	Unknown	0.1	1.1	0.7	1.1	0.5	0.2

We provided proof that pink salmon mtDNA haplotype variations can be used for identification of mixed-stock marine aggregations. Samples from 595 juvenile pink salmon were obtained from the autumn trawl survey of the R/V *Professor Kaganovsky* in 2009. The baseline data we used were the haplotype frequencies in samples of adult even-year pink salmon from nine rivers of Kamchatka and eight sites in Sakhalin and the Amur River (980 individuals in total). Analysis showed the stock composition of the juvenile pink salmon was mostly West Kamchatka (52.4%), followed by Sakhalin (27.1%), Amur River (11.9%), East Kamchatka (7.2%), and other (unknown; 1.4%).

Assuming the mortality rate is equal for the contributing stocks in the mixture of juveniles, we hypothesized that the regional stock proportions would be approximately the same for adults returning of following year. A comparison of the stock proportions in the juvenile pink salmon mixture from our analysis of 2009 samples with the proportions observed in the regional catch and escapement of adult pink salmon runs in 2010 showed there was a high degree of similarity (Fig. 1).
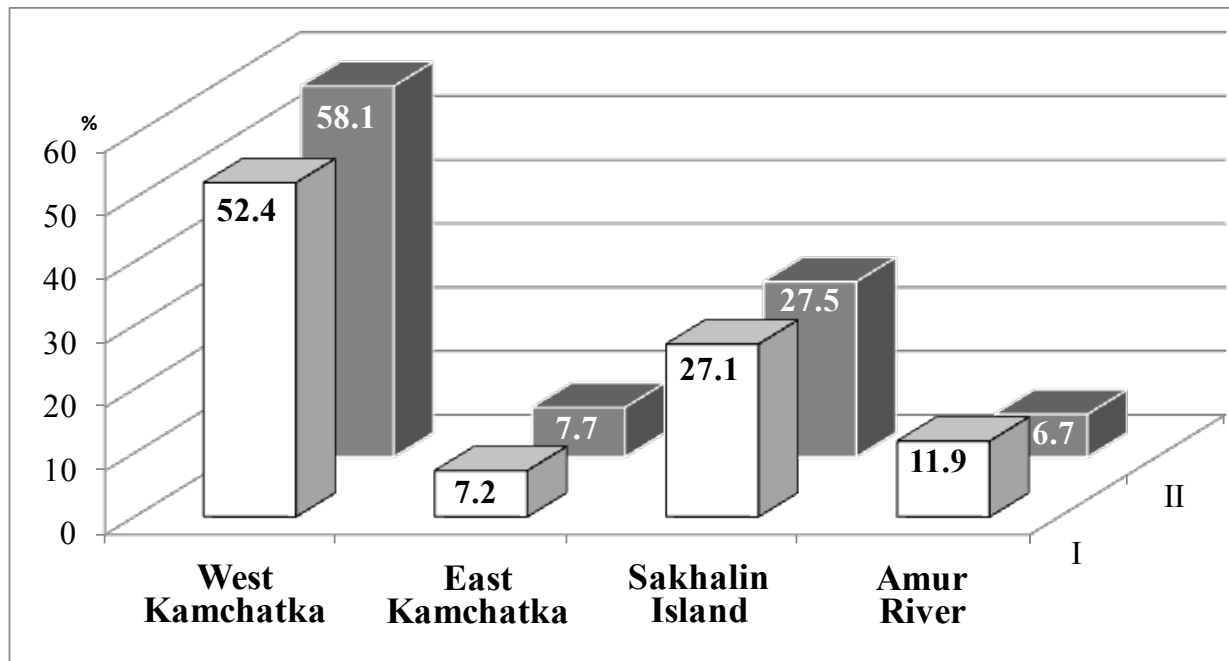

Fig. 1. Comparison of proportional estimates of pink salmon based on genetic analysis of juveniles in marine feeding aggregations in fall 2009 (row I) and regional catch and escapement of adults in 2010 (row II).