

Genetic Identification of the Okhotsk Sea Juvenile Pink Salmon Mixed-Stock Aggregations in the Course of the Early Marine Period of Life

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Pink salmon is the most abundant Pacific salmon species and one of the most important components of the North Pacific and Bering Sea ecosystem. Postcatadromous juvenile pink salmon leave coastal waters for winter foraging at ocean ranches after a short stay near the coast. In this paper we demonstrate results of juvenile pink salmon regional origin identification, provided on the base of RFLP (restriction fragment length polymorphism) analysis of the mtDNA Cytb/D-loop region. The identification was aimed to make quantitative evaluation of the contributions of juvenile pink salmon from different regions of spawning to mixed-stock foraging aggregations in the Okhotsk Sea.

The quantitative evaluation was made on the base of analysis of genetic markers frequencies in samples collected in three autumn trawl surveys in the Okhotsk Sea in 2011 on the R/V «Professor Kaganovsky» (TINRO-Center) and the STR «Uzon» (KamchatNIRO) and in 2012 on the R/V «TINRO» (TINRO-Center). Regional identification of pink salmon in the mixed-stock aggregations of 2011 was provided for the total sample, consisted of 19 subsamples (Table 1). Some data, including September 20–28 and October 18–30 samples, required separate analyzing. Results of the identification for the mixed-stock aggregations of 2012 are demonstrated in Table 2.

Juvenile fish from the mixed marine aggregations 2011 represented generation what should return to native regions for spawning in 2012. Estimation of the error of the method was made on in fact catch data about the prespawning fish in the commercial districts of the Okhotsk Sea basin.

The data of the mtDNA haplotype diversity among individuals of the even-numbered years of spawning (the even-year brood line) from 24 local populations of West Kamchatka, Sakhalin, continental shore of the Okhotsk Sea and Primorye were used as a baseline. Regional identification of the fish from the generation of the odd-numbered years was provided on the data, obtained as a result of analyzing samples from 19 rivers of West Kamchatka, Sakhalin, continental shore of the Okhotsk Sea and Kuril Islands. In the total we have analyzed the mtDNA haplotype frequencies for the sample of the approximate size of 2,5 thousand individuals.

As a result there were 61 haplotype variants revealed (38 composite haplotypes in the even-, 32 – in the odd-year brood line, 9 – in both brood lines) in the analysis of the polymorphism of the lengths of the mtDNA restrict fragments in studied samples of mature pink salmon generations of the odd and even years of spawning. The data about the population diversity of pink salmon of both even- and odd-year generations indicate of genetic heterogeneity, expressed clearly and having regional character (Fig. 1). The statistical heterogeneity, estimated to differentiate regional origin, is visibly higher, than the heterogeneity to differentiate populations.

Likelihood evaluation of the identification accuracy for the individuals from regions (Table 3) was made on the base of different frequencies of composite haplotypes of pink salmon from the rivers of West Kamchatka and the northern part of the continental shore of the Okhotsk Sea (the regional group of the Okhotsk Sea basin «northern populations»), Sakhalin, Kuril Islands and Primorye (the «southern populations»). It is revealed in the course of the evaluation of the composition of simulated samples, that the identification accuracy for both «northern» and «southern» regions is 88–92% for generations of the even years. For generations of the odd years the accuracy is lower – 78–84%, what should indicate of the lower pink salmon regional differentiation level for this brood line. No doubts, judging on the results, that genetic differentiation for the even-year brood line of pink salmon can be

provided for the regional level. As for the odd-year generations, the possibility of the differentiation requires further clarification in a research with analysis of maximum possible number of samples from principal spawning watersheds.

№	Region	1	2
Even-year pink salmon			
1	Northern populations	92.0 _(4.45)	11.8
2	Southern populations	7.4	87.8 _(6.72)
	Unknown	0.6	0.4
Σ		100	100
Odd-year pink salmon			
1	Northern populations	78.6 _(13.06)	15.0
2	Southern populations	20.8	84.2 _(10.86)
	Unknown	0.6	0.8
Σ		100	100

October in the central part of the Okhotsk Sea. In general the part of the «southern» populations was less than the part of the «northern» ones in both attempts: 39,6% in the September samples and 46,9% in the October samples (Fig. 2). The difference can be result of the different time and area of sampling, but in this way it also can illustrate when juvenile fish emigrate from the native regions and start to leave coastal area for feeding at sea.

To estimate methodic error for the genetic identification on the base of catch frequency dynamics for the mtDNA composite haplotypes we compared results, which we have obtained for juvenile fish, and the in fact data about the catch in the nursery regions for the same one generation of pink salmon (the fishery campaign 2012). In the preliminary assessment the part of the «northern» pink salmon populations from West Kamchatka and Magadan Region in the total catch is 57,3%, whence the part of the «southern» pink salmon populations from Sakhalin, Khabarovsk and Primorye Regions is 42,7%, what is rather similar to the results of provided genetic identification and says about potential possibility to use genetic data in the assessment of juvenile pink salmon stocks from different regions in the mixed-stock marine aggregations in the early phase of foraging.

On the data, collected during the autumn trawl survey for odd generation of juvenile pink salmon in the Okhotsk Sea in 2012 we have provided genetic identification of the regional composition of the mixed-stock marine aggregations. The results are demonstrated in figure 3. In view of the results the part of the «northern» populations seems rather impressive – >30% (the standard deviation is 9%).

On our view the results can be used for the assessment of the abundance of juvenile fish from different regions in the mixed aggregations in the case if:

Table 1. Sampling locations with the latitudes and the longitudes, period of collection and the number of juvenile pink salmon samples (N) in 2011.

Latitude/Longitude	N
20–28 September 2011	
53°01′/152°60′	50
53°00′/154°02′ and 53°02′/155°19′	47
54°04′/153°56′ and 53°60′/152°59′	46
54°00′/152°01′ and 53°60′/151°03′	45
54°00′/150°16′ and 54°00′/148°38′	50
54°60′/148°31′ and 55°00′/149°59′	49
55°00′/150°59′ and 55°00′/152°02′	49
55°00′/152°60′ and 55°02′/153°60′	49
55°01′/155°05′ and 56°01′/154°57′	50
56°33′/153°02′	48
51°04′/153°57′	49
Σ	532
13–30 October 2011	
52°22′/151°08′	35
49°53′/151°06′	50
49°34′/149°13′	50
50°54′/150°39′	50
50°26′/148°55′	50
54°43′/147°39′	47
52°14′/147°47′	50
50°14′/145°39′	50
Σ	382
Total	914

Table 2. Sampling locations with the latitudes and the longitudes, period of collection and the number of juvenile pink salmon samples (N) in 7 October – 5 November 2012.

№	Latitude/Longitude	N
1	53°13′/154°16′	47
2	51°22′/154°51′	50
3	49°41′/151°09′	50
4	55°17′/152°19′	50
5	54°52′/151°05′	49
6	51°08′/149°36′	48
7	48°45′/148°11′	46
8	50°58′/147°44′	50
9	52°37′/148°40′	47
10	52°39′/146°26′	48
11	48°35′/146°04′	48
Total		533

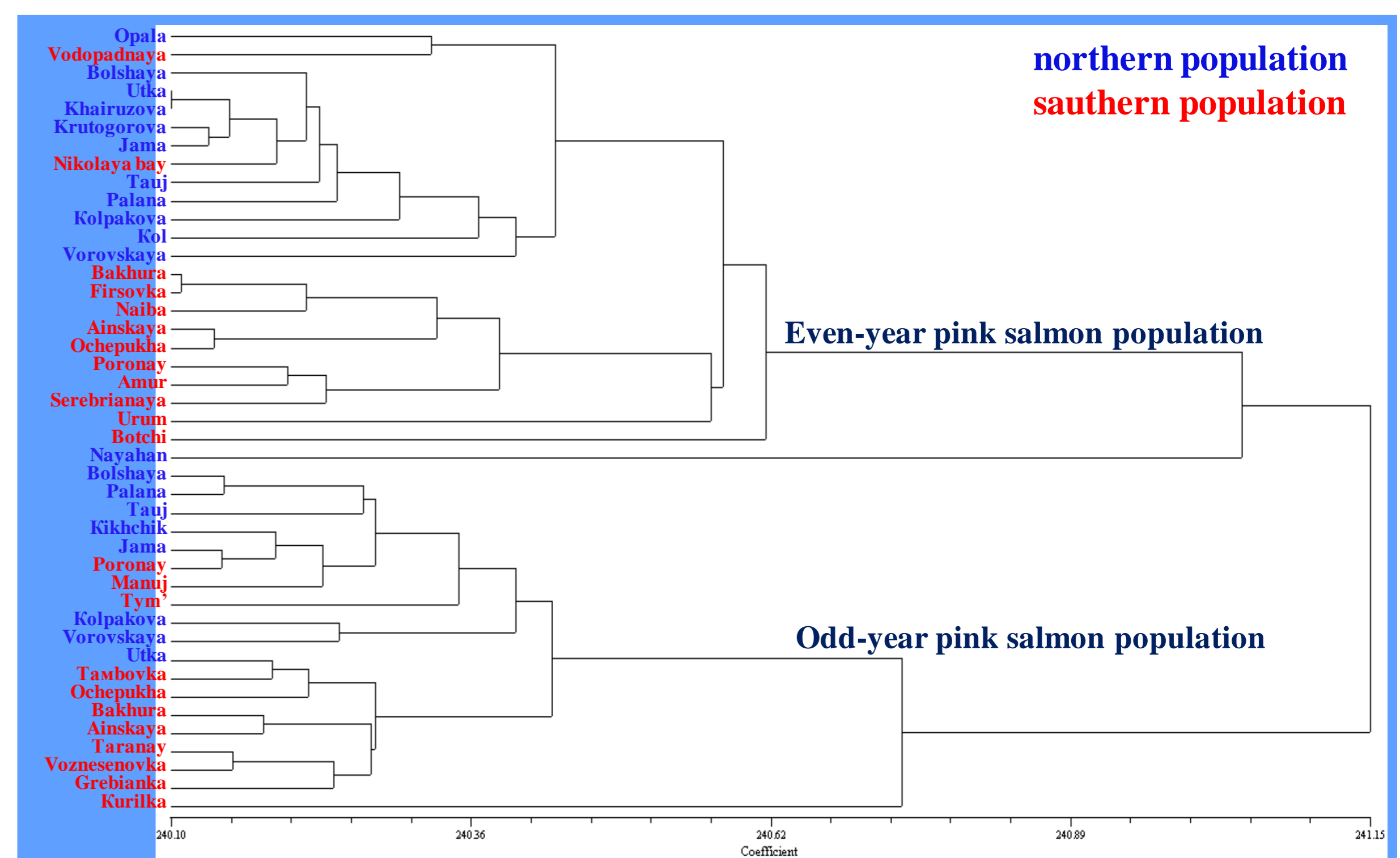


Fig. 1. The unweighted pair-group method with arithmetic mean (UPGMA) dendrogram created using genetic chord distances and based on the frequencies of composite haplotypes of even- and odd-year Asian pink salmon (43 rivers)

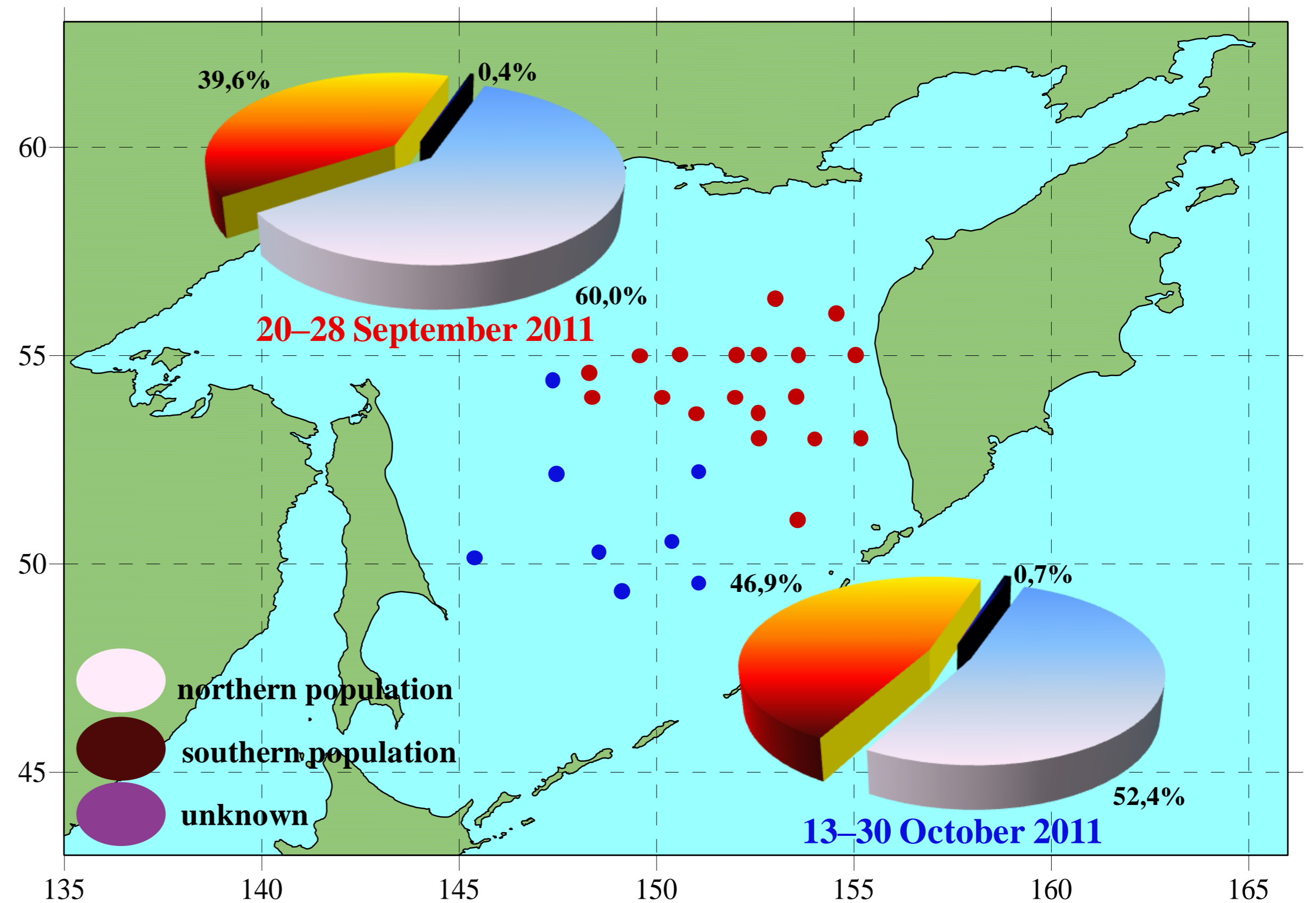


Fig. 2. Regional proportional estimates of pink salmon based on genetic analysis of juveniles in marine feeding aggregations in fall 2011 (the sites of sampling in September are marked with red, and in October – with blue).

judging on the results, that genetic differentiation for the even-year brood line of pink salmon can be provided for the regional level. As for the odd-year generations, the possibility of the differentiation requires further clarification in a research with analysis of maximum possible number of samples from principal spawning watersheds.

The RELF-analysis of the mtDNA in all studied mixed marine samples of juvenile pink salmon has revealed 21 composite haplotypes, which frequency distribution variety in the baseline samples from different regions was a basis for identification or likelihood evaluation of the percent regional contribution according to the principle of the maximum similarity in frequency of the composite haplotypes.

The results we have obtained on the evaluation of the population genetic differentiation of pink salmon in this research allow us to provide regional identification for the components of mixed-stock marine samples of juvenile pink salmon (Fig. 2–3). As it was said above, the results on the regional composition have been obtained from two attempts to analyze: samples, collected in September within more northern and close to Kamchatka Peninsula district of the Okhotsk Sea, and samples, collected in

October in the central part of the Okhotsk Sea. In general the part of the «southern» populations was less than the part of the «northern» ones in both attempts: 39,6% in the September samples and 46,9% in the October samples (Fig. 2). The difference can be result of the different time and area of sampling, but in this way it also can illustrate when juvenile fish emigrate from the native regions and start to leave coastal area for feeding at sea.

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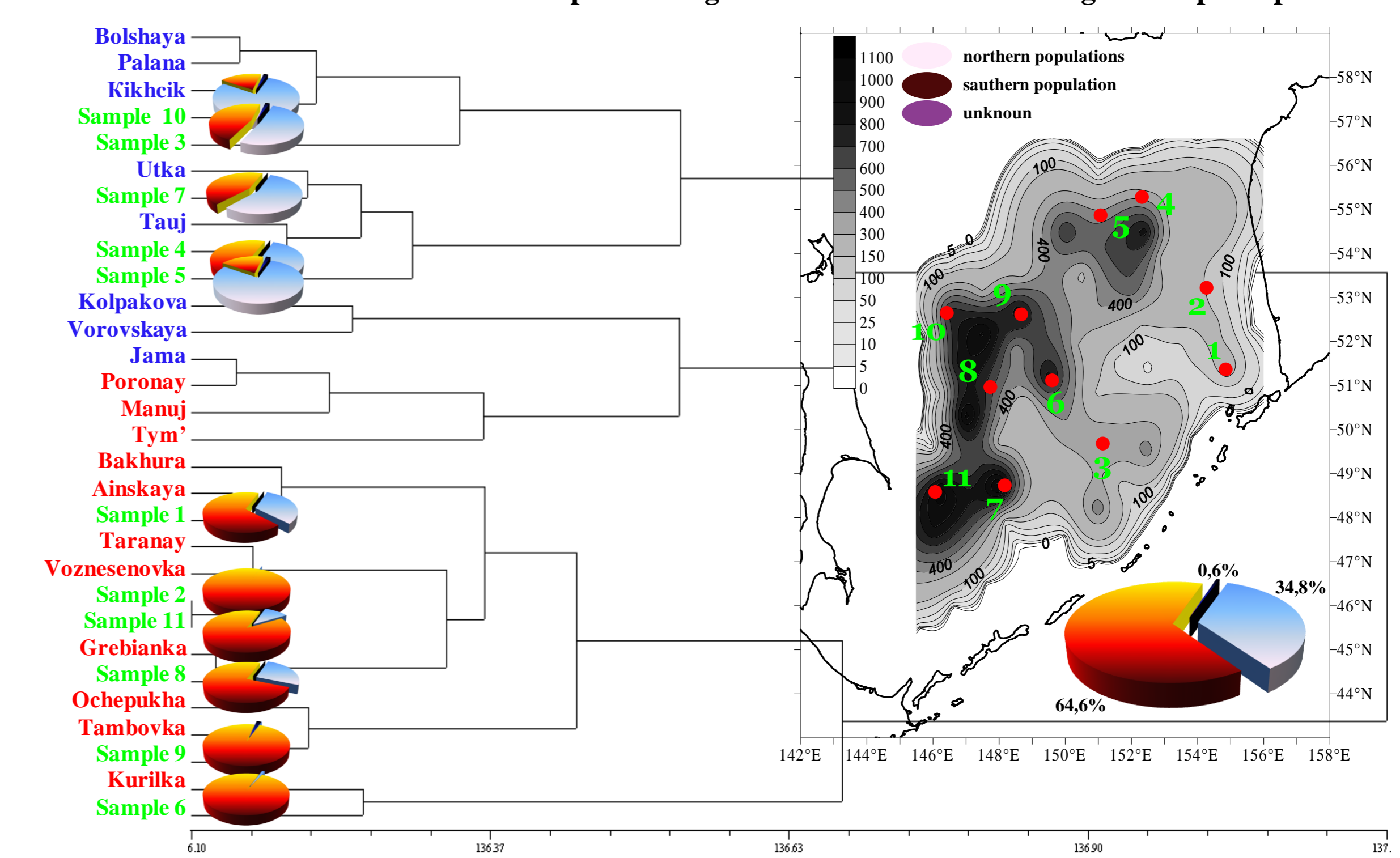


Fig. 3. The unweighted pair-group method with arithmetic mean (UPGMA) dendrogram created using genetic chord distances and based on the frequencies of composite haplotypes of odd-year Asian pink salmon and samples of juvenile pink salmon mixed-stock aggregations.

– the accuracy of the regional identification for the odd-year brood line of pink salmon is relatively low, comparing to the even-year brood line;

– the result has strongly influenced by the time of sampling, as the time of the emergence from the rivers and migration seaward is extensively different in regions within the Okhotsk Sea basin; moving the time of sampling for earlier or later periods cause increase contribution of the «northern» or «southern» population respectively.