Sockeye salmon is characterized by extremely complex population structure populations reproducing in different river watersheds (metapopulations) are subdivided into seasonal races, ecotypes, and subpopulations of isolated spawning grounds. Because of genetic and morphological differentiation of the intraspecies samples collected in downstream reach of a river are normally heterogeneous. The includes both mixed samples from an eyed and samples collected during sockeye salmon spawning run in lower river. The objective of the paper was to analyze subdivision of sockeye salmon from the low course of East and West Kamchatka rivers, where (in tributaries and taken) the most commercially important Asian stocks are reproduced. Samples for the analysis were collected during mass spawning run of sockeye salmon in the lower course of Ozernaya River, Bol' eya River, and Polynesia River at the mouth of 2002 (Fig. 1) and at the Kitilgino River (Khalaktyrsky District, Khabarovsk Territory, Russia) in 2006 (Khrustaleva et al. 2014). In addition, juvenile fish (undercatches) were caught during downstream migration in the upper reach of Plotkino River, 10 km from Nikolskoe Lake, and in the lower course of Bol' eya River, all in its flow; the main spawning river, Bol' eya River, 10 km from Kamchatka settlement (Khrustaleva et al. 2014) (Fig. 1b). Moreover Dr. Chris Hatfield (Hatfield et al. 2010) open data on allele frequencies of some loci in samples of Kitilgino and the upper reach of the Kamchatka River - Khalaktyrsky District, Khabarovsk Territory, Russia. DNA analysis was performed at the School of Aquatic & Fishery Sciences (University of Washington) [see] (2009). Statistical analysis included clustering of the samples in the STRUCTURE 2.3.4 software (Pritchard et al. 2000).

Morphological and genetic heterogeneity of sockeye salmon samples collected in different periods of its salmonid life cycle as well as from different outfalls of West and East Kamchatka rivers were observed. The size-masses characteristics of sockeye salmon in western Kamchatka rivers did not differ significantly between the periods of the mass movement, with a number of exceptions (Fig. 2). Sockeye salmon from the rivers East and West Kamchatka were noticeably smaller than caught during the mass run (2002 and 2003) but significant differences were revealed only in the fish of a length of (p=0.02). In Ozernaya River, the fish in 2002 was significantly larger (F-test, p=0.005) than caught two days later (31 June). Composition of the fish two samples revealed significant differences in genetic mass (p = 0.02), probably, due to different ratios of males and females in the catch. The total genetic diversity of the fish of Ozernaya River was the highest, and the genetic diversity in the fish of the Middle River was the lowest.

In the Middle River, the sockeye salmon caught on the 2002 mouth of Ozernaya River are the main representatives of the species. The stocks of the Middle River, the mouth of Ozernaya River, and the Kamchatka River have the lowest genetic diversity. The results of the analysis of the genetic diversity of the samples are not described either in length or in mass. There wasn’t any periodicity in estimates of allele frequencies of 45 SNP loci during mass spawning migration of sockeye salmon in the rivers of west and east Kamchatka. The heterogeneity of allelic frequencies of 54 polymorphic SNP loci was revealed by the periods of the mass run of sockeye salmon in the month of the Kamchatka River: the samples of the first (first runners and 1 July) and second (2-3 July and 3-4 July) were mass run significantly different. However these differences were mostly due to the variability of only two loci (one SNP-KF-293 and one MHC-II.21v). The identification of morphological and genetic heterogeneity of the samples may be explained by a successive approach to the river mouth of sockeye salmon, reproduced in different parts of the river basin.

According to the analysis in STRUCTURE in the mixed samples from the mouth of Kamchatka R. in 2004, two groups of individuals were distinguished - group 1 and more numerous group 2 (Fig. 5). Moreover, in the beginning the run group 2 was predominant, whereas in the second half of the run the individuals assigned to group 2 was increased much more frequently (Fig. 6). The consequent genetic was significantly differentiated by max loci (20 of 34), with the most contributions of HMCII.21v and GPHH.44. Analysis of the phenotypic traits in both groups of the fish for variations in dimension size, body color size, age, and mass, revealed, an average, older and larger. In addition, the proportion of individuals spent in fresh water for 2 years was significantly higher in group 1. We assumed that these groups belong to different subpopulations of summer sockeye salmon in Kamchatka R. watershed (Bugayev, 1993). Group 1 can be attributed to the grouping 2, reproduced in the middle and lower reaches of the river, some of them enter the Azobof bay for several months. Group 2 can be classified as grouping 3, which occupies upstream tributaries. Juveniles of the group 2 spend life stage on spawning grounds and migrate at stage of the age of 1 + (Bugayev, 1995). Our findings are supported by the results of multidimensional scaling (MDS) the results of Baltic Distribution calculated by the allelic frequencies of SNP loci in sockeye salmon samples from different parts of Kamchatka R. (Fig. 6). According to the first coordinate, 4 groups of sockeye salmon samples from the outfalls of the salmon were divided: 1) samples from upper tributaries, represented by one sample from Klikino R, and a shared cluster with group 2; 2) samples from the tributaries of the lower reach; and from the Kryevsky R. We can hypothesize that the most numerous in the watershed of sockeye salmon of Azobof Bay can be sporadically present in both groups. Most likely, it migrates a bit later, and our samples did not cover it. Differences between the samples collected during mass spawning run in the course of Kamchatka R. indicate a successive segment of migration of different sockeye salmon groups reproducing in distinct parts of the watershed: at the beginning, the individuals that reproduce in the spawning grounds of the middle reaches of the river predominates, then the upstream groups migrates and, probably, some groups are isolated. This can be a factor of the genetic diversity of sockeye salmon in Kamchatka R. watershed.