

;hjbkh\Z bHp_gdZ \ebygby]_h]jZnbq_kdhc baheypbb gZ kl_i_gv]_g_lbq_kdhc

;hjbkh\Z.¹, F_s_jkdB^{e2}, RiZdH<², =eZahF.², Eblh\c.B³, Jh`ghA<²

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Evaluation of effect of geographical isolation on level of genetic distinctness in beluga whale (*Delphinapterus leucas*) populations in Russian Far East

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The beluga whale is a species commonly occurring in the Sea of Okhotsk and the Bering Sea (De_c_g_g[_j] b ^j 1964). But beluga whales are rarely seen off southwest coast of the Kamchatka Peninsula and are almost never off the eastern coast of Kamchatka, which indicates that the Sea of Okhotsk beluga whale stock is geographically separated from the Bering Sea stock and the Arctic stock (F_evgb2001). However, the possibility of existence of separate stocks within the Sea of Okhotsk has been denied. Analysis of allelic distributions of microsatellite loci has shown that beluga whales that form the Sakhalin summer aggregation and the Shantar Islands summer aggregation belong to the same population (A_u_d_h_b_Z; this book). Of even greater interest is the issue whether beluga whales that aggregate in the above-mentioned sites are isolated from the stock summering off the D P F K D W N I coast. Although the Sakhalin summer aggregation is separated from the D P F K D W N D V suzhmer AggF gation by a distance of over 1000 km, the fact that Sakhalin Amur stock spends the winter in the northern part of the Sea of Okhotsk (as was indicated by satellite tracking data RiZ d ^j 2010) leaves open a possibility of the encounters and mating between the Sakhalin Amur stock and Kamchatka D V Z H stock during the winter and spring months.

To assess the degree of genetic isolation both between different groups of the Sea of Okhotsk population and between the Sea of Okhotsk and the Bering Sea populations of beluga whales, we estimated allele frequencies at eight nuclear DNA microsatellite loci: DlrFCB4, DlrFCB5 and DlrFCB17, EV94Mn, 415/416, 417/418, 464/465 and 468/469.

ljb wlfh mjh_gv]_g_lbq_kdbo hZebgkdh]h aZeb\Z hl`b\ghghuoihaZjDZfqZldb hdZau\Z_lky ^Z`_g_kdh_gv hlebqbc ©dZfqZlkdbo^a [_emob]h ebfZgZ

Moreover, the genetic differences between the Sakhalin VWRFN DQG WKH .DPFKDWND¶V even somewhat greater than the genetic differences between the Anadyr Estuary stock and the Kamchatka ND¶V ZHVW FRDVW VWRFN

:gZeba f_lh^hf deZkl_jbaZp Structure 2.3.3,Pritchard et al IZd`_h[gZjm`b\]_l_jh]_ggghklv \ hj[s^_oeZb\hdmigZk ebabjm_fZy \u[hjdZ k [hevr_c _jy_lky gZ ljb algZq_eh]ZjbnfZ _jhyhg g`_eb gnP=^A_]jmiiu \ e_ggZy]_l_jh]_ggghklv gZijyfmk[hjZ h[jZa@Zvg^ujk@bZfqZlkdb_`ebgkdb_^a [_emob hlebqZxlky koh^ghklvx hlg_k_gby bf_ggh d ©k\h_jbk

Using a clustering method (the software Structure 2.3.3, Pritchard et al. 2000), we confirmed the existence of obvious heterogeneity of the entire universal set: there was a higher probability that the samples being analysed were divided into three groups (the log probability LnP = -537.2) rather than two (LnP = -600.3). The heterogeneity directly correlated with the sample collection locations. All the three sets of samples (samples from the Anadyr Estuary, Kamchatka FDKWND¶V ZHVW FRDVW DQG 6 D ly high probability of belonging to their own stock (Fig. 1).

Table 3. Samples pairwise FSTs (above diagonal) and statistical significance level (below diagonal) for the samples comparison by frequencies of eight microsatellite loci alleles.

Locality	Sakhalin Bay	W. Kamchatka	Anadyr' Estuary
Sakhalin Bay	***	0,06768	0,07422
W. Kamchatka	0,00000	***	0,06556
Anadyr' Estuary	0,00000	0,00000	***

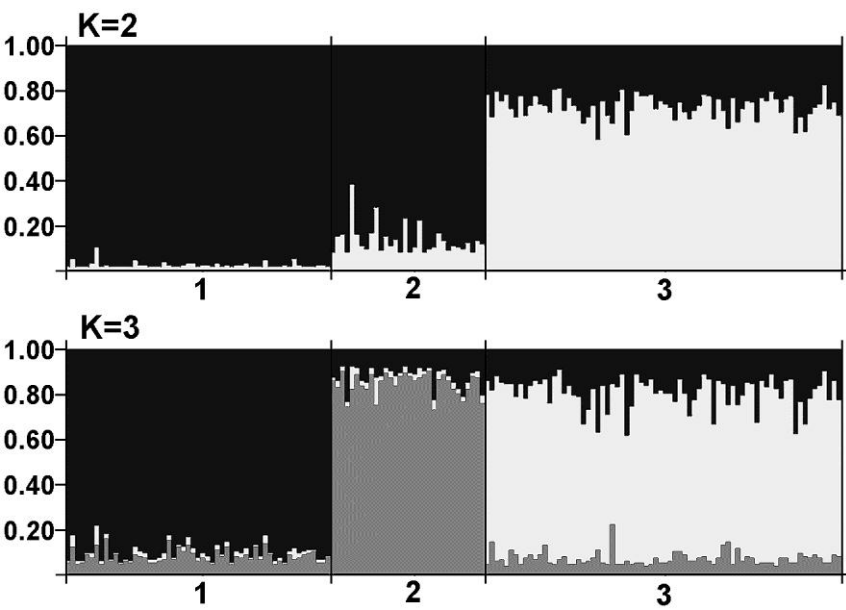


Fig. 1. Probability of individuals of total sample (n=161) to belong to one of two (K=2) or three (K=3) hypothetic genetic clusters. Admixture-LOCPRIOR model, 500000 replications. Sampling localities: 1 – Sakhalin Bay, 2 – Western Kamchatka, 3 – Anadyr' Estuary.

LZdbf h[jZahf ijb hlkmlkl\bb \uz nbq_kdbo ij\]jZ^_eZo _^bghc Z\hafh`ghc [ebahklb jZchgh\ abth

Thus, despite the absence of obvious geographical obstacles between two stocks inhabiting the same Sea Okhotsk and despite the possible nearness of their

]jZpbc f_`^m ^\mfy]jmiiZfb [_
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 jZa^_e_ggufb ihimeypbyfb HohM
 fhj_c

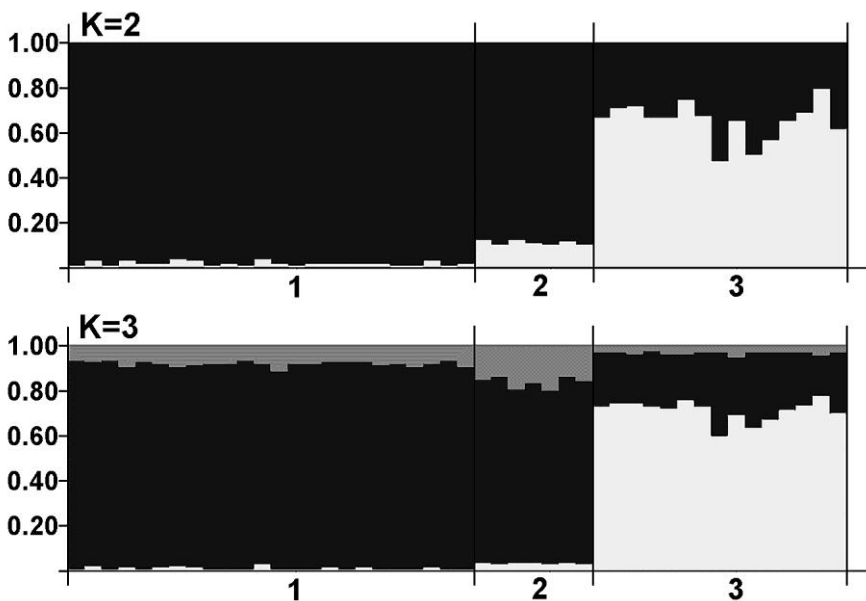
<Z`gh hlf_lblv qlh ijb jZa^_evgh
 b kZfhd klZlkbq_kdb ^hklh_jg
 lj_fy jZchgZfb khojZgyxlky ^ey Zh
 dh mjh_gv hlebqbc kZfph\ DZf
 (Fst= hdZau\Z_lky \ ^\Z jZa^_evgh
 fhdba wlbo jZfgh_ ljb wlhf
 aZiZa^_gZfqZikdhc \uf[h^h kZfpZfb
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 \ qZklhlZo \klj_qZ_fhklFst=0.0356
 P=0,018 \ lh \j_fy dZd \u[hjdb kZf
 KZoZebgkdh]h ba Zeb\gZ^ujkdh]h_e
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tering grounds and migration routes. These two stocks have a level of genetic isolation that is as high as the level of genetic isolation between the geographically separated the Sea of Okhotsk stock and the Bering Sea stock.

It is of importance that separate analyses for males and females still showed statistically significant differences between the three areas tested. Although the level of genetic isolation between the Sea of Okhotsk males and Sakhalin beluga males was two times higher (Fst=0.08046) than the level of difference between the Kamchatka and Sakhalin females (Fst=0.0372). Moreover, there was a significant difference in allele frequencies (Fst=0.0356 P=0.018) between males and females of the Sakhalin Gulf stock or between males and females of the Anadyr Estuary stock.

The clustering method did not reveal any genetic isolation between the Sea of Okhotsk stock and females of the Sakhalin Gulf stock, though we have already mentioned that there were statistically significant differences in the Fst values between two groups (the Anadyr and the Sea of Okhotsk ones) had the minimum value of the log probability: LnP= -1059.9, D=2 and LnP= -1062.2, D=3, Fig. 2. However, the analysis of males by the clustering method showed isolation of all the three groups: LnP= -2449.6, D=3 and LnP= -2485.4, D=2, Fig.3.



Jbk <_jhylghklv
 e_`ghklb hkh[_c \
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]bihl_lbq_kdbo_]_c
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 jZchg[hjZ[jZa^_evgh
 jbk1.

Fig. 2. Probability of individuals of sample of females (n=46) to belong to one of two (K=2) or three (K=3) hypothetical genetic clusters. Model and localities – see fig.1.

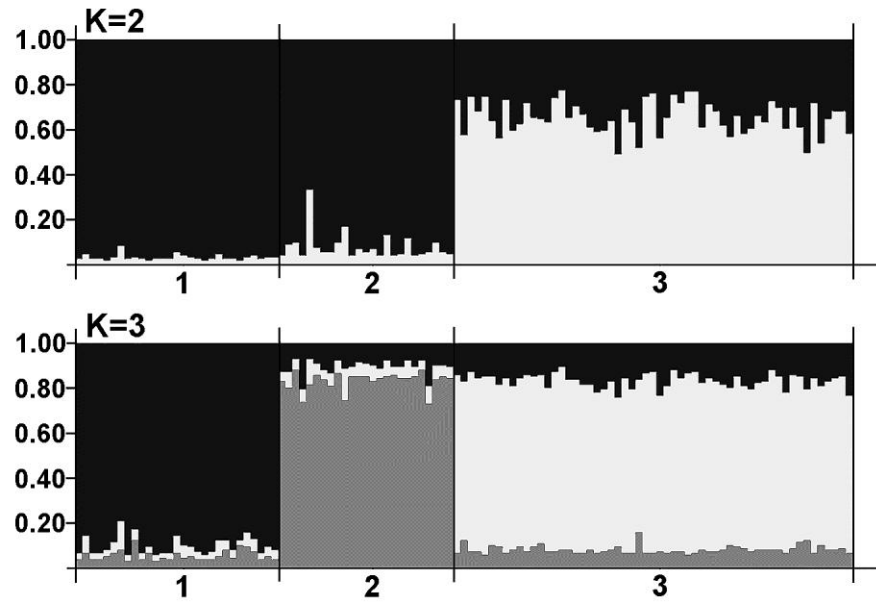
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To understand the possible causes of the isolation,

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guo `b\hlguo nZmgu Jhkkbb ijtk
kdh]h]_h]jZnbq_kdh]h h[s_kl\Z

ther research and large sample sizes are required.
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ences, with the support of the Russian Geographical
Society. The program is part of the Permanent exped
ition of Russian Academy of Sciences studying Red Book
animals and other focus species of Russia



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kdbo deZkl_jh\bFh^_c
jZchg[hjZ[jZch\k f
j b k 1.

Fig. 3. Probability of individuals of sample of males (n=111) to belong to one of two (K=2) or three (K=3) hypothetic genetic clusters. Model and localities – see fig.1.

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investigation of the species. Academy of Sciences of the USSR, Moscow. Translated by Israel Program for Scie
tific Translations. 455 pp.]
F _ e v g b c h \ 2001. ;_e m o Z H o h l k d h] h - f h j y J K a m e v I Z l u b k k e _ ^ h \ Z g b c f h j k d b
s b o > Z e v g _] h < h k l - h d Z]] < G , B F I H k d [M e l n i k o v V . V . 2001. Beluga Whale of the Sea of
Okhotsk. Pp. 5-58 in Research work on marine mammals in the North Pacific in 2000. VNIRO, Moscow
R i Z d h < , W g ^ j x k > , = e Z a h F . , E b l h \ c . Z , O h [[k D , F m o z f _ E F 2010. K _ a h g g u _ f b] j Z p
h o h l h f h j k d h c [_ e m o b ' H O S K L Q D S W H U X V Z O n h j * B D M e k d l r g i e] h g b k y Z o Z l e b e k h
36(1): 5662 [Shpak O.V., Andrews R.D., Glazov D.M., Litovka D.I., Hobbs R.C., Mukhametov L.M. 2010.
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Y a u d h F . Z , F _ s _ j k d B e , R i Z d h < , = e Z a h F . , E b l h \ c . Z , ; h j b k h ? Z . , J h ` g h a < 2012.
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Litovka D.I., Borisova E.A., Rozhnov V.V. 2012. Molecular genetic analysis of Sakhalin and Shantar be
J D ¶ ' H O S K L Q D S W H U X V O n h X F i e V O k h o t s k S e a H T H i s B o o k U H J D
Pritchard J.K., Stephens M., Donnelly P. 2000. Inference of population structure using multilocus genotype da
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Rosel P.E. 2003. PCR-based sex determination in Odontocete cetaceans.. Genetics 4: 647-649.