

## 5604 Patterns of Beluga Whale Distribution in the Okhotsk Sea: As Shown by Genetic Analysis

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Belugas (*Delphinapterus leucas*) living in Bering, Chukchi and Beaufort Seas are strongly philopatric to their summering areas, but are believed to share a single gene pool presumably mating on common winter grounds or during seasonal migration in spring (Brown Gladden et al., 1999; O'Corry-Crowe et al., 1997, 2010). Also, the groups known to occupy the same summering area may consist of animals of distant phylogenetic lineages, which suggests that the pattern of spatial distribution is recent compared to phylogenetic structure of the species in the region. Belugas occupying the Okhotsk Sea are isolated of the main range and seem to have more complicated population structure. Whales that spend summers in Sakhalinsky Bay and off the Western coast of Kamchatka with almost no exception belong to two distant mitochondrial lineages, and each lineage is presented by a set of related haplotypes of a high diversity in each of the two regions. In the Shantar region (western part of the Okhotsk Sea) both lineages are present, but the diversity of each one is reduced and presented mainly by the most common in the two other regions haplotypes. At the same time, analysis of recombining part of genome has shown that belugas summering in the Shantar region and in Sakhalinsky Bay belong (as separate genetic units) to one population, whereas the whales found off the western Kamchatka coast are notably isolated. Thus, the Okhotsk Sea belugas have more evident phylogeographic structure than belugas from Bering, Chukchi and Beaufort Seas.