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The Quaternary of the Urals: Global trends and Pan-European Quaternary records

**Четвертичный период Урала:
глобальные тенденции и их отражение
в общеевропейской четвертичной летописи**

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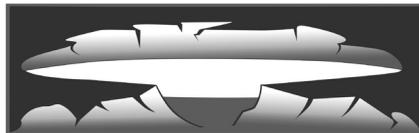
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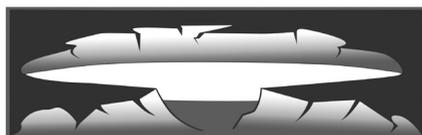
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МЕЖДУНАРОДНЫЙ СОЮЗ ПО ИЗУЧЕНИЮ ЧЕТВЕРТИЧНОГО ПЕРИОДА
СЕКЦИЯ ЕВРОПЕЙСКОЙ ЧЕТВЕРТИЧНОЙ СТРАТИГРАФИИ
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ИНСТИТУТ ЕСТЕСТВЕННЫХ НАУК

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GENETIC VARIABILITY OF BURBOT, *LOTA LOTA*, AND THE CONNECTION OF THE MAIN HOLARCTIC RIVER BASINS IN THE QUATERNARY

Key words: Lota lota, mtDNA control region, climate change, Ob River, Irtysh River

Climatic oscillations during the Pleistocene ice ages affected species' geographical distribution and abundance, which could be expected to have genetic consequences (Hewitt, 2004). Burbot (*Lota lota*, Linneus, 1758), the Holarctic freshwater gadoid, was restricted within glacial refugia peripheral to the ice sheets and depended on aquatic habitats during post-glacial dispersal, and, therefore, serves as an excellent model to study the impact of glaciations. The distribution of burbot mitochondrial haplotypes, revealed in previous studies, suggests that Western Siberia most likely was a transit region, through which burbot could spread from Europe to Siberia during the post-glacial period (Van Houdt et al., 2005). Previously, it was suggested that the distribution of burbot in Siberian rivers began after the Dneprovsk glaciation dated to 300,000–250,000 BP (Svetovidov, 1948; Tyulpanov, 1967). Indeed, paleontological data points to the importance of Western Siberia as one of the key regions in the formation of Eurasian biota during the Quaternary period (Borodin et al., 2001; Borodin et al., 2013). Importantly, the finding of burbot ancient bones at Chembackchino-94A (lower reach of Irtysh River, TL age — 650,000±110,000 years) (Borodin et al., 1998) is one of the oldest findings ever made in Eurasia. This therefore indicates that the Ob-Irtysh River basin could play much more important role in the formation of *Lota* biodiversity compared to the mere extrapolation of genetic data, obtained for the localities in Eurasia and North America.

The objective of the present study was to determine the diversity of the non-coding mtDNA control region among burbot populations inhabiting Western Siberia.

The left half of the mtDNA control region was sequenced for 116 burbot samples from several localities of the Ob-Irtysh River basin including the Irtysh River at Tobolsk, Severnaya Sosva, Voykar, Sob, Khodyta (tributaries of the Ob River), the Taz River and the Ob River at Karantinskiy island. Sequencing has revealed that the mtDNA control region is highly variable in this species. Indeed,

28 haplotypes were observed in the 116 individuals analyzed. Fig. 1 represents median joining network covering burbot control region haplotypes from two lineages, *L. l. lota* and *L. l. maculosa*, together with sequences, derived from the Western Siberian localities. Most of the control region haplotypes, revealed in the Ob-Irtysh River basin, fall into Eurasian and Beringian haplogroups. Our data show that 78 out of 116 control region sequences represent haplotypes, revealed earlier, such as EB30, EB35, EB43, EB44 and EB41 (Van Houdt et al., 2005). Not surprisingly, the majority of samples belong to the EB30 haplotype (55 samples), which is one of the central Eurasian haplotypes and the habitat of which covers not only European (the Isar, the Vistula), but also Asian (the Lena) rivers, as well as Lake Baikal. The ratio of this haplotype is 47%. Besides, 11 samples have Beringian haplotype EB41, which is found in the Kurenjoki and Porkkala Bay in Finland. This haplotype, also named as Xi1, was observed in large quantities in the Irtysh River in the North-Western China (Fang et al., 2013). 21 new haplotypes from the Ob-Irtysh River basin were named as WS 1–21 (Western Siberian). Among 21 new haplotypes, WS1, is the most widely distributed and was found in samples from the Sob River (3 sequences) and the Irtysh River at Tobolsk (4 sequences). This haplotype, together with its derivative haplotypes, WS2, WS3 and WS21, form a separate haplogroup. 17 sequences demonstrated singular haplotypes. The distribution of separate haplogroups coincides with major river basins (Fig. A5, Appendix 4). It is best shown for the haplotypes from the Mississippi, Missouri and Amur. However, also in Eurasia and Alaska a group of haplotypes are specifically found only in separate river basins, which reflects the Quaternary history of the species.

Our data indicate that studies on burbot phylogeography are incomplete and require further research, focused on genetic analyses of burbot inhabiting central part of Eurasia, in particular the Western Siberian Plain and the Eastern European Plain.

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