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MAPEEG-2015

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ABSTRACTS

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MODERN ACHIEVEMENTS IN
POPULATION, EVOLUTIONARY AND
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**THE ARCTIC CHAR (*SALVELINUS ALPINUS*) FROM THE POLAR URALS
AND ITS POSITION IN THE SPECIES PHYLOGEOGRAPHIC STRUCTURE**

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First data on the mitochondrial DNA (mtDNA) variability in the Arctic char (*Salvelinus alpinus*) from the Polar Urals are presented. MtDNA sequences (507 bp of the control region) were obtained from 18 individuals from two localities: Bolshoe Shuchye Lake and Bolshaya Hadata River. We describe four unique haplotypes of the mtDNA control region, and compare the original data (18 sequences) with the data reported in previous mtDNA studies (92 sequences) (Brunner et. al., 2001; Alekseyev et al., 2009).

Our results show that the previously described Atlantic and Siberian mitochondrial groups (Brunner et. al., 2001) are not separated from each other. Moreover, they do not represent different sub-groups in the Eurasian group as it was proposed by Alekseyev et al. (2009). We show that there is one Atlantic-Siberian supergroup, which has high genetic diversity. In the Brunner's work (2001) Atlantic and Siberian groups were separated from each other because the data were collected from the distant regions (from the western and eastern borders of the Atlantic-Siberian supergroup range). We show that the differences between these groups decrease after adding the data from some new regions such as the high Arctic Archipelago of Svalbard, Taimyr Peninsula (Alekseyev et al., 2009) and the Polar Urals (our data). Our results show that the major part of the Northern Eurasia and possibly the seas of the Arctic Ocean, are inhabited by one Atlantic-Siberian mitochondrial supergroup of the Arctic char.