

Original article

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Data on Variability of Nuclear Ribosomal DNA ITS 1–2 Markers of *Betula turkestanica*, *B. tianschanica*, *B. procurva*

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Abstract. The article includes preliminary results of nuclear ribosomal DNA ITS 1–2 region analysis of *Betula turkestanica* Litv., *Betula tianschanica* Rupr., *Betula procurva* Litv. implemented for clarification of taxonomic status, phylogenetic relationship and origin of these birch species. The range of *B. procurva*, *B. turkestanica*, *B. tianschanica*, is confined to the mountain system in southeast Central Asia (Pamir-Altai). *B. procurva* has a disjunctive range and is also found isolated from the main range in the mountainous part of the Urals (boreal forests zone and the Trans-Ural forest-steppe). These birch species have morphological features of *B. microphylla* Bunge and *B. pendula* Roth, however they also possess distinctive morphological traits. The paper shows the level of differentiation and the distribution of genetic variability between groups of haplotypes, and also provides a genetic network which demonstrates the relationships between the studied samples. Based on the results of genetic analysis, the origin and phylogenetic relationships of *B. procurva*, *B. turkestanica*, *B. tianschanica* are suggested. The resulting haplotype network confirms the hypothesis of a possible common ancestor of *B. procurva*, *B. pendula* from the section *Betula* (white birches) and *B. nana* from the section *Apterocaryon* (dwarf birches). A conclusion is made about the informativity of the ITS 1–2 region of nuclear ribosomal DNA for the differentiation of the studied birch species on the territory of Kyrgyzstan. At the same time, it is emphasized that the highest haplotype diversity is typical for *B. procurva* specimens with divergent position of the sample from the Kurgan region, which indicates the long-term existence of this disjunction.

Key words: *Betula*, ITS-marker, nuclear ribosomal DNA, phylogenetic analyses, taxonomy.

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