

Abstract

Taxonomic Investigations of *Betula obscura* and *B. pendula* var. *carelica* †

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† Presented at the 1st International Electronic Conference on Biological Diversity, Ecology and Evolution, 15–31 March 2021; Available online: <https://bdee2021.sciforum.net/>.

Abstract: Trees and shrubs belonging to the *Betula* L. genus present highly confusing interspecific relationships. The complex evolutionary history of birches may be due to several factors: interspecific gene flow, the independent occurrence of both polyploidy and dwarf forms in different lineages, incidents of major speciation events within a very short time period and different selection pressures in the distant populations of widespread species. We assessed phylogenetic relationships between the uncommon dark-barked *B. obscura* and *B. pendula* var. *carelica* with patterned wood texture and widespread birch tree species: white-barked *B. pendula* and *B. pubescens* as well as dark-barked *B. nigra* and *B. dahurica*, using the internal transcribed spacer ITS1 and ITS2 regions of nuclear ribosomal DNA, nuclear ADH (alcohol dehydrogenase) gene sequences and AFLPs (amplified fragment length polymorphisms). In the phylogenetic trees based on the ITS and ADH gene sequences, *B. pendula* var. *carelica* and *B. obscura* clustered with *B. pendula*, but were distinct from *B. pubescens*, *B. nigra* and *B. dahurica*. In turn, both clustering and multivariate ordination methods using the AFLPs revealed clear distinctness of *B. obscura* from the remaining species. *Betula pendula* var. *carelica* grouped with *B. pendula* and *B. pubescens* individuals in both AFLP analyses. Values of the leaf morphology indices of *B. obscura* and *B. pendula* var. *carelica* were within the range of *B. pendula* variation. All genetic and morphological analyses confirmed the intraspecific status of *B. pendula* var. *carelica*. We also suggest that *B. obscura* represent intraspecific variation of *B. pendula*, although discrepancies between nuclear sequences and AFLP results were noted.

Citation: Jadwiszczak, K.; Bona, A.; Brzeziński, D. Taxonomic Investigations of *Betula obscura* and *B. pendula* var. *carelica*. *Proceedings* **2021**, *68*, x. <https://doi.org/10.3390/xxxxx>

Published: date

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