

# Glacial and postglacial history of *Betula humilis* in Poland and Belarus

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## Introduction:

There are four *Betula* species in Europe: *B. pendula*, *B. pubescens*, *B. humilis* and *B. nana*. *B. pendula* and *B. pubescens* are common tall trees inhabiting almost entire area of the continent. *B. humilis* and *B. nana* are boreal species; hence, they are more northerly distributed. Tree birches are generally ubiquitous species. *B. nana* occupies raised bogs. *B. humilis* populates natural and drained fens and transitional mires. *B. humilis* and *B. nana* are glacial relicts in central and western Europe, and decay of their populations has provoked governments to strict protection.

Shrub birch *Betula humilis* Schrk. reaches the south-western border of its continuous range in Poland, but remnant populations localised in the Alps, the Carpathians, and in northern Germany strongly suggest that the species had been more widespread in the past (Hultén and Fries 1986, Zaluski et al. 2001). Macrofossil record of *B. humilis* is rather scarce and the pollen is included into *Betula nana* type; hence, it is very difficult to describe the glacial and postglacial history of the plant using solely palaeobotanical data. The present study reveals glacial and postglacial history of *B. humilis* inferred from molecular markers.



## Aims:

- 1) To test a hypothesis of the *B. humilis* glacial refugium in south-eastern Poland,
- 2) To discuss reasons of a high genetic variation in north-eastern Poland,
- 3) To describe potential routes of Holocene recolonisation

## Methods:

Studies were carried out in 26 populations of *B. humilis* in Poland and Belarus. The PCR-RFLP method was used to analyse chloroplast (cp) DNA diversity. Three non-coding cpDNA regions (*trnT-trnF*, *psaA-trnS*, *trnC-trnD*; Taberlet et al. 1991, Demesure et al. 1995) were screened for possible variation. Diversity and differentiation parameters ( $h_s$  - the average intra-population gene diversity,  $h_T$  - the total diversity,  $G_{ST}$  - the differentiation for unordered alleles and  $v_s$ ,  $v_T$  and  $N_{ST}$ , the corresponding parameters for ordered alleles) were estimated in northern, north-eastern and south-eastern Poland as well as in Belarus according to Pons and Petit (1996) using Permut software.

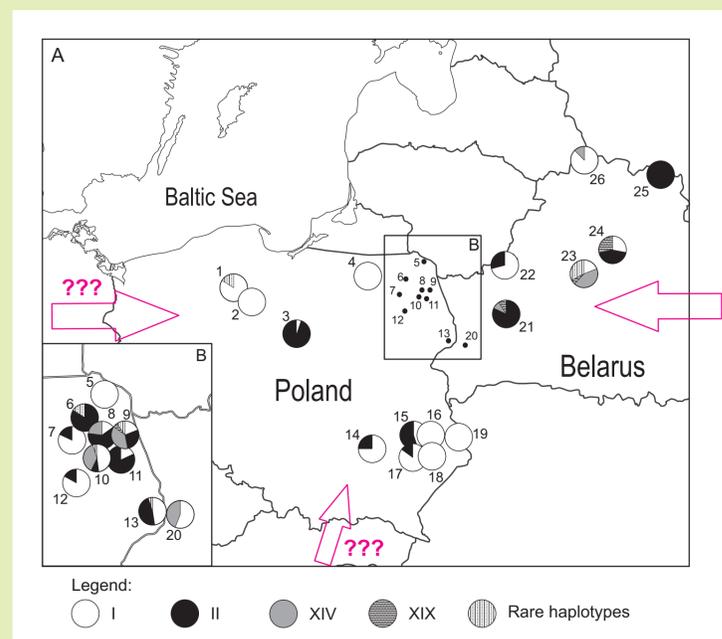


Fig. Distribution of cpDNA haplotypes of *B. humilis* in Poland and Belarus. A) whole study area, B) enlarged area of north-eastern Poland. Arrows show possible routes of postglacial recolonisation.

Region of study	Levels of population subdivision					
	unordered alleles			ordered alleles		
	$h_s$	$h_T$	$G_{ST}$	$v_s$	$v_T$	$N_{ST}$
N Poland	0.133±0.09	0.689±0.18	0.807±0.16	0.057±0.03	0.725±0.25	0.922±NC (*)
NE Poland	0.305±0.14	0.633±0.16	0.518±0.15	0.280±0.13	0.638±0.15	0.561±0.16
SE Poland	0.203±0.10	0.282±0.12	0.281±NC	0.203±0.10	0.282±0.12	0.281±NC
Belarus	0.401±0.17	0.804±0.11	0.502±0.22	0.317±0.14	0.831±0.07	0.619±0.22
Total	0.290±0.07	0.570±0.07	0.492±0.09	0.253±0.06	0.572±0.08	0.559±0.10 (*)

Table. Estimation of parameters of cpDNA diversity for unordered and ordered alleles in *B. humilis* populations.  $h_s$  and  $v_s$  - average intrapopulation diversity,  $h_T$  and  $v_T$  - total diversity,  $G_{ST}$  and  $N_{ST}$  - level of population subdivision of diversity NC - not computed, (\*) - statistically significant lower value of  $G_{ST}$  and  $N_{ST}$ .

## Conclusions:

1. Lack of isolation by distance strongly suggested that *B. humilis* could have survived the Last Glacial Maximum at higher latitudes.
2. Based on low haplotype diversity, a hypothesis of glacial refugium in south-eastern Poland was rejected.
3. Contribution of chloroplast haplotypes showed that the area of Poland and Belarus was populated from at least two disconnected refugia. Most probably one of them was situated in eastern Europe. Subsequent refugium or refugia of the shrub birch could have existed in western Europe and/or in the Carpathians.
4. Chloroplast markers showed high genetic diversity in some populations of *B. humilis* in north-eastern Poland, within the area being in close proximity to the Scandinavian ice-sheet during the LGM. Most probably this phenomenon can be explained in term of admixture zone. It is supported by the high haplotypic richness and the slightly higher value of  $v_T$  than  $h_T$ .

