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Geographical pattern of haplotypic variation in Austrian native stands of *Picea abies*

Abstract: In the present study we analysed the mitochondrial intraspecific variation in natural populations of Norway spruce. We used the second intron of the *nad1* gene, which contains two polymorphic short tandem repeats. Due to the maternal inheritance of mitochondrial DNA in Norway spruce, the spatial distribution of haplotype DNA allows insights into seed dispersal and artificial seed transfer. A total of 504 trees distributed all over Austria were genotyped, and 9 different haplotypes could be found. A geographical map of the haplotype variation pattern of *Picea abies* is presented.

Additional key words: Norway spruce, mitochondrial DNA, biogeography, genetic diversity

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Introduction

Norway spruce (*Picea abies* (L.) Karst.) is the major and economically most important tree species in Austria, prevailing in about 56% of the Austrian forests. However, a part of these forests, mainly at lower elevations, have been cultivated artificially. In the context of gene conservation and for the selection of well-adapted and stable forest reproductive material, the identification of native stands has become an important issue.

The present study aimed at analysing the genetic diversity of native (autochthonous) spruce stands in Austria.

Methods

We analysed the haplotype intraspecific variation with a mitochondrial DNA marker. We used the second intron of the *nad1* gene, which contains two polymorphic short tandem repeats (Sperisen et al. 2001).

Due to the maternal inheritance of mitochondrial DNA in Norway spruce, the spatial distribution of

haplotype DNA indicates gene flow by seeds, and allows insights into natural seed dispersal and artificial seed transfer. The samples were collected in a grid of 4 × 4 km by the National Austrian forest inventory (Österreichische Waldinventur 2000/2002, FBVA, Vienna). We analysed only samples from native spruce stands at high elevations. Because of the inaccessibility of these stands in the alpine regions, it is very likely that they are autochthonous.

Results and discussion

A total of 504 trees were screened, and 9 different haplotypes could be found. The geographical map of the haplotype variation of *Picea abies* shows that one single haplotype dominates nearly the entire alpine region of Austria. Only in the east and southeast we found a greater variation (Fig. 1).

The spatial analysis of molecular variance SAMOVA (Dupanloup et al. 2002) revealed three geographically and genetically homogeneous groups of haplotypes, where haplotype 815 is dominating with a frequency of 85%. The other two more fre-

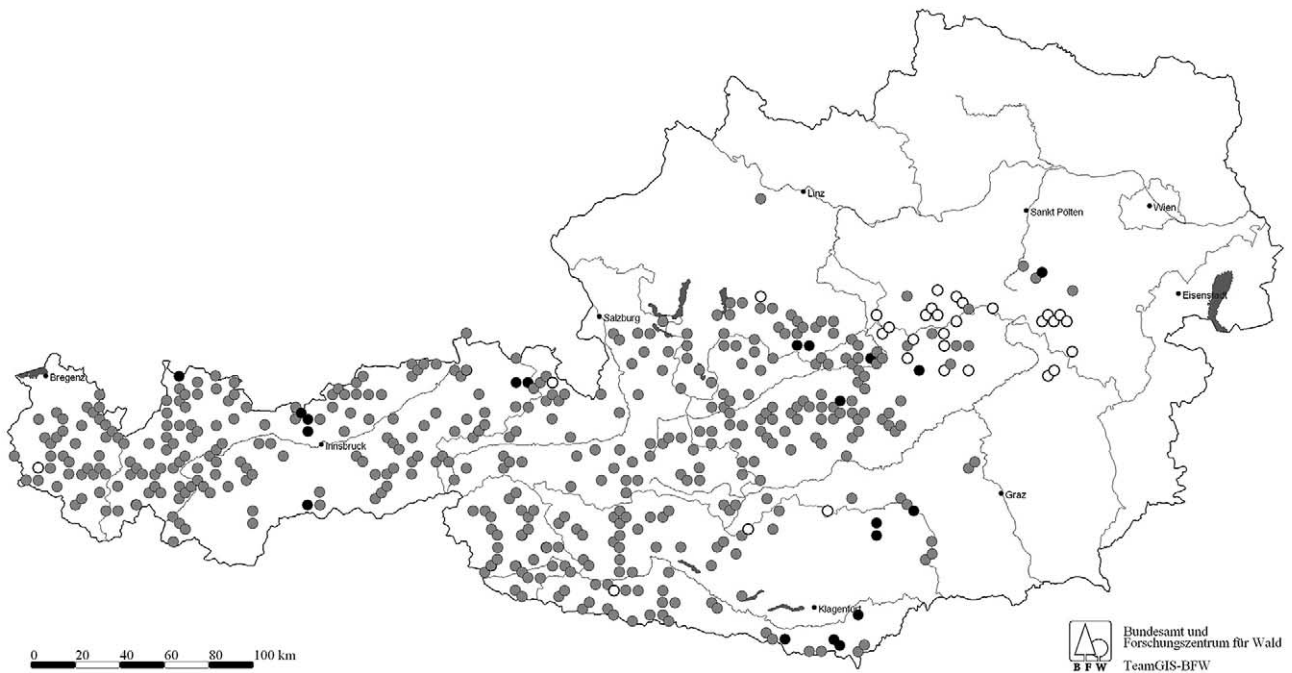


Fig. 1. Geographical map of three most frequent haplotypes of Norway spruce in Austria (black dots – 778bp; grey dots – 815bp; white dots – 842bp)

quent groups are located in areas with widest genetic variation in the east and southeast of the Alps. The higher genetic variation found east and southeast fits the present models of postglacial re-immigration routes from the Balkan and the Carpathian Mountains (Terhürne-Berson 2005).

The obtained map of mitochondrial haplotype variation is the first step to distinguish native autochthonous populations from allochthonous stands, and to identify artificial seed transfer in Austria. However, in its current state, it might only be possible to detect seed transfer if the transferred seeds have another haplotype and in regions where one single haplotype is dominant.

This work will be the basis for further investigations with additional marker systems of allochthonous stands in and beyond the natural range of spruce in Austria.

References

- Dupanloup I., Schneider S., Excoffier L. 2002. A simulated annealing approach to define the genetic structure of populations. *Molecular Ecology* 11: 2571–2581.
- Sperisen C., Büchler U., Gugerli F., Mátyás G., Geburek T., Vendramin G.G. 2001. Tandem repeats in plant mitochondrial genomes: application to the analysis of population differentiation in the conifer Norway spruce. *Molecular Ecology* 10: 257–263.
- Terhürne-Berson R. 2005. Changing distribution patterns of selected conifers in the Quaternary of Europe caused by climatic variations. Rheinische Friedrich-Wilhelms-Universität, Bonn. (Diss.)