

Twenty years German-Russian co-operation for genetic diversity in forests

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Abstract

Since 1994 there is a close cooperation among the forest genetic groups in Grosshansdorf (Germany) and Ufa (Russia). In the beginning of the common research, questions linked to genetic impacts air pollution on forests have been addressed. Then comparative studies on genetic variation and genetic differentiation of trees (oak, pine, larch) and insects (green oak leaf roller) have been conducted. A study of an isolated small pedunculate oak population on the south-eastern edge of the species distribution in the South-Urals brought insights on the extend of long distance pollen flow and a surprisingly high level of genetic diversity of its pest (green oak leaf roller). In the recent years, the work on large scale genetic structure of larch and different white oak species has been a focus. These results find their application for tests on tree species and geographic origin on wood samples and have the purpose to secure the trade of legally harvested timber.

Key words: Genetic diversity, genetic differentiation, green leaf roller, oak, pine, timber tracking

Research topics

Impact of air pollution

In the period from 1980 to 1995, a lot of research has been done on the impact of air pollution on forest ecosystems. One aspect studied was the influence of air pollution on the genetic composition of tree populations and genetic differences among tolerant and sensitive trees (SCHOLZ et al. 1989). In Germany, specific focus has been given to beech, spruce and pine (BERGMANN and SCHOLZ 1987, GEBUREK et al. 1987, IPSEN et al. 1998, MUELLER-STARCK 1985). The main result was – based on allozymes studies – that there was a significant risk in losing genetic diversity due to air pollution and another general finding was that the tolerant trees had higher levels of heterozygosity. Thus, for example, genetic inventories were made in six old beech stands in Germany exposed to long-term air pollution stress, identifying genotypes by paired comparison between tolerant and sensitive trees (MUELLER-STARCK and HATTEMER 1989). In this study, genetic comparisons were also made on germinating seed samples, and on young plants surviving under different stress conditions in the field. All the comparisons gave statistically significant differences for the genetic composition, especially those between germinating seed and surviving young plants. The results revealed losses of genetic variation in the group of sensitive individuals, and confirmed the importance of a high degree of heterozygosity and great genetic diversity for the survival ability of beech populations.

Using isozymes of five polymorphic loci the frequency of mutations and mutation-like events in populations of Scots pine (*Pinus sylvestris* L.) in South Urals (Russia) were studied (BAKHTIYAROVA et al. 1995). The frequency of rare electrophoretic variants of isozymes was shown to be significantly higher in two populations growing under industrial air pollution conditions ($p=5.0 \times 10^{-3}$) and $p=5.2 \times 10^{-3}$) than that of the control (1.6×10^{-4}).

Green oak leaf roller (*Tortrix viridana*)

A geographically isolated population of an herbivorous insect (*Tortrix viridana*, Lepidoptera: Tortricidae) in the Bashkir Transural region and five further populations were investigated for genetic variation using eight microsatellite markers (SCHROEDER et al. 2010). The sample size per population was between 48 and 62 individuals. The genetic variation was higher within the isolated population than within populations in the centre of the distribution area. No bottleneck effects were discovered during analyses that could have formatted the gene pool of this population. Balancing or directed selection toward preservation of specific alleles or higher fitness of heterozygous individuals could be an explanation for the unexpected high genetic diversity within this small and isolated population.

In another study, a total of 401 individuals of the green oak leaf roller from four stands in North Rhine-Westphalia (Western Germany) were examined. In three of four populations, the AFLP markers revealed clearly spatial genetic structure up to 40 m, which can be explained by the mating behaviour within this species (SCHROEDER and DEGEN 2008).

Genetic diversity and differentiation of oaks

The large scale genetic structure of European white oaks was studied for chloroplast gene markers with samples from more than 2600 populations (PETIT et al. 2002). The observed pattern is the result of the re-colonisation process from different refugia after the last glacial period. The group in Grosshansdorf contributed to this work samples and results for Germany and the Benelux countries (KOENIG et al. 2002). Oak chloroplast DNA (cpDNA) variation was studied in a grid-based inventory in western Central Europe, including Belgium, The Netherlands, Luxembourg, Germany, the Czech Republic, and the northern parts of Upper and Lower Austria. A total of 2155 trees representing 426 populations of *Quercus robur* L. and *Q. petraea* (Matt.) Liebl. were screened for polymorphism in up to four PCR-amplified cpDNA fragments. Eleven haplotypes belonging to four lineages were detected; these lineages were formerly restricted to glacial refugia in the Iberian Peninsula, the Apennine Peninsula and the Balkan Peninsula (Figure 1). The haplotypes originating from the Apennines are particularly well represented in the study region, but there is also a significant contribution from the other refugia, which explain the high overall level of cpDNA diversity. The strong human impact in western Central Europe during the past centuries, which has resulted in the clearance of most forests, was followed by reforestation, sometimes involving seed transfers. Despite this strong human impact, broad geographic patterns of lineages and haplotypes could still be detected.

We studied also material collected in Russia. This material could be clearly genetically separated from the genetic composition in Central Europe. The extent and spatial pattern of genetic variation at polymorphic allozyme loci in a population of pedunculate oak *Quercus robur* from the Bashkir Transural region was investigated using autocorrelation analysis (REDKINA et al. 2008). In the stand examined, statistically significant local concentration of most of the alleles in two-dimensional space was identified. Conservation strategies for this small population located outside of the western border of the species range, in the mountain-steppe habitat, and characterized by specific gene pool, were suggested.

To detect and avoid illegal logging of valuable tree species, identification methods for the origin of timber are necessary. In a German-Russian-US American cooperation project we used next-generation sequencing to identify chloroplast genome regions that differentiate the origin of white oaks from the three continents; Asia, Europe, and North America (SCHROEDER et al. 2016). For details on this see paper of SCHROEDER et al. in these proceedings.

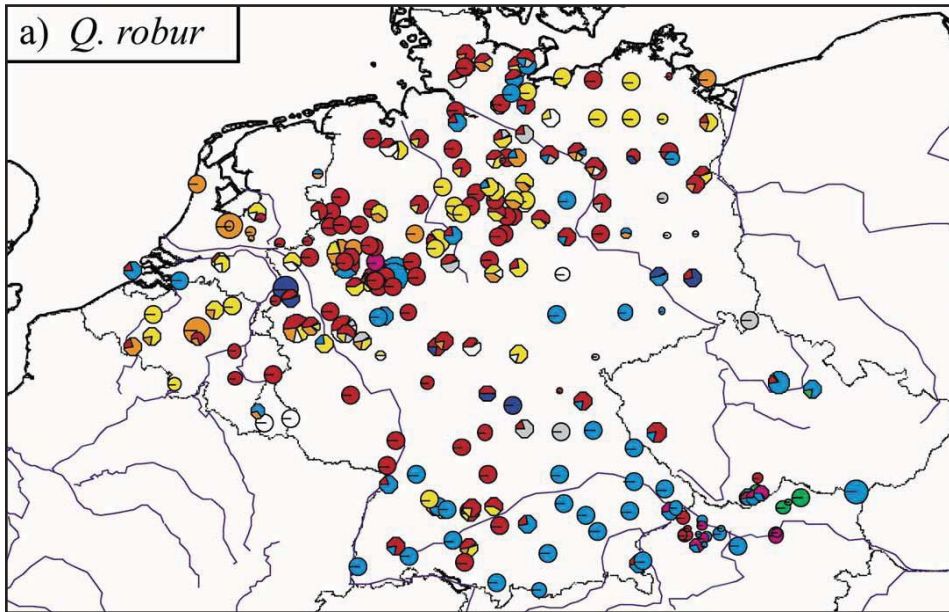


Figure 1: Distribution of chloroplast haplotypes of *Quercus robur* in Central Europe (from KOENIG et al. 2002)

Gene flow

In another German-Russian cooperation study we analysed long-distance pollen-mediated gene flow into an isolated relict stand (Figure 2) consisting of seven individuals of *Quercus robur* based on a total sample of 177 trees and 9 microsatellite loci (BUSCHBOM et al. 2011). We showed that pollen-mediated gene flow across more than 80 km in this wind-pollinated tree species contributed at least 35% of all successful pollinations in the investigated isolated and small oak stand at the eastern limit of the species' distribution. The observed pollen immigration shaped the genetic diversity of acorn progenies in the stand and might explain the comparably high genetic diversity in the persisting adult population.



Figure 2: Isolated pedunculate oak populations studied in the south-east Ural region.

Larix

More than 2000 larch samples have been collected in a transect from Western Europe to Japan. Using RAD sequencing, a large set of SNPs has been developed and the material has been genotyped on more than 250 SNPs. The results enable us to differentiate among six larch species and to check the geographic origin. For more details see the paper of Blanc-Jolivet et al. in these proceedings.

Outlook

Our future cooperation will continue to work on large scale genetic structure of spruce, pine, birch and aspen, with focus in the Western part of Russia. Further, we intend to intensify the technology transfer to the genetic lab of the Bashkiria state university in Ufa.

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