ELSEVIER

Forest Ecology and Management 156 (2002) 1–3

Forest Ecology
and
Management

www.elsevier.com/locate/foreco

Preface

In June 1994, the European Commission organized in Brussels a workshop entitled "Inter- and intraspecific variation in European oaks: evolutionary implications and practical consequences" as a final meeting of a previous EU-supported project on oak genetics under the FOREST program (Kremer and Mühs, 1996). The contributions made at this workshop presented a comprehensive overview of the distribution of genetic variation in the two most important oak species in Europe (sessile oak, *Quercus petraea* and pedunculate oak, *Q. robur*). They clearly outlined the vast amount of diversity existing throughout the natural range, and the contrasting patterns of geographic distribution that was observed between molecular markers and adaptive traits. It was also shown during the meeting that historical impacts could be separated from other evolutionary factors responsible for the distribution of genetic diversity, by analyzing separately chloroplast DNA (cpDNA) polymorphism and nuclear diversity. Since earlier results (Kremer et al., 1991) already indicated that cpDNA diversity exhibited clear-cut differences among oak forests, the construction of a range-wide geographic map of cpDNA polymorphism became feasible. Following the workshop, 13 research institutions decided to submit a proposal to the EU, entitled "Synthetic maps of gene diversity and provenance performance for utilization and conservation of oak genetic resources in Europe" (Project FAIR1 PL95-0297). There were basically two main reasons that motivated the proposal. Fundamental issues as the impact of colonization dynamics on genetic diversity was the first one. Because oaks are long-lived species, there was ongoing debate that oak forests would be far from genetic equilibrium and that their extant distribution of diversity would largely reflect their recent colonization dynamics. The construction of a dense cpDNA geographic map in conjunction with the retrospective description of oak distribution by fossil pollen analysis was intended to reveal the past colonization routes of the species. More applied issues as seed transfer rules was the second reason. Because of irregular flowering, oaks are generally being planted and there was a strong need for developing tools enabling to trace seed movements.

The papers in this edition of *Forest Ecology and Management* summarize the results obtained within the frame of this project. To our knowledge, this was the first attempt to construct synthetic range-wide maps of genetic diversity. There were a number of technical reasons that indicated that the goal could be achieved. First, as already indicated, it was known that cpDNA was highly differentiated among oak forests based on earlier investigations. Second, theoretical investigations have also shown that cpDNA was not only differentiated among populations, but was almost fixed within forests (Petit et al., 1993). Third, rapid molecular screening methods were available (Demesure et al., 1995) for large-scale analysis. Based on this background information, it was predicted that cpDNA diversity could be monitored in several hundreds of forests throughout Europe. The project started in 1996 with an expectation of 1200 forests to be analyzed. The planning for the construction of the map was to genotype all populations existing in provenances tests installed in Europe (500 populations) and then in a second step to complete the sampling by a systematic collection of populations based on a grid system (700 populations). Finally, the project ended with the molecular screening of 2613 forests. On average, this sampling strategy represents one sample population every 40–50 km throughout the natural range of white oaks in Europe. During the course of the project, other groups joined the program and bilateral cooperation between western and eastern Europe permitted to extend the maps beyond the limits imposed by the administrative constraints of the EU research project. Overall, joint efforts of 16 laboratories permitted to inventory cpDNA diversity in

PII: S0378-1127(01)00647-8

eight related white oak species (*Q. robur, Q. petraea, Q. pubescens, Q. frainetto, Q. faginea, Q. pyrenaica, Q. canariensis* and *Q. macranthera*) throughout Europe, with the exception of southern Balkans. But there are ongoing efforts to complete the survey. There were, however, a number of technical difficulties to achieve the goal. Standardization of protocols and identification of additional molecular variants were the major obstacles. A common strategy for molecular screening, based on restriction analysis of four PCR-amplified cpDNA fragments, was used to allow comparison among the different studies. A major achievement of this project was the comparative analysis of genetic data and palynological data on a range-wide scale. Geographic maps of oak fossil pollen deposits were constructed at 500-year-intervals between 15,000 and 6000BP throughout Europe. These maps are based on 600 pollen sequences available from the European pollen database (EPD, 483 sequences), the alpine palynological database (ALPADABA, 50 sequences) and about 70 sequences supplied for use in the project or digitized from published pollen diagrams. This was intended to identify post-glacial migration routes and colonization dynamics.

This Special Issue of *Forest Ecology and Management* is subdivided into two major parts. The first four papers aim at a synthesis of the results at the continental scale. Range-wide patterns of cpDNA diversity and fossil deposits are described. The eight subsequent papers concentrate on the regional distribution of cpDNA diversity by addressing specific regional issues. Results obtained within the frame of this project encompass the original expectations and suggest additional benefits not only for foresters, but also for managers, ecologists, paleobotanists, geneticists and historians.

Past and future colonization dynamics in Europe. The geographic distribution of the cpDNA polymorphism together with maps of fossil pollen deposits have allowed to localize refugial zones and retrace the post-glacial recolonization routes. Because oaks are carrier species in European forest ecosystem, the identification of their post-glacial recolonization routes may have further implication on the distribution and diversity of other plant or animal species associated to the oak ecosystems. Furthermore, the recolonization dynamics that were identified in this project can be considered as indicators of future migration movements of oaks as a result of climatic changes. Certainly, the large data set that was accumulated in the course on this project could be used to validate simulations of migration dynamics under various climatic changes.

Geographic distribution of diversity and conservation issues. The fine scale map provides basic data on where genetic diversity has been concentrated, or built-up. Clearly, the southern European regions (Iberian and Italian peninsula, Balkan regions) were confirmed as hot spots of diversity. There were, in addition, other European zones, where different maternal lineages merged which also exhibited high levels of diversity. These results need further to be compared with diversity estimates of other traits, in order do draw conclusions on conservation strategies at a range-wide scale.

Retrospective identification of historical seed transfer in oaks. Historically, oaks have been transferred over long distances in Europe, in particular from Eastern and Southern countries to Western countries and this is still going on today on a minor scale. In most countries, the present oak forest is, therefore, a mixture of predominantly native and exotic materials. In most cases, the existing archives do not permit the historical origin of the seed source to be identified. The maps that were constructed within the frame of this project were based on collections made in stands of presumably natural origin. They can, therefore, be considered as "reference genetic structure" that built up during natural post-glacial colonization. Hence, these maps will allow any population of "unknown origin" to be assigned to an alien or a local source. This information will be highly valuable for oak decline surveys and ecological studies, since sensitivity to dieback or diseases may result from the non-native origin of the stand.

Traceability in forestry. European regulation on the use of reproductive material recommend that collections for plantations should be based on stock which is of local origin. Long distance seed transfer may lead to adaptation problems of the introduced material. The verification of the geographic origin of a seed lot (or a seedling bench in a nursery) is based today on official documents. The synthetic map of cpDNA haplotypes can be considered as a tool to check the origin. In most cases, the strict identification of the geographic origin is not possible, but the comparisons of the cpDNA fingerprint of the seed lot to the reference map will certainly allow the exclusion of certain geographic regions as putative origins.

The overall objective of European Union research programs in the field of forestry is to support the protection, conservation and sustainable management of European forestry resources. Forest biodiversity is a central element of this overall strategy to which substantial research efforts have been devoted over the last years. The different papers presented in this edition are an excellent example of the research activities carried out in this area at EU level and demonstrate also the exciting possibilities that recent developments in molecular biology offer in the study of the genetic diversity of forest tree species.

References

Demesure, B., Sodzi, N., Petit, R.J., 1995. A set of universal primers for amplification of polymorphic noncoding regions of mitochondrial and chloroplast DNA in plants. Mol. Ecol. 4, 129–131.

Kremer, A., Petit, R., Zanetto, A., Fougère, V., Ducousso, A., Wagner, D., Chauvin, C., 1991. Nuclear and organelle gene diversity in *Quercus robur* and *Quercus petraea*. In: Müller-Starck, G., Ziehe, M. (Eds.), Genetic Variation in European Populations of Forest Trees. Sauerländer's Verlag, pp. 141–166.

Kremer, A., Mühs, H. (Eds.), 1996. Proceedings of the Workshop on Inter and Intra-specific Variation in European Oaks: Evolutionary Implications and Practical Consequences, Brussels, June 15–16, 1994. European Commission, Directorate General XII, EUR 16717 EN, 373 pp.

Petit, R.J., Kremer, A., Wagner, D.B., 1993. Finite island model for organelle and nuclear genes in plants. Heredity 71, 630–641.

Antoine Kremer*
Institut National de la Recherche Agronomique
Station de Recherches Forestières
BP 45, 33611 Gazinet Cedex, France

Xabier Goenaga
Directorate General for Research
European Commission, Rue de la Loi 200
1049-Brussels, Belgium

*Corresponding editor. Tel.: +33-5-5797-9074
fax: +33-5-5797-9088
E-mail address: antoine.kremer@pierroton.inra.fr
(A. Kremer)