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ORIGINAL ARTICLE

## Assessment of genetic diversity in two-species oak seed stands and their progeny populations

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### Abstract

In this article, we examined the effects of the two modes of regeneration (natural *vs.* artificial) on the genetic diversity of *Quercus robur* (L.) and *Quercus petraea* (Matt.) Liebl. populations. Using nuclear microsatellite markers, we investigated the genetic diversity of two-species oak seed stands (Jamy and Legnica, Poland) and their progeny – naturally regenerated stands and progeny plantations. A statistically significant excess of homozygotes was noted for all progeny plantations, but the naturally regenerated populations were in Hardy–Weinberg equilibrium. On average, gene diversity in the five progeny plantations from Jamy decreased on average 3.73% and increased 1.26% in plantations from Legnica. However, almost in all plantations from both stands statistically significant excess of homozygotes was noted, and natural regenerations were in Hardy–Weinberg equilibrium. Additionally, the effective population size was several fold higher for naturally regenerated stands compared with progeny plantations. Impact of regeneration mode and potential hybridisation in modelling the level of genetic diversity of progeny populations are discussed.

**Keywords:** *Genetic diversity, microsatellites, natural regeneration, progeny plantations, white oaks.*

### Introduction

Silvicultural techniques are a considerable driving force of alterations in the forests genetic resources (Savolainen & Kärkkäinen, 1992; Finkeldey & Ziehe, 2004; Bürgi & Schuler, 2003; Lefèvre, 2004; Hosius et al., 2006). With regard to clonal forestry and breeding programmes, changes in the genetic structure of populations are obvious but the consequences of routine management practices may be unknown. Meanwhile, one must be aware of the possible genetic changes related with various management practices due to the threat of the loss of genetic diversity (Ståhl & Koski, 2000; Bradshaw, 2004).

Yet, the extent and distribution of genetic diversity are preconditions for the adaptation that determines the long-term stability of individual species and entire ecosystems (Vellend & Geber, 2005). From an economic perspective, the loss of genetic diversity in species reduces the prospects for future selection and breeding of the ideal forest resources for timber and other forest products (Rajora & Mosseler,

2001). To meet future demands, the consequences of anthropogenic changes in managed populations of forest trees must be monitored to prevent over-exploitation and to establish rules on the rational use of available resources. The answer to these needs is the rising number of national and international networks, programmes, and strategies for the conservation and rational use of forest genetic resources that has been launched (Matras et al., 1993; Koski et al., 1997; Sigaud et al., 2000; Icggen et al., 2006; Anonymous, 2009).

In addition to their importance for production, forests are the main reservoir of biodiversity in Poland (Czerepko et al., 2008). Thus, one needs to accept that forest ecosystem biodiversity should affect the silvicultural regimes that are used in forests. In the face of global environmental changes, concerns over the maintenance of reservoirs of genetic variability have attracted special attention by modern forestry and environmental policy in Poland. Guidelines for the conservation of major forest tree species – outlined in “The programme for the conservation of the forest genetic resources and