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ARTICLE

Small-scale variability in phenological, leaf morphological properties and isoenzyme pattern of sessile oak complex (Lepidobalanus sub-genus) in a sessile oak-Turkey oak forest stand

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ABSTRACT In this work small-scale variation of leaf morphological, phenological and isoenzyme pattern was investigated win trees belonging to the Lepidobalanus sub-genus in a sessile oak-Turkey oak stand in order to make an exact taxonomic identification for further studies on physiological tolerance to climatic fluctuations. Classification functions based on leaf morphological traits suggest that most of the trees belongs to *Q. petraea*, but the introgression effects of *Q. dalechampii* and *Q. polycarpa* is also significant in the forest stand which might favour the drought tolerance in these groups of trees. Two representatives (*Q. pubescens, Q. virgiliana)* of Lanuginosae series are also present in the forest stand. The maximum difference in budburst time was two weeks among the trees. Representatives of Lanuginosae series can be described by late budburst. The isoenzyme analysis did not reveal taxon-specific allels, but some loci exhibited considerable differences in the frequency of allels among the different series and budburst groups. **Acta Biol Szeged 52(1):221-223 (2008)**

KEY WORDS

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In several European countries there are efforts to put oak species in the focus of the nature friendly forest magament practice in the future. It is an especially important issue in Hungary where the potential cover of the largest distributed forest communities, sessile oak-Turkey forests (Quercetum-petraeae-cerris) amounts to 19%. Gradual drying in climate of habitats of these forests has been reported within the past decades which greatly contributed to the large-scale decline of sessile oak (Jakucs et al. 1986; Mészáros et al. 1993). Climate scenarios suggest the strengthening of this tendency and consequent deterioration of sessile oak stands and decrease in potential forested area of our country (Mátyás and Czimber 2004). Since the present sylvicutural practice make decisions on selection of oak species and ecotypes for reforestation which influence the future tree species composition of our forests it should consider all available information on climatic sensitivity of different oak taxa including the results of ecophysiological studies on differencies in climate tolerance. The taxonomic uncertainity of identification of most oak species occurring in Hungary makes the selection difficult since the lack of reproductive isolation results in diverse hybridisation among different oak taxa which may influence the adaptation ability to changing habitat conditions.

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Oak species of Lepidobalanus sub-genus occurring in Hungary are categorised into three series (Schwarz 1936): Pedunculatae: *Q. robur*; Sessiliflorae: *Q. petraea*, *Q. dalechampii*, *Q. polycarpa*; Lanuginosae: *Q. pubescens*, *Q. virgiliana.* Some authors describe *Q. delaschampii* and *Q. polycarpa* as subspecies of *Q. petraea*, while others categorize *Q. virgiliana* as subspecies of *Q. pubescens*. Beside the different approaches there are differences in the area of distribution which indicate variation of requirements for habitat conditions. In West-Europe in addition to *Quercus robur*, *Quercus petraea* s.str., and *Quercus pubescens* s.str. are present. The area of *Q. delaschampii*, *Q. polycarpa* and *Q. virgiliana* shows a South-East European distribution but at the Northern and North-Western border they reach the Carpathian Basin too. Therefore in Hungary the effects of latter ones should also be considered (Mátyás 1967). Identification of individual taxa and intermediate forms involves many difficulties. Although there have been many trials, genetic identification has seemed impossible so far, since species-specific markers has not been found. Since leaf at least some leaf traits exhibit intermediate inheritance, leaf morphological studies may offer the most valuable results for the identification (Borovics 2000). In this work the small-scale variation of leaf morphological, phenological and isoenzyme pattern was investigated in trees representing the Lepidobalanus sub-

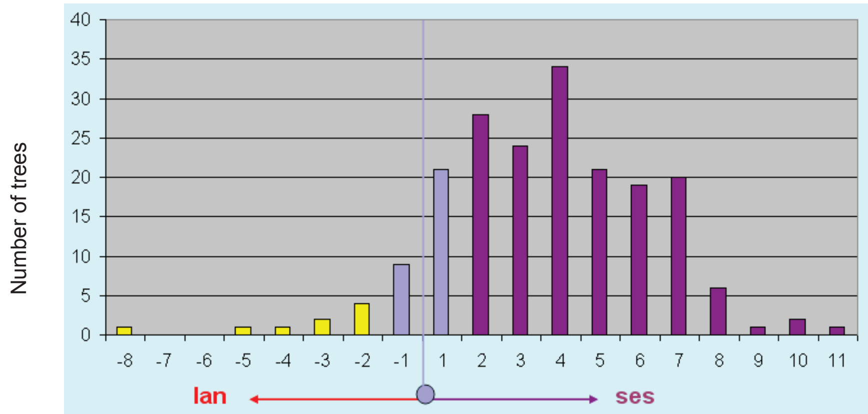

Figure 1. Distribution of trees on the basis of dominance of Sessiflorae (ses) – Lanuginosae (lan) leaf morphological traits.

genus in a sessile oak-Turkey oak stand. The main objective was to study the applicability of these parameters for taxonomic identification and to reveal the relative dominance of different taxa within the forest stand.

Materials and Methods

The studies were performed in the Síkfőkút Research Site, Bükk-Mountains, N-Hungarian Central Range. The site is covered by a 90-95 year old sessile oak-Turkey oak forest (Jakucs 1985). Field observations and samplings were made in an area of one hectare where the position of every tree is mapped and health conditions of trees are continuously registered.

In leaf morphological studies numeric taxonomic method was used which was introduced by Borovics (2000). After the full leaf development 5- 5 leaves were collected from shade layer of 198 trees, each identified earlier as *Quercus petraea*. In the analysis altogether means of 16 measured and derived traits of leaves were used in the Borovics' classification functions worked out for each taxon to identify the taxonomic position of every tree. Classification was performed in two steps: first trees were grouped into series, and then into species.

Phenological surveys were carried out during budburst of trees in 2003, 2004 and 2007. On the basis of budburst time three groups have been distinguished: group with early budburst, group with late budburst and group with intermediate budburst time.

Before budburst bud samples were collected from the canopy of 151 trees. Isoenzyme analysis involved 10 loci (AAT-B: Aszpartát-amino-transzferáz EC 2.6.1.1, ADH-A: Alkohol-dehidrogenáz , AP-A és AP-B: Leucin-aminopeptidáz EC 3.4.11.1, EST-A: Észteráz, IDH-B: Izocitrát-dehidrogenáz EC 1.1.1.42, MNR-A: Menadion-reduktáz EC 1.6.99.2, PGI-B: Foszfo-glükóz-izomeráz EC 5.3.1.9, PGM-A: Foszfo-glüko-mutáz EC 2.7.5.1, SKDH-A: Sikimát-dehidrogenáz EC 1.1.1.25) and were performed by gel electrophoresis after Müller-Starck and Ziehe (1991).

Table 1. Percentage distribution of trees among taxa distinguished by classification functions on the basis of leaf morphological traits.

Taxon	Relative number of trees %
Q. petraea s. str.	70,2
Q. dalechampii	0
Q. polycarpa	1,0
Q. pubescens s. str.	4,0
Q. virgiliana	2,5
pet-dal hibrid	5,1
pet-pol hibrid	2,5
pet-pub hibrid	5,6
pet-vir hibrid	7,1
vir-pub hibrid	2

Results and Discussion

Classification functions based on leaf morphology revealed an uneven distribution of trees among the three series: series of Sessiliflorae 79,8%, series of Lanuginosae 4,5%, Sesssiliflorae- Lanuginosae hibrid 15,7%. There are no trees with the effects of Pedunculatae series (*Q. robur*) in the forest and most of the trees belong to Sessiliflorae series. More exact distribution can be observed when the individuals are analysed on the basis of dominance of Sessiliflorae-Lanuginosae traits (Fig. 1). The whole stand is strongly dominated by Sessiliflorae traits.

When classification functions analysing the species were used most of the trees are grouped into *Quercus petraea* taxon but further species of the Sessiliflorae and Lanuginosae series are also represented in stand with the exception of *Q. dalechampii* (Table 1).

Comparisons of phenological groups and taxonomical groups it was found that trees of Lanuginosae series generally exhibit budburst later than representatives of Sessiliflorae.

Some enzyme loci (MNR-A, SKDH-A, EST-A) exhibited interesting regularity. All of the 10 enzyme loci can be considered polimorph. The dominance of main allel is 71%, although the distrbution among loci is heterogenous and amonting from 46 to 92%. Mean of the effective number of allels is 1,86. The fixation index suggests a strong lack of heterosigocy in half of the studied enzyme loci (ADH-A, AP.A, AP-B, MNR-A, PGM-A) which reflects selection pressure possibly occurring during the sprouting after clear-cutting of the former mature stand or during the oak decline starting in the 80'ies. There are not significant genetic distances among the three budburst groups, although the group of trees with early budburst separated clearly from the other two groups. This is mainly attributed to three enzyme loci (MNR-A, PGM-A, EST-A). These results and comparative ecophysiological measurements on the distinguished taxa can provide information for selection of sylvicultural reproductive materials used in future deforestation.

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