

ORIGINAL PAPER

Assessing the growth of pedunculate oak trees from Polish provenances and families on the 'Chrostowa II' experimental trial after 22 years

Jacek Banach[✉], Patrycja Bongilaj

Department of Ecology and Silviculture, Faculty of Forestry, University of Agriculture in Krakow, Al. 29 Listopada 46, 31-425, Krakow, Poland

ABSTRACT

Studies were conducted on the progeny of pedunculate oak trees at an experimental trial located in the Brzesko Forest District in southern Poland. The study aimed to compare the adaptability of oak trees from 58 different trees, grown in five provenances across Poland, to new environmental conditions after being transplanted to the experimental trial situated in the Carpathian Foothills. The height and breast height diameter of the trees and calculated their slenderness quotient and basal area were measured. The research determined the range of interprovenance and intraprovenance variability and established the provenance and family heritability for each trait. The results showed that oak trees from the Krotoszyn provenance in the Kalisz Highlands had the highest values for growth traits such as height, breast height, and basal area, while the oaks of the Młynary-1 and Młynary-2 provenances from the northern part of the country had the lowest values. The provenance had a significant effect on the variation in height, breast height diameter, and basal area of the pedunculate oak. Moreover, the family had a significant effect on the latter two traits. The study also revealed that almost all oaks growing in the experimental trial had good stability, as indicated by their slenderness coefficient. The provenance heritability for all traits ranged from 0.80 for height to 0.21 for slenderness quotient. Meanwhile, the family heritability was slightly lower, ranging from 0.15 for tree height to 0.60 for the basal area. These high heritability values demonstrate the potential for the effective selection of oak trees at the provenance and family levels.

KEY WORDS

basal area, breast height diameter, height, heritability, *Quercus robur*

Introduction

The primary objective of forest management is to breed stands with desirable phenotypic properties and to achieve this, the results of selection work are used to identify the most valuable genotypes. These genotypes can provide higher stand resistance and improve the quality and productivity of the stand in the future (Barzdajn, 2008, 2009). It is essential to promote deciduous species such as oaks to reduce the proportion of coniferous species, but populations with verified breeding values must be used to minimize the negative effects of using untested regeneration material (Barzdajn and Bruder, 2018).

[✉]e-mail: jacek.banach@urk.edu.pl

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Provenance, family, or provenance-family experiments are the primary method of identifying intraspecific variation in forest trees. These experiments periodically evaluate the progeny value of partial populations or individual trees based on the analysis of various traits, with a focus on the variability and heritability of economically important characteristics such as conformation, phenology, resistance, and growth. Provenance-family studies can provide a better understanding of the extent of interpopulation and intrapopulation variability in a species, enabling the selection of the best families and populations for use in improving the productivity and quality of future stands. Therefore, it is advisable to consider the achievements of selection work in economic planning to achieve optimal outcomes.

Studies on pedunculate and sessile oak have assessed various traits, including survival, height, biomass production, spring flushing, susceptibility to fungal pathogens and insect pests, wood properties, genetic differentiation, and provenance, family, and individual heritability. These studies include the work of Foer (1999), Jensen (2000), Chmura (2002), Bogdan *et al.* (2004), Barzdajn (2008), Banach and Lenowiecki (2011), Jankowiak *et al.* (2013), Chmura *et al.* (2014), Kesić *et al.* (2021), Memišević Hodžić *et al.* (2021), Girard *et al.* (2022), Hietz *et al.* (2022).

In Poland, there are few oak experiments, and one of the earliest is an experimental trial established in 1968 in Kórnik, which includes two populations of sessile oak and seven of pedunculate oak (Foer, 1998). The largest experiment was established in 1995 in the forest districts of Oborniki Śląskie and Milicz, where 78 provenances of pedunculate and sessile oak were tested (Barzdajn, 2000). Another research series consists of provenance and family trials established between 1996 and 2000, with a total of 18 provenances and 270 families, including one French provenance from the Massif Central (Foer, 1999; Barzdajn, 2008; Banach and Lenowiecki, 2011; Jankowiak *et al.*, 2013; Chmura *et al.*, 2014). The pedunculate oak in the trials of this experimental series is still in the early stages of growth, but periodic surveys provide crucial information on the intraspecific variability of this species.

The slenderness quotient (SQ), which is calculated as the quotient of height and breast height diameter, is a characteristic of the shape of the longitudinal section of the trunk. This quotient is used to assess a tree's stability and its resistance to wind and snow damage (Zajączkowski, 1991; Wang *et al.*, 1998; Cantiani and Chiavetta, 2015; Skrzyszewski and Pach, 2020). Analyses have shown that the slenderness of a tree can affect its wood properties (Krajnc *et al.*, 2019; Yahya *et al.*, 2020) and can be used to predict tree growth (Pretzsch *et al.*, 2021). Studies have been conducted on coniferous species (Kaźmierczak *et al.*, 2011; Jarmuł and Kaczmarski, 2020; Zhang *et al.*, 2020; Masternak and Sobala, 2021; Skrzyszewska and Banach, 2021) and deciduous species (Nazari Sendi *et al.*, 2014; Korzeniewicz *et al.*, 2016; Stăncioiu *et al.*, 2021), including pedunculate oak (Rymer-Dudzińska and Tomusiak, 2000; Kaczmarski *et al.*, 2018; Dudek *et al.*, 2021) to determine the magnitude of this coefficient as a function of different factors shaping tree growth in stands.

The study aimed to evaluate the growth of pedunculate oaks after 22 years on the experimental trial 'Chrostowa II' in the Brzesko Forest District. Four oak characteristics, including height, breast height diameter, basal area, and SQ were analyzed. The study compared the adaptability of oak trees, which were the progeny of 58 trees grown in five stands (provenances) in different regions of Poland, to new environmental conditions after being transplanted to the experimental trial established in the Carpathian Foothills. The range of interprovenance and intraprovenance variability were determined and tested the research hypothesis on the lack of variation between different families and provenances for the analyzed oak traits.

Materials and methods

The study material consisted of the generative progeny of pedunculate oak grown from acorns collected from 58 trees in five stands in Poland (Fig. 1). In 1999, three-year-old seedlings (1,920 seedlings) were planted into hand-prepared plots (0.6×0.6 m) with a spacing of 2.0×2.0 m in the experimental trial 'Chrostowa II' (N 49.902207; E 20.292614). The trial is located in the Regional Directorate of State Forests in Kraków, subdivision 83i, Chrostowa forest range (Brzesko Forest District, Bochnia subdistrict). Further information about this experiment, *i.e.* geographical coordinates of provenances, scheme of the experimental area, distribution of oaks, *etc.*, can be found in an earlier publication (Banach and Lenowiecki, 2011).

In April 2021, when the trees were 25 years old, the height (h , m) and breast height diameter ($d_{1.3}$, cm) of the pedunculate oaks were measured. From these measurements, the basal area of the stand (G , m²·ha⁻¹) and the SQ were calculated. The study used a Vertex IV clinometer from Haglöf, with an accuracy of 0.1 m, to measure the height of the oaks. The breast height diameter was measured with a caliper in two perpendicular directions to the nearest 0.1 cm. The value of G was calculated by multiplying the average tree breast height cross-sectional area for the family ($g_{1.3}$, m²), the number of trees planted per hectare (2,500 with spacing 2×2 m), and the percentage of trees remaining in the trial from those planted in 1999. The value $g_{1.3}$ for a single tree was calculated using formula (1):

$$g_{1.3} = \frac{\pi d_{1.3}^2}{40000} \quad (1)$$

where:

$d_{1.3}$ – is the tree breast height diameter [cm].

The SQ for each tree by dividing its height by its breast height diameter ($h/d_{1.3}$) were calculated. Kaźmierczak *et al.* (2008) reported that the average value of SQ in oaks aged 20-30 years should be around 1.10. In this study, a range of 1.10 ±0.10 was assumed as appropriate for pedunculate oaks aged 25 years. The study calculated the number and proportion of trees in three classes of the SQ (better than average, average, and worse than average) for each provenance: <1.00, 1.00-1.20, and >1.20, respectively. The χ^2 fraction test for more than two populations (Steczowski and Zeliaś, 1997) were used to determine the significance of differences in the obtained proportions of trees.

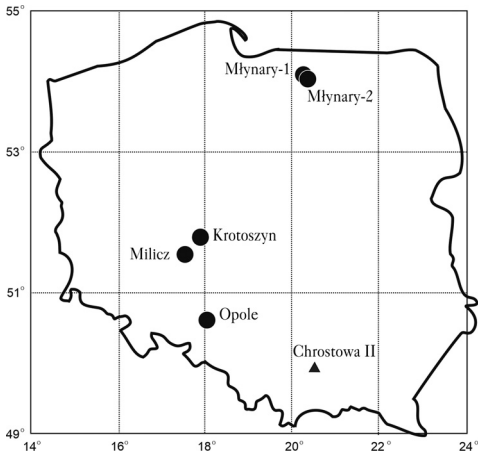


Fig. 1. Location of the 'Chrostowa II' experimental trial (▲) and provenances of pedunculate oak (●) used in the experiment

Mean value and standard error (SE) for each trait analyzed (h , $d_{1,3}$, G , SQ) for each provenance and family were calculated. The significance of differences between provenances and families within provenance were tested using analysis of variance method. The analysis used a hierarchical model (random model) that considered three sources of variation: individual trees, families within provenance, and provenances (Equation 2). The study performed the calculations using the GLM module in Statistica 13.3 software (TIBCO Software Inc., 2017):

$$y_{ijn} = \mu + \alpha_i + \beta(a)_{j(i)} + \varepsilon_{ijn} \tag{2}$$

where:

- y_{ijn} is the observation of the quantitative trait,
- μ is the overall mean,
- α_i determines the influence of the i th provenance,
- $\beta(a)_{j(i)}$ specifies the influence of the j th family in the i th provenance, and
- ε_{ijn} is the random component (error).

Homogeneity of variances using the Brownian-Forsythe test were checked. For the basal area, a significant differences in variances between provenances and families were found. Therefore, performed a logarithmic transformation (ln) on the data before further calculations.

The study calculated provenance (h_p^2) and family (h_f^2) broad sense heritability for each trait (Giertych, 1985, 1991; Dobrev, 2007; Barzdajn, 2008; Banach and Lenowiecki, 2011; Wojda *et al.*, 2012; Bogdan *et al.*, 2017; Apostol *et al.*, 2020; Morales and Swarts, 2022; Zhang *et al.*, 2022). The expected mean squares for the sources of variation (provenience, family) were determined using the Hicks method described by Giertych (1991). Because of the random effect of the factors, three variance components (for provenance, family and error) were calculated. Due to the unbalanced experimental set-up, *i.e.* the different number of families in provenances and the number of trees in families and provenances, the respective numerical coefficients (k_1 , k_2 , k_3) for each variance component were also calculated. The calculations were performed in Statistica 13.3 (TIBCO Software Inc., 2017) with the ‘Variance Components’ module:

$$h_p^2 = \frac{\sigma_p^2}{\frac{\sigma_e^2}{k_3} + \frac{k_2\sigma_f^2}{k_3} + \sigma_p^2} \tag{3}$$

$$h_f^2 = \frac{\sigma_f^2}{\frac{\sigma_e^2}{k_1} + \sigma_f^2} \tag{4}$$

where:

- σ_p^2 is the provenance variance component,
- σ_f^2 is the family variance component,
- σ_e^2 is the error variance component,
- k_1 is the average number of trees in the family,
- k_2 is the average number of trees in the family including provenance, and
- k_3 is the average number of trees in the provenance.

In addition, to calculate provenance heritability using Equation 3, intrapopulation heritabilities, (*i.e.*, family heritability within each provenance) were calculated, separately for each provenance using Equation 4. For each value of provenance and family heritability, the study also calculated the standard error (SE_{h^2}) using the formula from Falconer and Mackay (1996).

Results

VARIABILITY BETWEEN PROVENANCES. After 22 years of growth on the experimental trial 'Chrostowa II', the tallest oaks were from the Krotoszyn provenance, with a height of 13.7 m. These oaks significantly differed from those of the Młynary-2 (11.8 m), Młynary-1 (11.9 m), and Milicz (12.1 m) provenances, which formed a homogenous group (Fig. 2a). Oaks from the Krotoszyn provenance also had the highest mean breast height diameter, measuring 17.0 cm, which was significantly larger than the diameter obtained from oaks of the Młynary-2 (13.7 cm) and Młynary-1 (13.9 cm) provenances (Fig. 2b). Similarly, oaks from the Krotoszyn provenance had the largest basal area, measuring 27.6 m²·ha⁻¹, which was significantly lower for oaks of both provenances from Młynary (Fig. 2c). The average SQ for oaks ranged from 0.85 to 0.90 and did not differ between the provenances (Fig. 2d).

FAMILY VARIABILITY. Among the families tested, oaks from families 95 and 88 of the Krotoszyn provenance had the highest mean height of 14.9 and 13.8 m, respectively. In contrast, oaks from family 55 of Milicz and family 81 of Młynary-2 had the lowest mean height of 9.8 and 10.4 m, respectively. The greatest variation in breast height diameter was observed in the Młynary-1 provenance, where the difference between the largest (family 41) and smallest mean diameter (family 82) was 7.9 cm (75%). Significant differences in mean breast height diameter were also found in the Krotoszyn provenance between families 95 and 92 and in the Milicz provenance between families 59 and 55, with a difference of 6.2 cm in both cases. The highest basal area value was achieved by oaks from family 95 in the Krotoszyn provenance, with a value of 44.5 m²·ha⁻¹, while oaks from family 71 in Młynary-1 had the lowest basal area value of 4.3 m²·ha⁻¹, which represents a tenfold difference. The basal area trait had the highest interfamilies variation coef-

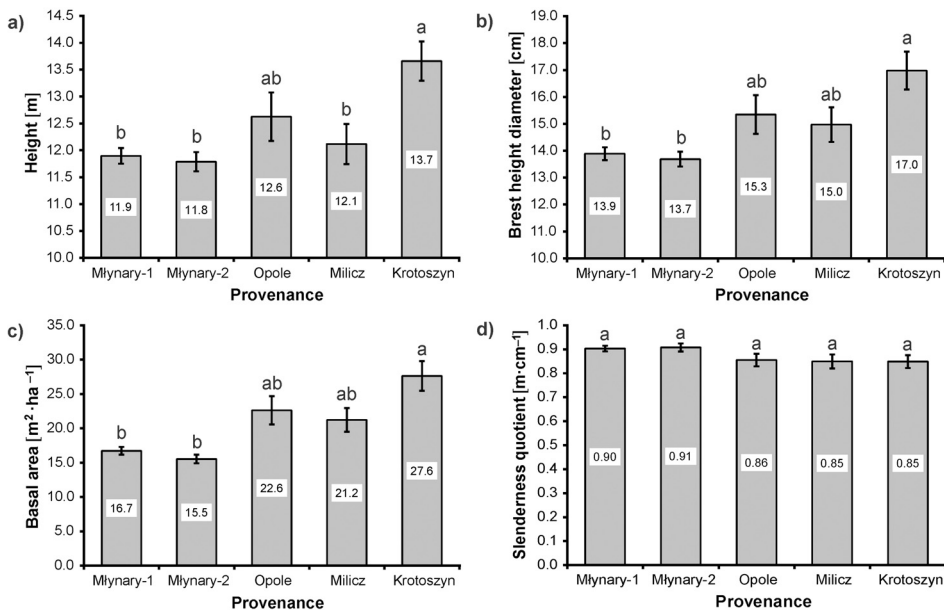


Fig. 2.

Comparison of mean values (\pm SE) of pedunculate oak traits of analyzed provenances; a, b – homogenous groups determined by Tukey's test for $p=0.05$

ficient at 51.1%. The highest SQ coefficient at the family level (1.05) was observed in oaks from family 82 in Młynary-1, while the lowest coefficient (0.76) was found in oaks from family 47 in Młynary-2 (Table 1).

The mean values of the breast height diameter and basal area varied significantly among provenances and families. However, only the provenance had a significant effect on the height of the oaks. In contrast, there were no significant effects of provenance or family on the slenderness quotient (Table 2).

Table 1.

Mean values (\pm SE) of pedunculate oak traits for the families tested on the 'Chrostowa II' experimental trial

| Name of provenance | Family no. | Trait | | | |
|--------------------|------------|------------|-----------------------------|--|--|
| | | height [m] | breast height diameter [cm] | basal area [m ² ·ha ⁻¹] | slenderness quotient [m·cm ⁻¹] |
| Młynary-1 | 31 | 10.7 ±0.9 | 12.6 ±1.2 | 15.3 ±3.1 | 0.86 ±0.04 |
| | 33 | 12.2 ±0.6 | 14.7 ±1.1 | 17.8 ±2.5 | 0.87 ±0.05 |
| | 34 | 11.7 ±0.7 | 12.9 ±0.8 | 15.0 ±1.7 | 0.95 ±0.06 |
| | 36 | 11.8 ±0.8 | 14.4 ±1.4 | 24.9 ±4.7 | 0.92 ±0.08 |
| | 37 | 11.2 ±0.8 | 13.4 ±1.2 | 18.2 ±3.0 | 0.88 ±0.06 |
| | 38 | 11.7 ±0.8 | 13.7 ±0.8 | 16.9 ±2.0 | 0.87 ±0.06 |
| | 39 | 11.4 ±1.1 | 12.7 ±1.3 | 9.8 ±1.9 | 0.93 ±0.07 |
| | 40 | 13.1 ±0.3 | 16.1 ±1.1 | 32.6 ±4.1 | 0.87 ±0.06 |
| | 41 | 13.7 ±0.6 | 18.5 ±1.5 | 39.4 ±5.7 | 0.79 ±0.05 |
| | 45 | 12.7 ±0.7 | 13.7 ±1.0 | 18.8 ±2.7 | 0.96 ±0.05 |
| | 60 | 11.9 ±0.7 | 14.2 ±1.2 | 20.2 ±3.0 | 0.89 ±0.05 |
| | 61 | 11.9 ±0.6 | 13.9 ±1.0 | 21.1 ±3.0 | 0.92 ±0.07 |
| | 62 | 12.6 ±1.3 | 14.8 ±1.5 | 14.7 ±2.7 | 0.87 ±0.06 |
| | 64 | 12.7 ±0.6 | 16.0 ±1.2 | 28.0 ±3.7 | 0.84 ±0.04 |
| | 66 | 12.8 ±0.9 | 17.2 ±1.3 | 25.3 ±3.9 | 0.77 ±0.06 |
| | 67 | 12.7 ±0.9 | 12.5 ±0.9 | 10.0 ±1.4 | 1.03 ±0.05 |
| | 68 | 10.7 ±0.6 | 11.6 ±1.0 | 11.7 ±2.1 | 1.00 ±0.09 |
| | 69 | 10.7 ±0.9 | 12.4 ±1.9 | 7.5 ±2.1 | 0.92 ±0.08 |
| | 70 | 10.9 ±0.7 | 10.7 ±0.8 | 8.9 ±1.2 | 1.04 ±0.06 |
| | 71 | 11.9 ±0.6 | 14.6 ±3.3 | 4.3 ±1.8 | 0.89 ±0.17 |
| | 72 | 12.1 ±1.1 | 13.7 ±1.5 | 14.2 ±2.7 | 0.91 ±0.06 |
| | 73 | 11.3 ±1.0 | 13.5 ±1.2 | 13.4 ±2.3 | 0.86 ±0.08 |
| | 74 | 11.5 ±0.5 | 14.4 ±1.0 | 27.4 ±3.6 | 0.84 ±0.05 |
| | 76 | 11.1 ±0.7 | 12.8 ±0.8 | 16.0 ±1.9 | 0.89 ±0.05 |
| 77 | 11.0 ±1.2 | 11.3 ±1.5 | 6.0 ±1.5 | 1.02 ±0.12 | |
| 78 | 12.5 ±0.8 | 13.5 ±1.0 | 14.2 ±1.8 | 0.94 ±0.05 | |
| 79 | 11.4 ±1.3 | 13.0 ±1.9 | 5.6 ±1.4 | 0.89 ±0.04 | |
| 82 | 11.1 ±0.7 | 10.6 ±0.7 | 11.0 ±1.4 | 1.05 ±0.04 | |
| Młynary-2 | 2 | 11.4 ±0.8 | 13.2 ±0.9 | 18.3 ±2.3 | 0.88 ±0.05 |
| | 28 | 12.3 ±0.8 | 13.3 ±1.4 | 14.6 ±3.0 | 1.02 ±0.10 |
| | 30 | 11.9 ±0.6 | 13.2 ±1.1 | 15.1 ±2.9 | 0.94 ±0.06 |
| | 32 | 12.0 ±0.8 | 14.7 ±1.2 | 18.6 ±2.9 | 0.86 ±0.06 |
| | 35 | 12.1 ±1.2 | 14.3 ±1.8 | 12.6 ±2.9 | 0.89 ±0.08 |
| | 42 | 11.9 ±0.5 | 12.4 ±0.8 | 8.9 ±1.1 | 1.04 ±0.11 |
| | 43 | 12.6 ±0.5 | 16.6 ±0.9 | 32.0 ±3.1 | 0.79 ±0.04 |
| | 46 | 11.6 ±0.6 | 12.8 ±1.0 | 10.6 ±1.6 | 0.94 ±0.06 |
| | 47 | 11.8 ±1.0 | 16.4 ±1.5 | 25.6 ±4.0 | 0.76 ±0.07 |

Table 1. continued

| Name of provenance | Family no. | Trait | | | |
|--------------------------------|------------|------------|-----------------------------|--|--|
| | | height [m] | breast height diameter [cm] | basal area [m ² ·ha ⁻¹] | slenderness quotient [m·cm ⁻¹] |
| Młynary-2 | 48 | 11.8 ±0.7 | 15.8 ±1.4 | 31.2 ±5.6 | 0.79 ±0.05 |
| | 49 | 11.3 ±1.0 | 12.9 ±1.4 | 11.2 ±2.4 | 0.92 ±0.08 |
| | 50 | 12.6 ±0.6 | 13.9 ±0.8 | 21.0 ±2.4 | 0.93 ±0.04 |
| | 75 | 11.5 ±1.0 | 13.4 ±1.6 | 16.6 ±3.7 | 0.91 ±0.06 |
| | 80 | 12.0 ±0.6 | 12.4 ±1.3 | 9.2 ±1.9 | 1.03 ±0.09 |
| | 81 | 10.4 ±1.2 | 12.8 ±1.4 | 8.7 ±2.0 | 0.83 ±0.06 |
| | 83 | 12.7 ±1.0 | 13.5 ±0.9 | 12.9 ±1.7 | 0.94 ±0.07 |
| | 84 | 11.2 ±0.8 | 12.2 ±1.0 | 12.7 ±2.0 | 0.96 ±0.08 |
| | 85 | 11.2 ±1.0 | 12.2 ±1.3 | 8.9 ±1.9 | 0.94 ±0.05 |
| Opole | 9 | 12.2 ±0.8 | 14.3 ±0.8 | 14.1 ±1.6 | 0.86 ±0.05 |
| | 13 | 13.2 ±0.9 | 15.7 ±1.2 | 21.0 ±2.9 | 0.87 ±0.04 |
| | 14 | 12.4 ±0.7 | 15.8 ±1.3 | 32.7 ±5.3 | 0.84 ±0.05 |
| | 54 | 12.4 ±0.7 | 16.4 ±1.3 | 23.1 ±3.8 | 0.79 ±0.05 |
| Milicz | 55 | 9.8 ±1.1 | 10.7 ±1.3 | 8.8 ±2.0 | 0.92 ±0.09 |
| | 56 | 12.3 ±0.7 | 14.4 ±1.2 | 17.7 ±2.8 | 0.90 ±0.06 |
| | 59 | 13.2 ±0.4 | 16.9 ±1.0 | 35.2 ±3.8 | 0.82 ±0.04 |
| | 88 | 13.8 ±0.4 | 17.4 ±1.3 | 36.4 ±5.2 | 0.85 ±0.05 |
| Krotoszyn | 91 | 13.6 ±0.8 | 15.4 ±1.6 | 14.3 ±2.6 | 0.95 ±0.09 |
| | 92 | 11.7 ±1.1 | 13.5 ±1.2 | 14.5 ±2.5 | 0.87 ±0.06 |
| | 95 | 14.9 ±0.6 | 19.7 ±1.2 | 45.4 ±4.8 | 0.79 ±0.04 |
| Family mean | | 12.0 | 14.0 | 17.8 | 0.90 |
| Standard deviation | | 0.9 | 1.9 | 9.1 | 0.07 |
| Coefficient of variability [%] | | 7.5 | 13.6 | 51.1 | 8.0 |

Table 2.

Results of hierarchical analysis of variance of pedunculate oak traits tested on the 'Chrostowa II' experimental trial

| Trait | Source of variance | F-test | Significance level (<i>p</i>) |
|------------------------|--------------------------|--------|---------------------------------|
| Height | provenance | 5.0234 | 0.002 |
| | family within provenance | 1.1761 | 0.189 |
| Breast height diameter | provenance | 3.2837 | 0.019 |
| | family within provenance | 2.3267 | <0.001 |
| Basal area | provenance | 3.4417 | 0.015 |
| | family within provenance | 2.4931 | <0.001 |
| Slenderness quotient | provenance | 1.268 | 0.297 |
| | family within provenance | 1.334 | 0.061 |

TREE STABILITY. Overall, the majority of oaks in all provenances had a low SQ, with 72.8% of trees below 1.00, while 18.0% had an average value ranging from 1.00 to 1.20. Only 9.2% of trees were found in the class with the least favourable quotient, *i.e.*, above 1.20. Although the proportion of trees in the different slenderness coefficient classes varied slightly between the individual provenances, the differences were not significant according to the χ^2 test (Table 3).

PROVENANCE AND FAMILY HERITABILITY. The study found that the magnitude of provenance and family heritability varied for the analysed traits, which included height, breast height diameter, basal area, and SQ. Provenance heritability was generally higher than family heritability, except for the SQ (Table 4). The highest provenance heritability value was observed for oak height ($h_p^2=0.80$), followed by breast height diameter and basal area. High values of family heritability were also obtained for the latter two traits. Family heritability was lowest for oak height ($h_f^2=0.15$).

Within each provenance, family heritability varied significantly. Family heritability was zero for all traits in the Opole oak provenance and for height in the Młynary-2 provenance. For the other provenances, family heritability ranged from 0.09 (basal area) to 0.81 ($d_{1,3}$) in the Milicz provenance. Oaks from the Milicz and Krotoszyn provenances had high intraprovenance heritability ($h_f^2>0.7$), except for basal area (Table 5).

Discussion

The study found that the origin of the pedunculate oaks had a significant impact on their height, breast height diameter, and basal area, while families within provenances differed only in the latter two traits. However, neither of the genetic factors analysed had a significant effect on the SQ. This finding is consistent with Barzdajn's (2008) study on a trial in Milicz. The high genetic variability observed in pedunculate oak, which is influenced by provenance and family within provenance, was also noted by Hautsalo *et al.* (2015), who studied the growth and survival of six provenances of *Quercus robur* L. from the Finnish area. In contrast, Banach (2011) reported a significant effect of genotype only on the height of pedunculate oak, with no effect on survival. Meanwhile, Bogdan *et al.* (2004) found that family significantly impacted the variation in height and breast height diameter of Slavonian pedunculate oak.

Table 3.

Number of trees and proportion [%] in each slenderness quotient class for the pedunculate oak provenances tested on the experimental trial 'Chrostowa II' ($\chi^2=8.5781$; $df=8$; $p=0.379$)

| Name of provenance | Slenderness quotient class | | |
|----------------------|----------------------------|------------|-----------|
| | <1.00 | 1.00-1.20 | >1.20 |
| Młynary-1 | 259 (70.8) | 72 (19.7) | 35 (9.6) |
| Młynary-2 | 176 (70.4) | 49 (19.6) | 25 (10.0) |
| Opole | 36 (83.7) | 5 (11.6) | 2 (4.7) |
| Milicz | 44 (78.6) | 8 (14.3) | 4 (7.1) |
| Krotoszyn | 47 (82.4) | 5 (8.8) | 5 (8.8) |
| Total for experiment | 562 (72.8) | 139 (18.0) | 71 (9.2) |

Table 4.

Variance components and provenance and family heritability of pedunculate oak traits tested in the experimental trial 'Chrostowa II' ($k_1=13.16$; $k_2=14.79$; $k_3=126.54$)

| Trait | Variance components | | | Heritability $\pm SE_{h^2}$ | |
|------------------------|---------------------|--------------|--------------|-----------------------------|-----------------------|
| | σ_p^2 | σ_f^2 | σ_e^2 | provenance (h_p^2) | family (h_f^2) |
| Height | 0.29746 | 0.10451 | 7.81014 | 0.80 \pm 0.11 | 0.15 \pm 0.04 |
| Breast height diameter | 0.86545 | 1.94109 | 19.25363 | 0.70 \pm 0.15 | 0.57 \pm 0.05 |
| Basal area | 0.01459 | 0.03205 | 0.28245 | 0.71 \pm 0.15 | 0.60 \pm 0.05 |
| Slenderness quotient | 0.00015 | 0.00135 | 0.05333 | 0.21 \pm 0.12 | 0.25 \pm 0.04 |

Table 5.

Variance components and intraprovenance heritability ($\pm SE_{h^2}$) of pedunculate oak traits tested in the experimental trial 'Chrostowa II'

| Provenance (average trees number for family) | Variance components (σ_f^2 ; σ_e^2) and heritability (h_f^2) | Trait | | | |
|---|---|-----------------|------------------------------|-----------------|-------------------------|
| | | height | breast height diameter | basal area | slenderness quotient |
| Młynary-1 ($k_1=13.02$) | σ_f^2 | 0.08464 | 2.01143 | 0.03424 | 0.00136 |
| | σ_e^2 | 7.70981 | 18.87335 | 0.26319 | 0.04880 |
| | h_f^2 | 0.13 \pm 0.05 | 0.58 \pm 0.07 | 0.27 \pm 0.07 | 0.63 \pm 0.07 |
| Młynary-2 ($k_1=13.10$) | σ_f^2 | 0 | 0.84887 | 0.01564 | 0.00181 |
| | σ_e^2 | 8.25907 | 18.18582 | 0.25150 | 0.06812 |
| | h_f^2 | 0.00 | 0.38 \pm 0.09 | 0.26 \pm 0.08 | 0.45 \pm 0.09 |
| Milicz ($k_1=13.79$) | σ_f^2 | 1.54587 | 5.79070 | 0.06636 | 0.00032 |
| | σ_e^2 | 6.67823 | 18.91104 | 0.29850 | 0.04717 |
| | h_f^2 | 0.76 \pm 0.16 | 0.81 \pm 0.13 | 0.09 \pm 0.12 | 0.75 \pm 0.16 |
| Opole ($k_1=13.93$) | σ_f^2 | 0 | 0 | 0 | 0 |
| | σ_e^2 | 8.96232 | 22.79353 | 0.36908 | 0.36908 |
| | h_f^2 | 0.00 | 0.00 | 0.00 | 0.00 |
| Krotoszyn ($k_1=13.89$) | σ_f^2 | 1.28801 | 5.64881 | 0.10301 | 0.00096 |
| | σ_e^2 | 6.66513 | 23.97883 | 0.45732 | 0.04034 |
| | h_f^2 | 0.73 \pm 0.17 | 0.77 \pm 0.16 | 0.25 \pm 0.19 | 0.76 \pm 0.16 |

The importance of provenance and family influence extends beyond the traits analysed in this study. Other studies have also shown high interpopulation and intrapopulation variability in pedunculate oak traits. For example, Jankowiak *et al.* (2013) found significant variation in shoot susceptibility to *Phytophthora cambivora* (Petri) Buisman colonisation within Polish pedunculate oak provenances. Banach and Lenowiecki (2011) reported significant variation in the incidence of insect pest galls caused by gall wasps (Hymenoptera, Cynipidae). In Austria, Hietz *et al.* (2022) found significant provenance effects on anatomical properties and wood density. Additionally, Barzdajn and Bruder (2018) reported significant differences in spring flushing, powdery mildew incidence, and stem form (number of stems) between progeny of plus trees of pedunculate oak growing in a generative seed orchard. Therefore, the genetic variability of pedunculate oak should be considered when selecting planting material for forest restoration and management.

The findings suggest that the source of pedunculate oak seeds, either provenance or family, can be optimized for forest management purposes, which is consistent with studies on other tree species such as *Abies alba* Mill. (Mihai and Mirancea, 2016), *Fagus sylvatica* L. (Kowalkowski, 2013; Szeligowski *et al.*, 2019), *Larix decidua* Mill. (Foff *et al.*, 2014), *Picea abies* (L.) Karst. (Jármay and Ujvári, 2006; Skrzyszewska and Banach, 2021), and *Pinus sylvestris* L. (Ballian and Šito, 2017; Gülcü and Bilir, 2017).

After 22 years of growth on the Chrostowa-II experimental trial, the oaks of Krotoszyn provenance were found to have the highest mean height, largest mean breast height diameter, and largest mean basal area, as well as the lowest slenderness quotient indicating their resistance to abiotic factors. These results suggest that the Krotoszyn oaks evaluated as provenance have the best adaptation to the habitat conditions of the experimental trial in the Carpathian Foothills, among all the provenances studied. Furthermore, significant differences were observed between the mean values of traits for individual families within this provenance, indicating high family

heritability. These findings are consistent with Barzdajn and Bruder's (2018) assessment of the Krotoszyn population, which also showed high phenotypic variability in the progeny of plus trees. The authors cited suggest that the high intraprovenance variability of Krotoszyn oaks may be due to their artificial origin. This hypothesis is supported by chloroplast DNA analysis of trees in three forest stands in the region, which revealed a high level of intrapopulation variability and the presence of haplotypes characteristic of the Balkan and Iberian refugium (Nowakowska *et al.*, 2007). Haplotypes associated with the Iberian refugium are commonly found in western European and northern German countries (Petit *et al.*, 2002), suggesting that they may have been introduced to the Krotoszyn Plate area by German foresters who previously managed the region.

The high genetic diversity is also evident from the high family heritability observed within each provenance, indicating the potential for effective individual selection for all growth traits analyzed. Barzdajn and Bruder (2018) and Bogdan *et al.* (2004) also reported high family heritability for tree height of 12-year-old oaks, as well as for height and breast height diameter of trees. At the Chrostowa-II trial, no significant differentiation between families was observed for the Opole provenance, resulting in zero heritability for all traits. This finding is consistent with the analysis conducted in an experiment with 22 pedunculate oak provenances from Austria and Croatia, where no significant differences were found between families for some provenances, resulting in zero ancestral heritability (Bogdan *et al.*, 2017). Low family heritability was also observed in an experiment with *Quercus frainetto* Ten. (Apostol *et al.*, 2020). On the Chrostowa-II experimental trial, the provenance heritability of oak traits was high, suggesting effective population selection is possible. In contrast, slightly lower provenance heritability (maximum of 0.34) was observed in a study covering 28 populations growing in Bosnia and Herzegovina (Ballian and Memišević Hodžić, 2022). However, high values of provenance heritability for growth traits exceeding family heritability are typical for both pedunculate oak (Jensen, 2000; Barzdajn, 2008; Banach, 2011; George *et al.*, 2020) and other woody species (Wainhouse and Ashburner, 1996; Zhao *et al.*, 2014; Sampaio *et al.*, 2019; Morales and Swarts, 2022; Teodosiu *et al.*, 2023).

On the Chrostowa-II experimental trial, the average slenderness quotient at the family level for oaks was $SQ=0.90$. The majority of trees on the trial (about 73%) were classified as having high stability, indicated by SQ values <1.00 . This suggests that most oaks were more stable than the average size reported by Kaźmierczak *et al.* (2008) for pedunculate oaks aged 20-30 years ($SQ=1.10$). However, it is worth noting that the magnitude of the slenderness quotient is crucial, as it affects the stability of a single tree and the whole stand. High values of this coefficient increase the risk of damage from wind or snow (Wang *et al.*, 1998; Skrzyszewski and Pach, 2020). For instance, Korzeniewicz *et al.* (2017) found a very high value of the slenderness quotient in an unmanaged spruce stand, regardless of the biosocial position of the trees. On the other hand, less frequent but intensive silvicultural treatments performed in young pine stands may also destabilize them (Masternak and Sobala, 2021). In the Chrostowa-II trial, there was no significant variation in the slenderness quotient of oaks between provenances and families within provenances. Furthermore, provenance and family heritability had a low value, indicating that selecting oaks based on this trait for growth on this trial is insignificant.

Conclusion

✦ The study found a significant effect of provenance on the variation in height, breast height diameter, and basal area of pedunculate oak, with family significantly affecting the latter two traits. Therefore, the research hypothesis of no significant variation was not confirmed.

- ✦ The highest values of growth traits (height, breast height, and basal area) of oaks originating from the Kalisz Highlands were confirmed, while oaks from the northern part of Poland were rated lowest in this respect.
- ✦ Most trees on the trial had a slenderness quotient lower than the value that a pedunculate oak should have at 25 years of age, indicating good stability. The lack of significant effects of provenance and family suggests that this trait is unimportant for oak selection.
- ✦ Provenance heritability for all growth traits was high, with breast height and basal area having high family heritability. These high heritability values offer the possibility of effective selection to improve these tree parameters.

Authors' contributions

J.B. – conceptualisation, methodology, statistical analyses, formal analysis, final text preparation, review and editing; P.B. – measurements, database preparation, writing-original draft preparation.

Conflict of interest

The authors declare that they have no conflict of interest.

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STRESZCZENIE

Ocena dębu szypułkowego polskich proveniencji i rodów po 22 latach wzrostu na powierzchni doświadczalnej „Chrostowa II”

Głównym zadaniem gospodarki leśnej jest hodowla drzewostanów o dobrych właściwościach fenotypowych. W tym celu wykorzystuje się wyniki prac selekcyjnych, w których do hodowli wybierane są najbardziej wartościowe genotypy. Podstawową metodą identyfikacji zmienności wewnątrzgatunkowej i wartościowania przydatności genotypów jest zakładanie doświadczeń proveniencyjnych, rodowych lub proveniencyjno-rodowych. Na takich powierzchniach ocenia się okresowo wartość potomstwa populacji cząstkowych (drzewostanów) lub pojedynczych drzew (rodów) na podstawie analizy różnych cech. W badaniach tych główny nacisk kładzie się na zmienność i dziedziczalność cech ważnych ekonomicznie. Badania dotyczące oceny potomstwa dębu szypułkowego przeprowadzone zostały na powierzchni doświadczalnej „Chrostowa II” w Nadleśnictwie Brzesko. Uprawa została założona w 1999 r. z wykorzystaniem 3-letnich sadzonek dębu szypułkowego wyhodowanych z żółędzi zebranych z 58 drzew rosnących w 5 drzewostanach (ryc. 1). Celem badań było porównanie możliwości dostosowania się dębów pochodzących z różnych regionów Polski do nowych warunków środowiskowych po ich przeniesieniu na uprawę doświad-

czalną założoną na Pogórze Karpackim. Wiosną 2021 r., tj. po 22 latach wzrostu dębu szypułkowego na uprawie, zmierzono wysokość i pierśnicę wszystkich drzew, a na ich podstawie obliczono współczynnik smukłości oraz sumaryczne pole przekroju pierśnicowego. Do oceny stabilności dębów zastosowano podział współczynnika smukłości (SQ) na 3 klasy: <1,00 – stabilność lepsza od przeciętnej, 1,00-1,20 – przeciętna stabilność, >1,20 – stabilność gorsza od przeciętnej. Dla każdej cechy określono wartości średnie dla proveniencji i rodów. Do oceny wpływu genotypu (proveniencja, ród) zastosowano hierarchiczną analizę wariancji. Po określeniu komponentów wariacyjnych obliczono odziedziczalność proveniencyjną i rodową, a także odziedziczalność rodową wewnątrz każdej proveniencji. Największymi średnimi parametrami wzrostowymi charakteryzowały się dęby pochodzenia Krotoszyn z Wysoczyzny Kaliskiej, a najniższymi Młynary-1 i Młynary-2 z północnego obszaru Polski (ryc. 2), potwierdzono zatem dobre walory dębów krotoszyńskich. Największe zróżnicowanie między rodami otrzymano dla sumarycznego pola przekroju pierśnicowego, a najniższe dla współczynnika smukłości (tab. 1). Jedynie dla tej cechy nie odnotowano istotnego wpływu genotypu (tab. 2). Wartości współczynnika smukłości pojedynczego drzewa wskazały na dobrą stabilność prawie wszystkich analizowanych dębów, a 90,8% drzew charakteryzowała stabilność przeciętna lub lepsza od przeciętnej. Różnica między proveniencjami dla wyróżnionych klas stabilności nie była istotna (tab. 3). Odziedziczalność pochodzeniowa dla wszystkich analizowanych cech wyniosła od 0,80 dla wysokości do 0,21 dla współczynnika smukłości. Odziedziczalność rodowa była nieco niższa i wyniosła od 0,15 dla wysokości do 0,60 dla pola pierśnicowego przekroju (tab. 4). Odziedziczalność rodowa wewnątrz każdej proveniencji wyniosła od 0 dla Opola do wartości powyżej 0,7 dla Krotoszyna i Milicza (tab. 5). Uzyskane wysokie wartości odziedziczalności umożliwiają prowadzenie efektywnej selekcji dębów, która może być realizowana zarówno na poziomie proveniencyjnym, jak i rodowym. Wyjątek stanowi smukłość drzewa, dla której odnotowano brak istotnego wpływu proveniencji i rodu oraz małą odziedziczalność. Sugeruje to, że na obecnym etapie wzrostu dębu szypułkowego cecha ta nie ma znaczenia selekcyjnego.