Differentation of Scots pine (*Pinus sylvestris* L.) seed orchard in Gidyle on basin of morphological needles trains

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Abstract   The subject of this study was to analyse the variation of Scots pine (*Pinus sylvestris* L.) seed orchard with regard to a complex of 9 morpho-anatomical traits of needles. The following measurements were carried out: needle length, number of resin canals, thickness of needle epidermis on adaxial side, mean width of needle epidermis cells on adaxial side, needle cross-section width, needle cross-section thickness, ratio of needle cross-section height to its cross-section width, or the. ratio of traits 6 to 5, distance of vascular bundles (in μm), Marcet's coefficient, i.e. cross-section width x distance of vascular bundles divided by cross-section thickness, or trait 5 x trait 8 divided by trait 6. The intra-population variation of 150 Scots pine (*Pinus sylvestris* L.) clones form a seed orchard in Giedyle, Orneta Forest District in the Regional Directorate of State Forests in Olsztyn, was examined. The applied complex of traits was evaluated using a test of discriminatory power and the characterisations of traits and coefficients of correlation between them were calculated, as well as the degree of participation of particular traits in the construction of canonical values was assessed. The data being obtained from biometrical examination were the basis to perform statistical analyses: multivariate analysis of variance together with testing of statistical hypotheses and canonical variate analysis. The Mahalanobis distance between the trees was set and, based on their shortest values, a dendrite was constructed. With the method of agglomerative clustering, which is based on the nearest neighbourhood, the population homogeneity was examined. The Marcet's coefficient and the distance between vascular bundles were found to be the traits which differentiate the population under stud y the best.

Zróżnicowanie cech plantacji nasiennej sosny zwyczajnej (*Pinus sylvestris* L.) w Giedylach na podstawie cech morfologicznych igieł

Słowa kluczowe   *Pinus sylvestris* L., plantacja nasienna, igły, zmienność igieł, zmienność genetyczna

Streszczenie   Przedmiotem badań była analiza zmienności plantacji nasiennej sosny zwyczajnej (*Pinus sylvestris* L.) pod względem kompleksu dziewięciu cech morfo-anatomicznych igieł. Przeprowadzono następujące pomiary: długość szpilki, liczba kanałów żywicznych, grubość epidermy po stronie płaskiej igły, średnia szerokość trzech komórek epidermy po stronie płaskiej igły, szerokość przekroju poprzecznego igły, grubość przekroju poprzecznego igły,

stosunek wysokość przekroju poprzecznego igły do szerokości przekroju poprzecznego czyli stosunek cechy 6 do 5, odległość wiązek przewodzących (w μm), wskaźnik Marceta tj. szerokość przekroju x odległość wiązek przewodzących podzielona przez grubość przekroju poprzecznego czyli cecha 5 x cecha 8 podzielona przez cechę 6. Zbadano wewnątrzpopulacyjną zmienność 150 klonów sosny zwyczajnej *Pinus sylvstris* L. z plantacji nasiennej w Giedylach, Nadleśnictwo Orneta na terenie RDLP Olsztyn. Zastosowany zespół cech oceniono testem mocy dyskryminacyjnej, obliczono charakterystyki cech, współczynniki korelacji między nimi oraz oceniono stopień udziału poszczególnych cech w konstrukcji zmiennych kanonicznych. Uzyskane w wyniku opracowania biometrycznego dane stanowiły podstawę do wykonania analiz statystycznych: wielozmiennej analizy wariancji wraz z testowaniem hipotez statystycznych i analizy zmiennych kanonicznych. Wyznaczono odległości Mahalanobisa między drzewami, a na podstawie ich najkrótszych wartości skonstruowano dendryt. Metodą grupowania aglomeratywnego, opartego na najbliższym sąsiedztwie, zbadano jednorodność populacji. Stwierdzono, że cechami, które najlepiej różnicują badaną plantację są: wskaźnik Marceta oraz odległości między wiązkami przewodzącymi.

Introduction

The genus Pinus comprises about 120–150 species worldwide, being predominantly distributed over the Northern hemisphere. In Europe, there are about 15 species growing here, occurring mainly in the Mediterranean climate. In our latitude, the most important species is *Pinus sylvestris* L. (Staszkiewicz 1968; 1970).

The Scots pine is an anemogamous and anemochorous species and, as in many species of the genus *Pinus*, a high level of variation in pollination within populations is also being observed (Mitton 1983; Muona, Szmidt 1985; Gulberg et al. 1985; Prus-Głowacki, Stephen 1994). Poland, except the Bieszczady Mountains, is covered by the Scots pine range. Based on the morphological traits, its four climatic ecotypes have been distinguished in our country, i.e. Swedish, Polish, Southern and Sub-Carpathian. The best known Scots pine, and the most valued by foresters, is represented by the Polish climatic ecotype (Boratyński 1993). At present, the Scots pine is the most important species of European forests because of its enormous economic value. In Poland, numerous studies have been carried out for all forest tree species but the genetic variation of Scots pine (*Pinus sylvestris* L.) has been described most extensively (Dziulak, Burczyk 2001, 2006; Odrzykoski 2002; Sułkowski et al. 2008). The Scots pine is a particularly important species in the sylviculture of our country. In 2009, its area percentage amounted to 60.4% of the forest area of Poland (Przybylski, Jastrzębowski 2012).

Forest stands of the Scots pine are developed mostly by artificial reforestation. Therefore, a special attention should be paid to the aspect of seed origin and quality. Pine seeds originate mostly from the facilities under selective breeding programme being carried out by State Forests. The most advanced element of selective breeding in Poland is seed orchards; through the seeds being produced there, they have to ensure the transfer of research works on forest tree improvement to practical use (Kowalczyk et al. 2011). Future forest stands that result from the seeds collected in seed orchards are the offspring of parent tree clones being the individuals with the best phenotype (Przybylski, Jastrzębowski 2012). Despite the great importance of seed orchards in sylviculture, there are not many detailed studies on them (Kowalczyk et al. 2011).

Striving to raise forest productivity is associated with an increase in the interest in tree breeding based on the principles of modern genetics. The main objectives of forest management are, among others, to provide national economy with as large volumes of timber of the best quality as possible without depletion of the production base. The results of national and international

studies indicate that the most effective way to increase and improve the forestry production is to use selection.

Seed orchards that are derived from selected champion trees can be of dual origin:

– clone seed orchards – they are established from vegetatively propagated trees, each of which is represented by a certain number of genotypically identical copies. Such orchards are an excellent "testing ground" for many studies,

– seedling seed orchards – they are derived from champion tree seeds. This category of seed orchards is rarely studied due to the young age of seedlings (Müller-Starck 1991).

In Europe, undoubtedly the largest area of seed orchards is in the countries of the former USSR (Novoselceva 1990, after Przybylski 1993) and the Nordic countries, mainly in Sweden (Hadders and Samuelson 1985, after Przybylski 1993).

The first clone seed orchards were established in Poland by the end of the 1950s. To 1991, about five thousand champion trees were selected, of which the seed for establishing seed orchards was obtained. At present, there are about 600 ha of clone seed orchards which give approximately 200 kg seeds per year and about 400 ha of seedling seed orchards which do not produce seeds yet (Matras 1992). Many seed orchards being established in the 1970s enter now into a phase of intense seed production (Burczyk 1990). These seeds are used in Poland mainly for establishing registered derived crops, of which forest stands of high breeding value will be created in the future (Kowalczyk et al. 2011).

The adaptability of future forest stands becomes particularly important under the conditions of constantly growing environmental contamination and in the face of the threat of massive destruction of forests. Dying of forest stands without the possibility of their regeneration leads to irreversible loss of the gene pool of tree populations. Thus, the idea of creating forest gene banks, being already implemented in Poland, was born. A gene bank is to primarily store for a long time the gene resources of endangered tree and shrub species as well as forest species populations which, for various reasons, will be considered now and in the future as threatened or particularly valuable (Wesoły 1996). Seed orchards are also a specific type of gene banks. The genetic diversity of Scots pine is being determined most often by using chromatographic methods: electrophoresis of enzymes and chromatography of phenolic compounds (Szweykowski, Urbaniak 1982; Krzakowa et al. 1994), and morpho-anatomical traits (Sokołowski 1931; Staszkiewicz 1961; Bobowicz, Korczyk 1994a, 1994b; Urbaniak 1997; Skrzyszewski 2004). In the evaluation of Scots pine diversity, molecular analysis, including DNA analysis, is also used (Krzakowa 1979; Nowakowska 2007).

The Scots pine is characterised by high plasticity, i.e. is distinguished by the adaptability to prevailing environmental conditions, which allows moving its seeds into other climatic regions, as well as by great variability, among others, of morphological and anatomical traits of its needle and cones (Bobowicz 1984, 1990; Bobowicz et al. 1983; Korczyk 1980, 1986).

The use of anatomical and morphological traits to describe the diversity of Scots pine *Pinus sylvestris* L. was applied quite early. From among many morphological traits being useful to describe the intraspecific diversity of Scots pine, particular attention is being paid to the length of needles, although this trait does not fully meet the expectations related to it because it is considerably subject to modifying influences of the environment, both climatic and edaphic ones, the consequence of which is its high variability. Examination of the needle length in the trees growing under the same soil and climatic condition in a seed orchard excludes the influence of habitat, thus it is possible to think that individual differences between trees, being manifested in the length of needles, are genetically conditioned.

The width and thickness of needles also proved to be useful to describe intraspecific diversity of Scots pine. Apart from that, the number of resin canals that is visible on the needle cross-section has become and important trait being used to describe its intraspecific diversity.

As has already been mentioned, the quantitative traits are characterised by continuous variation. They are conditioned polygenically, the genes produce additive effects or they specifically interact with each other. These effects, i.e. intensification of traits, can be expressed in numbers. Examination of the continuous variation of quantitative traits requires the application of appropriate biometrical and statistical methods. These methods were applied in this study to determine the degree of seed orchard variation, assuming that individual trees are governed by the same principles in such a population created by man as in nature (free gene flow). Although this population can be regarded as "artificial", it was expected to demonstrate its considerable genetic diversity due to randomness (random selection) of genotypes being gathered within it.

Material and methods

Two-year pine needles were sampled from 150 Scots pine clones in a seed orchard in Giedyle, Orneta Forest District located in the Regional Directorate of State Forests in Olsztyn. This seed orchard comprises champion tree seedlings of Scots pine obtained from the Tabórz Forests. The area of seed orchard included 30 sections, covering an area of 24.07 ha. On this area, after appropriate agrotechnical procedures, Scots pine seedlings were planted with a loose spacing of 5 x 5 m. Division of the area into sections and spacing of pine seedlings were prepared by the Forest Research Institute. The project of spacing of pine seedlings was designed so that, regardless of the thinning being made later, two seedlings of the same clone were not in the immediate vicinity. As a result, trees at the age of fruiting are randomly pollinated by the same mixture of pollen grains. In line with these principles, 173 clones represented by 9000 seedlings were planted in the Tabórz pine seed orchard in Giedyle.

Based on the results of isoenzymatic studies being carried out by the Tabórz Pine Seed Orchard in Giedyle, 150 clones were selected from which research material was collected – two-year pine needles for morphological and anatomical examinations were collected from each clone. Each specimen was represented by 10 short shots from which one needle from each short shot was collected for anatomical examinations, with the second needle of the same pair being intended for measuring their length. This material was placed in 70% ethanol. Examination of the anatomical traits was performed on needle cross-sections being made in the middle of its length. Thus, each individual was represented by 10 cross-sections being made in 10 different needles. Transverse sections were arranged on a glass slide in two rows, 5 sections per each row. They were embedded in polyvinyl alcohol and covered with a cover-slip. The microscopic slides being prepared this way were used for further anatomical examinations. In total, 1500 semi-permanent microscopic slides were made, on which anatomical traits were examined (traits 2 to 9) (Szweykowski et al. 1976) and just as much needles were examined to learn their morphological traits.

The following measurements were performed: 1 – needle length (in mm); 2 – number of resin canals; 3 – thickness of needle epidermis on the adaxial side (in μm), 4 – mean width of 3 needle epidermis cells on the adaxial side (in μm), 5 – needle cross-section width (in μm), 6 – needle cross-section thickness (in μm), 7 – ratio of needle cross-section height to its cross-section width, or the ratio of trait 6 to trait 5, 8 – distance of vascular bundles (in μm), 9 – Marcet's coefficient, i.e. cross-section width x distance of vascular bundles divided by cross-section thickness, or trait 5 x trait 8 divided by trait 6.

The applied complex of traits was evaluated using a test of discriminatory power and the characterisations of traits and coefficients of correlation between them were calculated, as well as the degree of participation of particular traits in the construction of canonical values was assessed. The data being obtained from biometrical examination were the basis to perform statistical analyses: multivariate analysis of variance together with testing of statistical hypotheses and canonical variate analysis. The Mahalanobis distance between the trees was set and, based on their shortest values, a dendrite was constructed. With the method of agglomerative clustering, which is based on the nearest neighbourhood, the population homogeneity was examined. The Marcet's coefficient and the distance between vascular bundles were found to be the traits which differentiate the population under stud y the best.

Results and discussion

Analysis of the discriminatory power of traits (Caliński et al. 1976) showed that $F_{cal} > F_{0.05}$ for all traits and that the main traits for determination of Scots pine variation from the Giedyle seed orchard are as follows: needle cross-section width (5), number of resin canals (2), needle cross-section height (6), distance of vascular bundles (8) and Marcet's coefficient (9). The values of F statistics are the highest for these traits (Table 1). Failure to reject any of the traits by the discriminatory power test is evidence of the relevance of their selection and the same of their usefulness in the examination of Scots pine variation.

Table 1. The result of discriminatory power examination for 9 needle traits of the Scots pine (*Pinus sylvestris* L.) from the Giedyle seed orchard

No	Traits	F_{cal}
1	needle length	15.10
2	number of resin canals	25.02
3	thickness of needle epidermis on the adaxial side	3.21
4	mean width of 3 needle epidermis cells on the adaxial side	2.94
5	needle cross-section width	30.44
6	needle cross-section thickness	23.28
7	ratio of needle cross-section height to its cross--section width, or the ratio of trait 6 to trait 5	7.51
8	distance of vascular bundles	18.80
9	Marcet's coefficient	16.49

$F_{0.05} = 1.21;\ \ F_{0.01} = 1.31$

Analyses of the variability of pine needle anatomical traits allow evaluating the ability to preserve potential range of their variation being observed in the trees occurring in substantially different environments. But the range of variation may be a consequence of phenotypic modifications. Nevertheless, anatomical traits are considered less susceptible to the influences of the environment than morphological ones (Stace 1993). The length of needles of the trees examined

in the Giedyle seed orchard amounted to 77.02 mm and it represents the value in the range of values being characteristic of the trees form the Polish Lowlands (Urbaniak et al. 2003). Mountain Scots pine populations have clearly shorter needles (e.g. in the Pieniny Mts population it is 40.34 mm), as shown by Zajączkowski (1949).

The characteristics of 9 traits shows that the variability of any trait does not exceed 29% and does not drop below 6% (Table 2). The most variable trait is the Marcet's coefficient (i.e. needle cross-section width x distance of vascular bundles divided by needle cross-section thickness, or trait 5 x trait 8 / trait 6), for which the coefficient of variation amounted to 28.54%, and distance between vascular bundles (trait 8). The Marcet's coefficient has also had the highest value in the study by Urbaniak et al. (2008) referring to description of the inter-population diversity of Scots pine from the Tuchola Forest based on 8 anatomical traits of pine needles and amounted to 37.09%, 30.18% and 28.43% for the Jelenia Wyspa population, the Jeziorka Kozie population and the Skraj population, respectively. Its values are similar to the result being obtained for the Tabórz pine seed orchard in Giedyle.

The lowest variation is characteristic of trait 7, i.e. the ratio of trait 6 to trait 5 (ratio of needle height to needle cross-section width). The value of this coefficient of variation in the Giedyle seed orchard amounted to 6.18%.

Table 2. Descriptive statistics for 9 needle traits of the Scots pine (*Pinus sylvestris* L.) from the Giedyle seed orchard

Traits	Mean	Standard deviation s.d.	Variation coefficient var. co.%	confidence interval		Minimum	Maximum
1	77.02	10.86	14.09	76.47	77.57	8.00	146.00
2	1.34	2.51	22.06	11.22	11.47	3.00	22.00
3	8.15	1.35	16.59	8.08	8.22	4.89	12.45
4	6.04	0.79	13.09	6.00	6.08	4.15	9.13
5	1750.65	211.86	12.10	1739.93	1761.38	1033.60	2401.60
6	826.53	89.09	10.78	822.02	831.04	532.00	1170.40
7	1.47	0.03	6.18	0.47	0.47	0.37	0.59
8	150.28	37.76	25.13	148.37	152.19	47.31	283.86
9	320.83	91.55	28.54	316.20	325.47	91.91	660.79

The correlation coefficient for 9 pine needle traits is shown in Table 3. It shows that, of the total number of 36 calculated correlation coefficients, 29 (80.55%) are above the critical value, i.e. they are highly significant at 0.01.

Most strongly correlated are the distances between vascular bundles with the Marcet's coefficient (trait 8 with trait 9), for which the absolute value of correlation coefficient amounts to 0.97. Also the needle cross-section width is strongly correlated with the needle cross-section height (trait 5 with trait 6), for which the absolute value of correlation coefficient amounts to 0.87. Most weakly correlated is trait 4 with trait 7, i.e. mean width of 3 needle epidermis cells on the adaxial side with the ratio of trait 6 to trait 5. Trait 4, i.e. mean width of 3 needle epidermis cells, is most

weakly associated with other traits. Also trait 3, i.e. thickness of needle epidermis on the adaxial side, and trait 7 (ratio of trait 6 to trait 5) show weak correlations.

Table 3. Coefficients of correlation between 9 needle morphological and anatomical traits of the Scots pine (*Pinus sylvestris* L.) from the Giedyle seed orchard. ** – statistically significant correlations, at the significance level α = 0.01.

1								
2	** 0.1722							
3	0.0425	* 0.0655						
4	0.0262	−0.0126	** 0.2834					
5	** 0.3348	** 0.5893	** 0.1826	** 0.0918				
6	** 0.3287	** 0.5893	** 0.1913	** 0.1033	** 0.8664			
7	** −0.0815	** −0.3044	−0.0352	0.0043	** −0.4681	0.0252		
8	** 0.2816	** 0.5366	** 0.1439	** 0.0946	** 0.8022	** 0.6213	** −0.5050	
9	** 0.2706	** 0.5279	** 0.1291	** 0.0828	** 0.7963	** 0.5298	** −0.6470	** 0.9744
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**

The testing of general hypothesis with multivariate analysis of variance (Caliński 1970; Caliński et al. 1976; Ceranka et al. 1976) shows that the trees examined differ significantly in the statistical sense with respect to 9 pine needle traits being treated jointly or separately. This can be seen from the value of calculated F statistics. Its value in the general hypothesis amounts to 10.48, while the critical value for this statistics amounts to 1.07, thus F_{cal} is substantially higher than $F_{0.05}$. The diversity of examined Scots pine trees form the Giedyle seed orchard with respect to each 9 pine needle traits is presented in Table 4. It shows that all traits, except the Marcet's coefficient, differentiate significantly the pine trees in the statistical sense. In determination of this diversity the needle length and the number of resin canals is of particular importance. Similar results have been obtained for the population of Scots pine located in the Janów Lubelski Forest District. The values of F statistics for each trait show that the needle length and the number of stomatal rows on the adaxial side of needle most strongly differentiate the trees of the Janów Podlaski population (Urbaniak et al. 2013). The length of needle statistically distinguished the Scots pine clones examined in the Giedyle seed orchard. However, this trait is subject to quite considerable effects of the environment, which could be one of the factors being responsible for its variation (Urbaniak et al. 2003; 2006). Except trait 7, other traits have considerable values of the coefficient of variation, which may reflect environmental modifications to a greater extent. The variability of these traits can be an index of plasticity that provides the Scots pine clones from the Giedyle seed orchard with ability to live and persist under different conditions and in different environments.

Table 4. The values of F statistics determining the diversity of 150 clones of the Scots pine (*Pinus sylvestris* L.) from the Giedyle seed orchard

No	Traits	F_{Cal}
1	needle length	34.30
2	number of resin canals	25.98
3	thickness of needle epidermis on the adaxial side	13.26
4	mean width of 3 needle epidermis cells on the adaxial side	8.58
5	needle cross-section width	6.52
6	needle cross-section thickness	4.88
7	ratio of needle cross-section height to its cross-section width, or the ratio of trait 6 to trait 5	3.23
8	distance of vascular bundles	2.36
9	Marcet's coefficie	0.89

$F_{0.05} = 1.22$

A graphic representation of intra-population variation is a scatter diagram for the trees examined on the plane of first two canonical variables V_1 and V_2 comprising 60% information from the set of 9 pine needle traits; 14 extremely located tress clearly differs from the other ones (Fig. 1).

A dendrite constructed on the basis of the shortest Mahalanobis distances (Celiński et al. 1976) confirms the great diversity of trees with respect to needle traits (Fig. 2), although the similarity between trees is slightly different than in Figure 2. Based on a comparison of the values of the shortest Mahalanobis distances being entered into the dendrite and the critical values for these distances $D_{0.05} = 1.85$, it can be concluded that 109 distances is smaller than the critical value ($D_{cal} < D_{0.05} = 1.85$). Thus, 109 associations between the clones suggest that they do not differ significantly from each other. The highest value is shown by the Mahalanobis distance connecting clone 2228 to clone 363 ($D_{cal} = 3.6696$), which supports the separateness of these clones from the rest of the population being already found earlier. Also specimens 343, 1702. 2170. 2202, 2215 and 2214, being distinguished by high separateness on a diagram of the analysis of canonical variables (Fig. 1), are characterised here – following tree 363 – by high values. High separateness is also characteristic of tree 2202 which is connected to tree 2203 by a distance of 2.90, while tree 2203 to tree 1704 by a distance of 3.010, and next to tree 2172 by a distance of 2.10. Clone 2172 is connected to clones 2212 and 1710 through tree 1720. The next group of clones being characterised by considerable Mahalanobis distances is formed by tree 339, to which clone 343 is connected by a distance if 3.05, as well as clones 2144, 1702 and 2125 being connected to clone 339 by large distances. Thus, the dendrite being constructed on the basis of the shortest Mahalanobis distances shows that the above-mentioned clones clearly differ from the rest of the analysed clones.

The separateness of clone 363 can also be well seen on a dendrogram being constructed on the basis of agglomerative clustering with the nearest neighbourhood method (Fig. 3). The clones, the separateness of which was shown on the dendrite being constructed on the basis of the shortest Mahalanobis distances, also here has a special place – these are clones 343, 339, 1702, 2144 and 2202. It can be concluded that, as a result of agglomerative clustering with

the nearest neighbourhood method, the Scots pine clones examined split into a number of small subgroups that combine the trees being most similar. All statistical methods being applied allowed demonstrating that the Scots pine from the Giedyle seed orchard significantly varies with respect to needle anatomy.
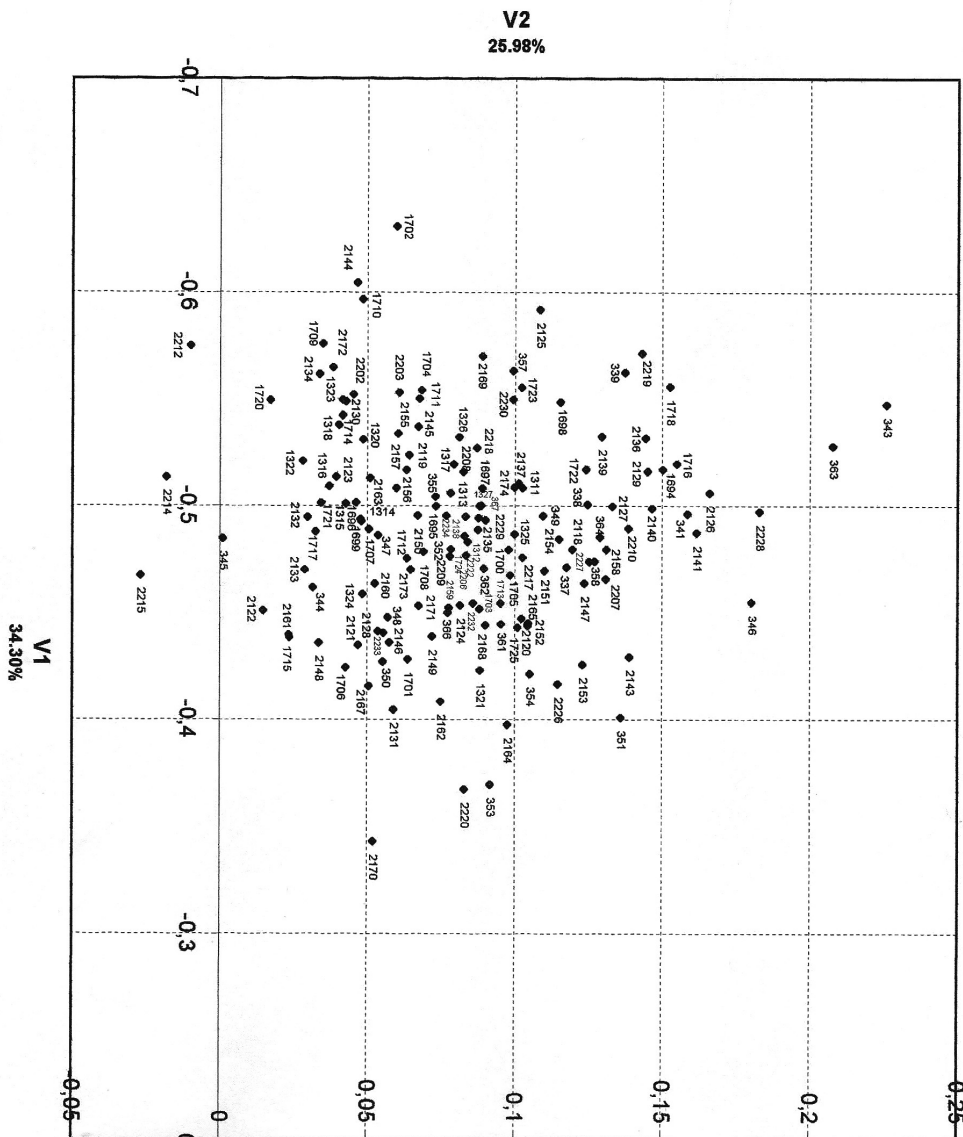

Figure 1. A scatter diagram for 150 clones of the Scots pine (Pin*us sylvestris* L.) from the Giedyle seed orchard in the plane of first two canonical variables V$_1$ and V$_2$, comprising 60.28% information from the set of 9 needle traits being applied
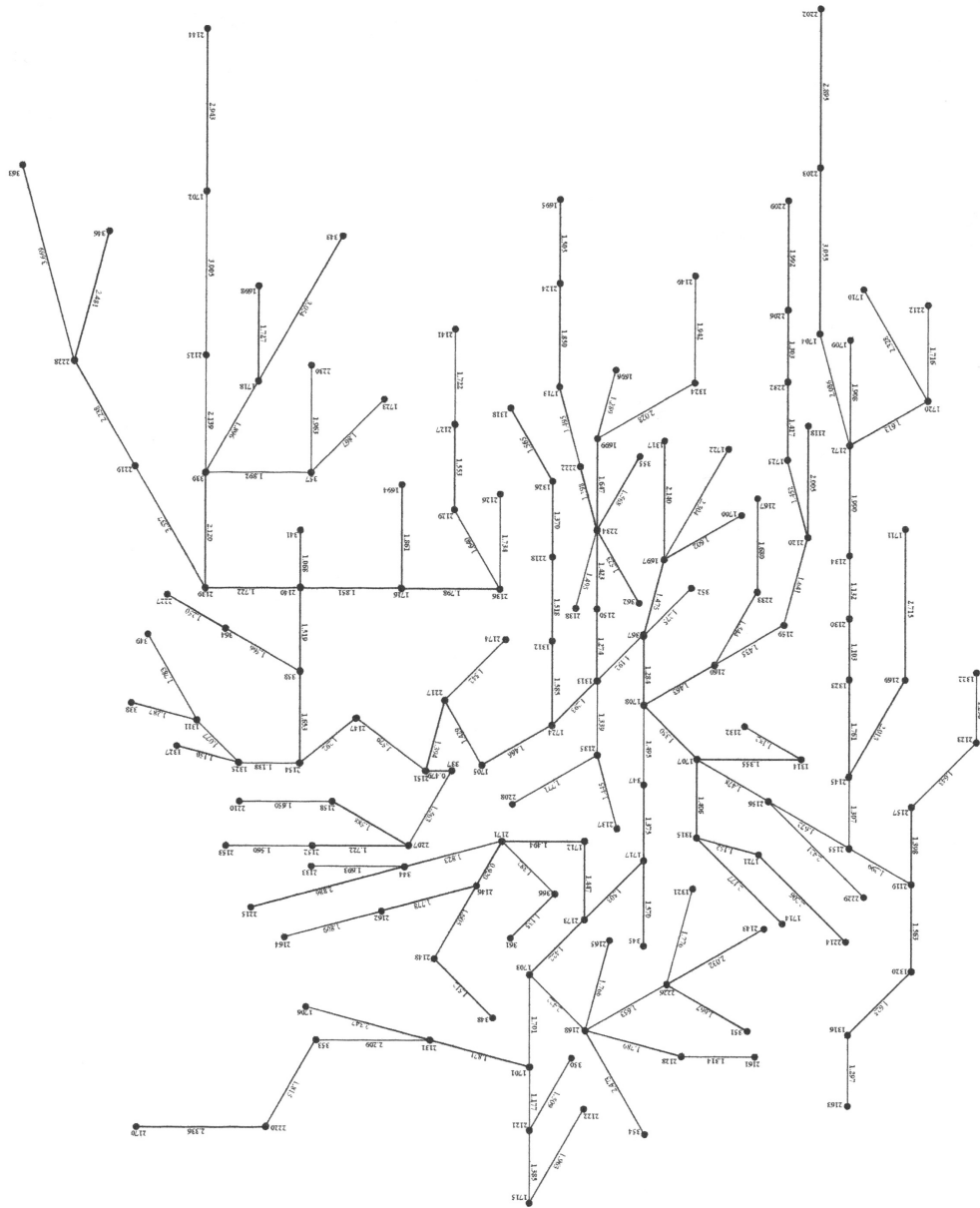
Figure 2. A dendrite [dendrite tree / dendrogram / tree diagram] of 150 clones of he Scots pine (*Pinus sylvestris* L.) from the Giedyle seed orchard constructed on the basis of the shortest Mahalanobis distances being determined for 9 needle traits
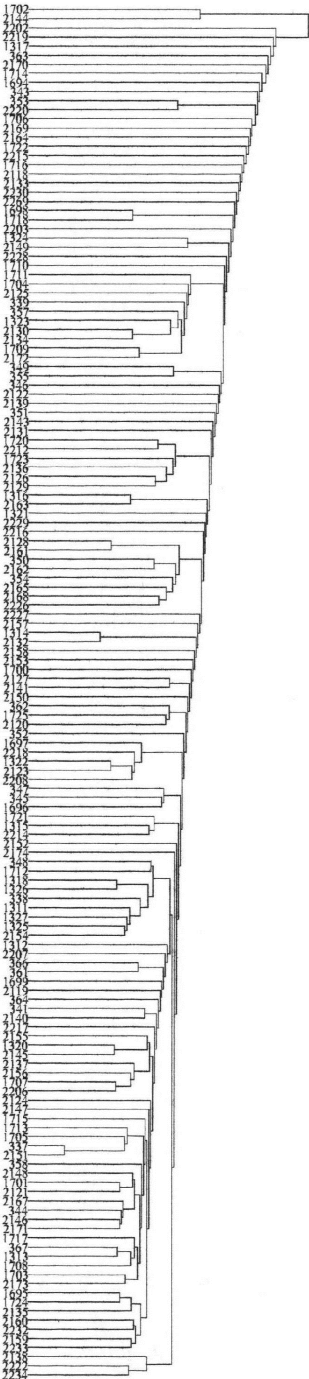
Figure 3. The result of clustering for 150 clones of he Scots pine (*Pinus sylvestris* L.) from the Giedyle seed orchard based on 9 needle traits

Based on the results being obtained in this study, it can be concluded that the examined Scots pine clones from the Giedyle seed orchard show statistically significant differences with respect to the set of nine morphological and anatomical needle traits. Individual differentiation can be seen on dendrites being constructed for the shortest Mahalanobis distances. For the needle traits being examined (Fig. 2), most of the associations between the trees are characterised by the Mahalanobis values being smaller than the critical values, so these tress do not differ significantly in the statistical sense with respect to the set of 9 needle morphological and anatomical traits being applied. However, it should be noted that there are certain significant differences and this refers in particular to clones 2228 and 363 and, to a lesser extent, to the trees of clones 1718, 343, 2125, 1702, 1704 and 2203. When taking into account the whole table of associations on the basis of the Mahalanobis distances, significantly different tree pairs represent 36.23% (41 trees) at a significance level of 0.01 and 16% (24 trees) at a significance level of 0.05.

When analysing the diagram of canonical variables, it can be concluded that the clones being distinguished by statistically significant distances on a dendrite also here show substantial differences from other clones; these are trees 343, 363, 1702, 2125 and 2228. The separateness of the same clones is confirmed by the result of agglomerative clustering on the basis of 9 needle morphological and anatomical traits.

The graphically demonstrated variation within the Giedyle seed orchard that comprises information from the set of nine needle morphological and anatomical traits being applied on the representatives of 1050 Scots pine clones is presented on a diagram of the analysis of canonical variables (Fig. 1), on a dendrite (Fig. 2) and on a dendrogram (Fig. 3).

The variability of needle traits in 150 Scots pine closed being examined does not exceed 28.54% and does not drop below 6.18%. The most variable trait is the Marcet's coefficient (trait 9 – 28.54%), next the distance of vascular bundles (trait 8 – 25.13%) and the number of resin canals (trait 2 – 22.04%). The traits mentioned above differentiate the clones under study the best with respect to the observed variability in needle traits. The dominant influence of these traits on the formation of variability in population has been also observed by Bobowicz (1988).

Practically all countries where the Scots pine is a tree of major economic importance have a programme of its genetic breeding for the needs of forest plantations. Seeds from selected forest stands or produced in special seed orchards are increasingly finding their way to afforestation, superseding the seeds from accidental harvesting in felling areas. A long period of checking the *Pinus sylvestris* L. offspring cannot yet ensure that the seeds being delivered will indeed give increased production or better tree quality. Therefore, the result of genetic works on the Scots pine being obtained so far is protection of the best natural resources through the use of seeds collected from selected individuals and populations chosen because of their genetic and adaptive values.

It is worth noting that the studies of diversity of the Scots pine from seed orchards have been conducted at the individual level, so they referred to differences between individual trees. As concluded on the basis of the obtained results, this variation jest substantial for all sets of traits, with single trees being extremely varied. The obtained results suggest that the Scots pine clones being examined differ significantly in the statistical sense.

Conclusions

1. The Tabórz pine seed orchard in Giedyle is characterised by a high level of genotype richness being determined by the variability of needle morphological and anatomical traits.
2. The analysis of qualitative traits, i.e. determination of the degree of variation needle morphology and anatomy showed large diversity of the Scots pine (*Pinus sylvestris* L.) clones from the Giedyle seed orchard under study. Among the needle traits being analysed, the Marcet's coefficient differentiates the examined clones the best.
3. The heterogeneity of the Giedyle population is being observed in the results of all methods being applied, in particular in the results of agglomerative clustering with the nearest neighbourhood method. Based on the calculated Mahalanobis distances, it can be concluded that there statistically significant different individuals are among 150 Scots pine clones.
4. The knowledge of tree genotypes should be used when planning the spacing and vicinity of clones in second-generation plantations.

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