

ORIGINAL PAPER

Variability in biometric traits of Scots pine needles in Poland

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ABSTRACT

The biometric traits of Scots pine needles have been studied mainly with regard to this species provenances and refugia as well as those that were growing in some nature reserves and experimental forests. Meanwhile, little is known about the variability of these traits on a larger scale. We focused on Scots pine throughout its whole natural range in Poland. Our aim was to present the scope and spatial distribution of the needle length and width variability of this species. The data on needle length and width were collected from model trees representing as many as 310 sample plots distributed throughout the entire country. Scots pine needle traits expressed a large variability with needle width being less variable than needle length. The average needle length for all model trees in the country was 68.68 mm. The average needle length in the first of these sets of model trees, whose needles were longer than average, was 74.58 mm with two of the three subsets distributed in the northern part of the country. The second set of model trees grouped model trees whose needles were shorter than average. Their average needle length was 62.05 mm with only one of four subsets distributed in the same part of the country. The average width of needles was 1.17 mm. Two of three subsets of model trees whose needles were longer than average, and whose needle widths were wider than average, were distributed in the northern part of the country. The distribution of model trees with both needle length and width smaller than the average values for these traits, was not as consistent as the needle widths from the set of model trees with longer needles. The distribution of the identified subsets with the borders of both the natural forest regions and with the dendroclimatic regions for Scots pine that were distinguished in Poland. The aforementioned relationships allowed the division of the country's territory into four sections: northeastern, northwestern, southwestern and southeastern. Three of these sections contained one determined pair of two subsets, one consisting of model trees with longer needles and another with shorter needles. The one exception was the southeastern country section, which was definitively dominated by just one subset consisting of model trees with shorter needles. The spatial patterns of the identified subsets in Poland indicated quite a strong correlation between the needle traits variability and regional growing conditions.

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Received: 9 November 2022; Revised: 30 January 2023; Accepted: 14 February 2023; Available online: 28 March 2023

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KEY WORDS

dendroclimatic regions, morphological traits, *Pinus sylvestris* L., spatial patterns

Introduction

Scots pine *Pinus sylvestris* L. is a species of significant ecological, social and economic importance. In Eurasia, Scots pine forests are estimated to cover over 145 million hectares (Mason and Alfa, 2000; Mullin *et al.*, 2011; Durrant *et al.*, 2016). Of all the coniferous tree species in the Northern Hemisphere, it has the second largest range (Boratyński, 1991; Hytteborn *et al.*, 2005; Labra *et al.*, 2006). Currently, its distribution extends from the Arctic Circle in northern Scandinavia (70° N) to central Spain and Turkey (40° N) and from western Scotland (6° W) to the shores of the Sea of Okhotsk (150° E) in Far East Asia with elevations from sea level in western Scotland to 2,700 m in the Caucasus Mountains (Boratyński, 1991).

At present, the actual range of Scots pine in Europe is much larger than this species natural range. The reason for this expanded distribution is that since the mid-nineteenth century, Scots pine seeds collected from unknown places over nearly all of Europe were broadly distributed by German, Austrian, Hungarian and Czech enterprises (Zawierucha, 1985). Then the seeds were used to establish Scots pine monocultures even beyond this species natural range (Fig. 1). Thus, European commercial forests had origins that were both native and alien (Zawierucha, 1985).

In Poland, the Scots pine is a dominant, forest-forming tree species occurring mostly in lowland and upland areas. However, it also forms some dispersed populations in the Carpathian and Sudeten Mountains. Its share in the species composition of Polish forests is as high as 58% (Raport, 2018) which is much higher than the 20% average area that Scots pine tree stands cover in European forests (Durrant *et al.*, 2016).

The knowledge gaps in the genetics and ecology of Scots pine resulted from centuries that followed in which a continuous resettlement of its various ecotypes from different climatic conditions and breeding characteristics occurred, mostly having negative traits when compared to the production potential of native ecotypes (Zawierucha, 1985). Populations from a continuous Eurasian Scots pine range express a high level of genetic variation (Mejnartowicz and Bergmann, 1985; Yazdani *et al.*, 1985; Müller-Starck, 1986; Dzialuk and Burczyk, 2006), while at the genome-wide level molecular genetic differentiation at nuclear loci is low ($F_{ST}=0.02$) in most parts of the distribution among sampling locations (Wang *et al.*, 1991; Prus-Głowacki and Stephan, 1994; Prus-Głowacki *et al.*, 2003, 2012; Labra *et al.*, 2006; Pyhäjärvi *et al.*, 2007; Kujala and Savolainen, 2012; Wachowiak *et al.*, 2014; Hebda *et al.*, 2017).

Human impacts on forest genetic resources may result from different activities such as breeding and selection, seed transfer, silvicultural measures, and alterations of the growing conditions. Out of these activities, the most important is the impact of seed transfer which affects the genetic structure depending on the origin and genetic diversity of the transferred material. Furthermore, its impact also depends on site conditions and genetic diversity of the local population in the destination site (Lefèvre, 2004; Jankowski *et al.*, 2019).

An impending threat to forests is climate change. According to Reich and Oleksyn (2008), even modest climate warming will likely influence Scots pine survival and growth but in distinct ways in different parts of the species range. The response of Scots pine to worsening climatic scenarios is still insufficiently investigated, while management strategies require more information on its adaptive capacity (Mátyás, 2021).

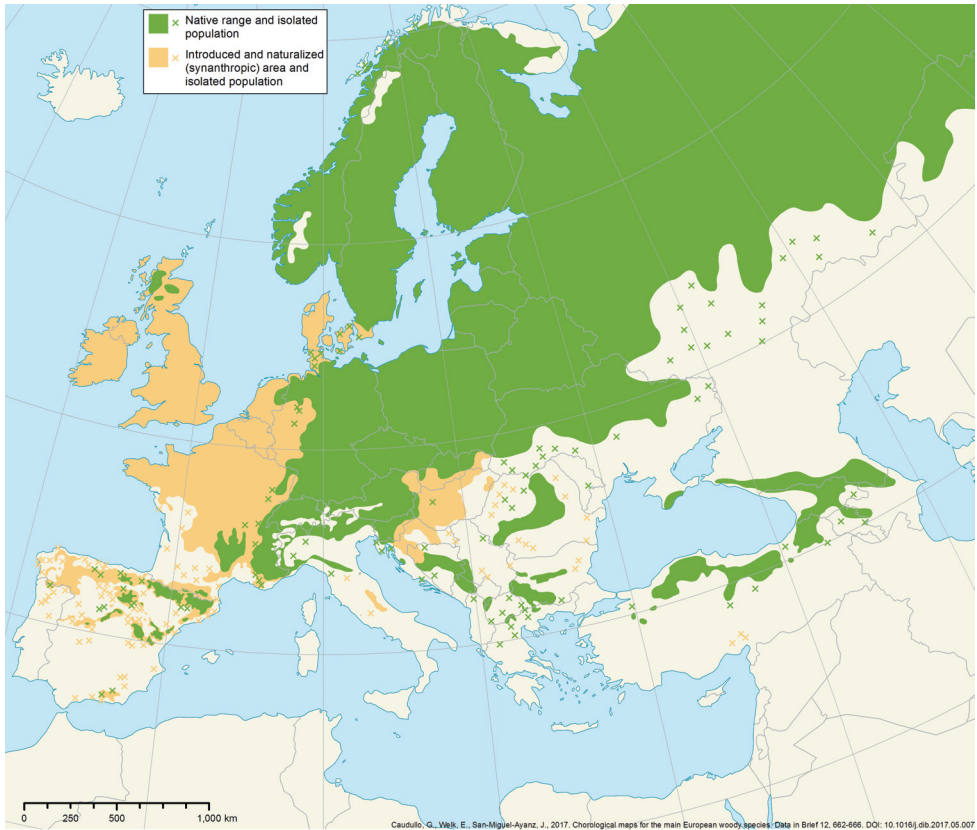


Fig. 1.

Present distribution of Scots pine tree stands in Europe according to NFI data (after Caudullo *et al.*, 2017)

Scots pine is characterized by a high variability of morphological and physiological traits (Eckenwalder, 2009), particularly its vegetative parts and most notably the needles (Novikova and Milyutin, 2006). Scots pine, with its extensive Eurasian range, shows predominantly clonal variability. The largest variability takes place in populations at the southern and western peripheries of its range, since Scots pine grows there under unfavorable climate conditions (Marcysiak, 2021). The study of the cone and needle traits (including needle length and width) in relic sites of this species revealed the highest differentiation between the Iberian and Anatolian populations and generally the geographical structure of the phenotypic variability (Jasińska *et al.*, 2014).

In Scots pine, as well as in other conifers, the needles of trees that grow under the same conditions are of a comparable size. However, the variability in needle length within a crown is quite high with coefficients of variation reaching tens of percent (Lemke, 1980). The variability in needle length in a tree stand is much lower than needle length variability within the crowns of individual trees (Lemke, 1980; Lesiczka *et al.*, 2017). Additionally, the needle length in Scots pine varies not only within the crown of one tree (they are usually longest in the lower part of the crown) but even on individual shoots (Mamaev, 1973). Moreover, the needle length from one annual shoot may differ from the needle length of an adjacent annual shoot (Pravdin, 1964; Mamaev, 1973).

Currently, studies on needle biometric traits in Scots pine in Poland have been conducted either in populations growing in sites that were decidedly different in terms of fertility and/or moisture content but located a short distance from each other (Urbaniak *et al.*, 2003; Woźniak *et al.*, 2005; Pawlaczyk *et al.*, 2010; Urbaniak *et al.*, 2018), on selected populations located in lowlands, foothills and mountains (Łabiszak *et al.*, 2017), and in tree stands occurring in university experimental forests (Lemke, 1980). Further, some of these studies were concerned, in particular, with populations of so-called 'relic' status (Androsiuk and Urbaniak, 2006; Urbaniak *et al.*, 2006, 2008; Urbaniak and Vončina, 2008).

Needle width has been less studied in earlier research, since it has proven to be less useful in describing variations in Scots pine needle morphology when compared to needle length. The lower importance of needle width as compared to needle length (*e.g.*, for monitoring purposes) results from the low variability of the former. For example, in Sweden the average needle width of this species increases southwards from 1.57 mm in the north, 1.71 mm in the center, and 1.72 mm in the south (Paule, 1971). Meanwhile, according to Żelawski and Niwiński (1966), in Poland it decreases southwards and is even less variable than in Sweden with average needle width 1.47 mm in the north, 1.48 mm in the center and 1.41 mm in the south of the country.

It can be concluded that apart from relatively numerous studies on needle biometric traits in Scots pine, knowledge of this subject in Poland is still fragmentary and does not sufficiently reflect needle length and width variability in this species. Therefore, a much larger set of phenotypically diverse reference samples (randomly selected and collected from various sites within the country) is required to fully represent the aforementioned variability (Li *et al.*, 2012). The aim of our research is to present the actual scope and spatial distribution of the needle length and width variability of Scots pine stands in Poland based on a large number of sample plots of the National Forest Inventory network.

Materials and methods

DESCRIPTION OF THE STUDY AREA AND SELECTION OF THE MODEL TREES. Stratified sampling was used to select sample plots representing the entire range of site conditions within the Scots pine distribution in Poland. Sample plots were sub-sampled from 12,543 National Forest Inventory (NFI) plots located in Scots pine tree stands based on bioclimatic factors, forest site type and stand age. A simple random sample was subsequently drawn from each category resulting in a total of 310 sample plots (Fig. 2).

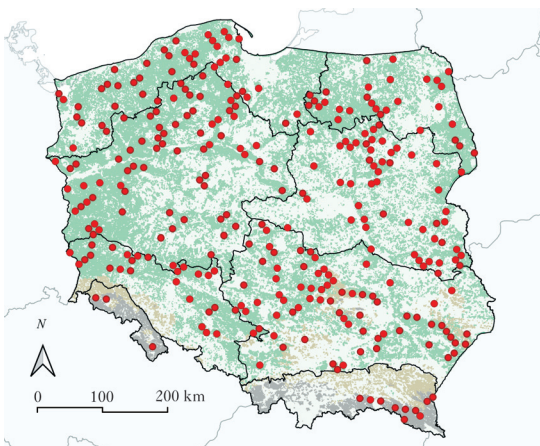


Fig. 2. Geographical distribution of 310 sample plots (red circles) in Poland

The selected stands occurred in the whole range of site conditions characteristic for the distribution of Scots pine forests in Poland. Thus, they represented a wide cross section of forest site types from coniferous and mixed coniferous forests (mainly in the central and northern range of Scots pine) to mixed and broadleaf forests (more common in the southern range of the species) (Fig. 2) and at altitudes ranging from 4 m to 654 m above sea level (a.s.l.). The annual mean temperature across Poland's territory varies from 5.5°C to 9.1°C and the total annual precipitation varies from 499 mm to 815 mm (Hijmans *et al.*, 2005).

The sample plots were established 70 m directly northwards from the NFI plot in order to ensure that the latter would not be affected. The sizes of the sample plots were multiples of 0.01 ha (ranging from 0.01 to 0.24 ha) selected so that each plot contained at least 30 Scots pine trees. The diameter at breast height (DBH) and height (H) of all trees growing on each sample plot were measured. Based on the calculated dendrometric parameters of the trees, one tree (without visible damage) from the group of dominant or co-dominant with an H close to the determined top height and the calculated average DBH was selected and felled on each sample plot, thereafter referred to as a model tree.

NEEDLE SAMPLING AND MEASUREMENT. Scots pine needles were sampled from the model trees after they were felled. This activity took place during the period between two growing seasons, *i.e.* in late autumn and winter 2015 and early spring 2016. According to the recommendations of ICP Manual Forest (Rautio *et al.*, 2010) needles were collected from the sunny part of the crown, from several locations on a selected branch, from the seventh whorl, and counting from the apex, *i.e.* in the upper 1/3 of the crown length (Fig. 3). Based on this approach similar environmental conditions of the collected needles were maintained (Marcysiak, 2021).

In order to determine individual variation in the biometric traits of Scots pine needles, 50 randomly selected dry, two year old needles were collected from each model tree, thus in total the measurements of 15 500 needles were carried out. The study focused on two biometric traits of Scots pine needles that are commonly used in research concerning needle morphology, *i.e.* needle length and needle width (*e.g.*, Pawlaczyk *et al.*, 2010; Lesiczka *et al.*, 2017; Łabiszak *et al.*, 2017).

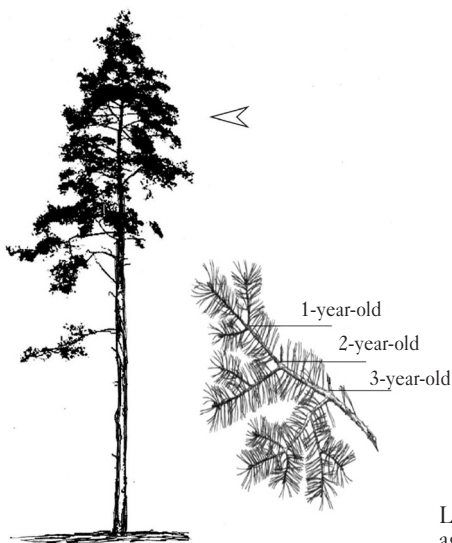


Fig. 3.

Location of branches (arrowhead) in the crown and needle age classification

The needles were scanned using an EPSON EXPRESSION 11000 XL scanner with 800dpi resolution. The captured needle images were converted to monochrome and analyzed using the computer program 'DigiShape' (Cortex Nova, 2005).

The length and width of the needles were determined according to the principle of the smallest enclosing rectangle, i.e. the rectangle containing the object and touching it with its sides. The longer side of the rectangle is parallel to the main (longer) eigenvector which is the direction in which the contour of the needle is most extended. The biometric traits were measured with an accuracy of 0.01 mm.

STATISTICAL ANALYSIS. The data set consisted of 310 samples with 50 needles in each. A cluster analysis was performed on averaged needle biometric traits and geographic coordinate data in order to correlate each model tree to the identified model tree sets and subsets as well as their distribution within the country. The analysis was accomplished using the full linkage method based on Euclidean distances. Principal component analysis (PCA) was performed to demonstrate the strength of the correlation of needle biometric traits and geographic coordinates on the resulting model tree sets and subsets. Cluster analysis and PCA were carried out using Orange Data Mining 2.7 software.

In order to describe the data set in regard to needle biometric traits, and to present the obtained results in tables, statistical analysis was performed using STATISTICA 12.0 (StatSoft Inc., 2013) to calculate the mean, minimum and maximum, standard deviation and coefficient of variation. The normality of the data and residuals was verified using the Shapiro-Wilk test ($p > 0.05$) with the data following a normal distribution. Tukey's honest significant difference (HSD) test was used to find significant differences in needle length and width variability between the identified model tree subsets. Significant differences were determined for $p < 0.05$ across the range.

Results

The age of the model trees ranged from 12 to 147 years with an average of 67 years. Accordingly, the size amplitude of the model trees was very large with DBH ranging from 8.05 cm to 40.3 cm and H from 6.3 m to 32.8 m.

The cluster analysis based on needle length and width of the model trees, as well as on geographic coordinates of the sample plots where these needles were collected, allowed us to distinguish between two model tree sets with one consisting of three subsets and the other of four (Fig. 4). Their distributions in Poland are presented in Figure 5.

The average needle length for all model trees in the country was as much as 68.68 mm. The average needle length in the first of these sets of model trees, whose needles were longer than average, was 74.58 mm. Two of the three subsets of which this set consisted, were distributed in the northern part of the country. The second set of model trees grouped the model trees whose needles were shorter than average with an average needle length of 62.05 mm. Only one of the four subsets of which this set consisted were also distributed in the same part of the country with an average needle width of 1.17 mm. Two of the three subsets of model trees whose needles were longer than average and those that were wider than average were distributed in the northern part of the country. In contrast, the distribution of model trees with both needle length and width smaller than the average values was not as consistent as the needle widths from the set of model trees with longer needles.

The principal component analysis (PCA) showed that the first principal component (PC1) explains that almost 38% of the information contained needle length in the needle biometric traits data, and to a lesser extent, geographic latitude. The second component (PC2) explains slightly more than 32% of the information, and it is positively correlated with geographic longitude (Table 1). In summary, the main component that differentiated the identified model tree sets was the needle biometric trait value, while the geographic coordinates of the sample plots were of lower importance in this respect.

The identified model tree subsets differed from each other not only in terms of their needle biometric trait values but also in terms of coefficients of these trait variations (V%) (Table 2).

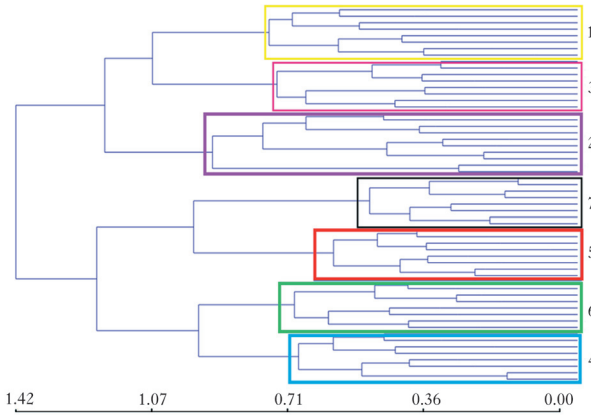


Fig. 4. Cluster analysis based on needle biometric traits and geographic coordinates

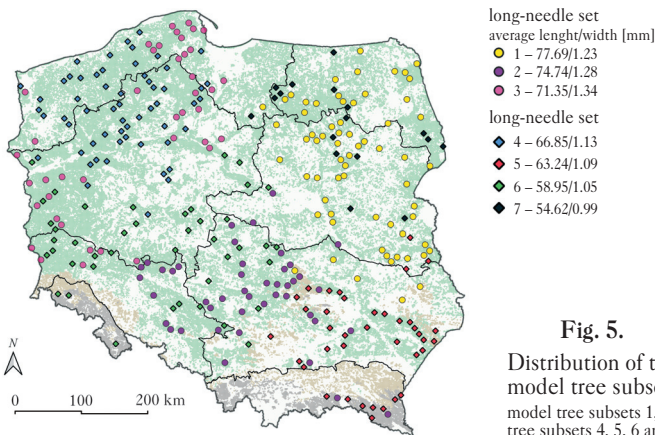


Fig. 5. Distribution of the identified model tree sets and model tree subsets in Poland
 model tree subsets 1, 2 and 3 circles – longer needle set; model tree subsets 4, 5, 6 and 7 diamonds – shorter needle subset)

Table 1.

Values of coefficients of principal component variables describing needle biometric traits and geographic coordinates of model trees in identified the aforementioned model tree subsets

Variable	PC1	PC2
Needle length	0.70	0.16
Needle width	0.69	-0.06
Longitude	0.01	0.69
Latitude	0.10	-0.69
Variance [%]	37.66	32.47

The mean coefficients of variation in needle length were higher than they were in needle width for all model tree subsets. The highest variation in needle length was observed in the fifth model tree subset, and the highest variation in needle width occurred in the first model tree subset. The lowest variation in needle length was found in the seventh model tree subset, and the lowest variation in needle width was found in the fifth model tree subset.

The results of Tukey's HSD test confirm the validity of the two aforementioned identified model tree sets in terms of needle length (Table 3) and needle width (Table 4).

Another reason in favor of identifying two model tree sets are the clearly noticeable differences in correlation between needle length and needle width in the identified model tree sets. In the first set of model trees with longer needles as average needle length decreased in subsequent model tree subsets (Fig. 6) the average needle width increased (Fig. 7). Conversely, in the second set of model trees with shorter needles as average needle length decreased in subsequent model tree subsets (Fig. 6) the average needle width also decreased (Fig. 7).

The distribution of the identified model tree sets and subsets largely coincide with the borders of natural forest regions as described by Zielony and Kliczkowska (2012) and by dendroclimatic regions (Wilczyński *et al.*, 2001) (Fig. 8). The relationships between the occurrence

Table 2.

Basic statistics of needle length (NL) and needle width (NW) in the identified model tree subsets

Trait	Subset	Number of plots	Average [mm]	Min. [mm]	Max. [mm]	SD	V [%]
NL	1	66	77.69	55.82	100.48	10.98	14.13
NW			1.23	1.01	1.52	0.10	8.22
NL	2	44	74.74	51.82	97.25	11.00	14.72
NW			1.28	1.10	1.48	0.10	8.01
NL	3	41	71.35	51.21	95.20	10.25	14.37
NW			1.34	1.18	1.52	0.09	6.80
NL	4	61	66.85	44.49	89.42	10.22	15.29
NW			1.13	0.93	1.35	0.09	7.69
NL	5	38	63.24	41.53	77.81	9.70	15.34
NW			1.09	0.90	1.21	0.07	6.59
NL	6	43	58.95	42.16	76.34	8.57	14.54
NW			1.05	0.87	1.18	0.08	7.60
NL	7	17	54.62	43.58	67.00	6.58	12.05
NW			0.99	0.86	1.09	0.07	6.89
NL	Total	310	68.68	41.53	100.48	12.32	17.92
NW			1.17	0.86	1.52	0.13	11.58

Table 3.

Results of Tukey's HSD test for needle length

Subsets	1	2	3	4	5	6	7
1		ns	<.05*	<.05*	<.05*	<.05*	<.05*
2			ns	<.05*	<.05*	<.05*	<.05*
3				ns	<.05*	<.05*	<.05*
4					ns	<.05*	<.05*
5						ns	ns
6							ns
7							

*Pair of MTSSs significantly different, $p < 0.05$; not significantly different, $p > 0.05$

Table 4.
Results of Tukey's HSD test for needle width

Subsets	1	2	3	4	5	6	7
1		ns	<.05*	<.05*	<.05*	<.05*	<.05*
2			ns	<.05*	<.05*	<.05*	<.05*
3				<.05*	<.05*	<.05*	<.05*
4					ns	<.05*	<.05*
5						ns	<.05*
6							ns
7							

*Pair of groups significantly different, $p < 0.05$; not significantly different, $p > 0.05$

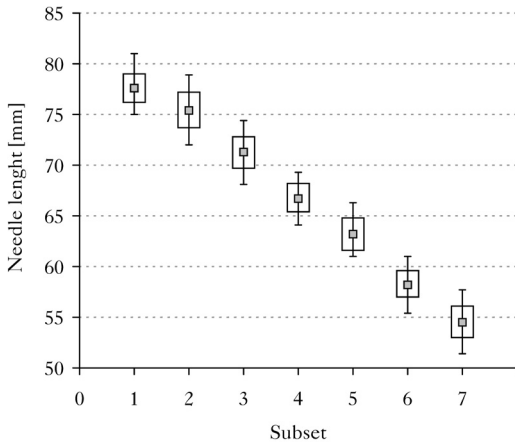


Fig. 6.

Graphical expression of differences between model tree subsets based on their average needle length

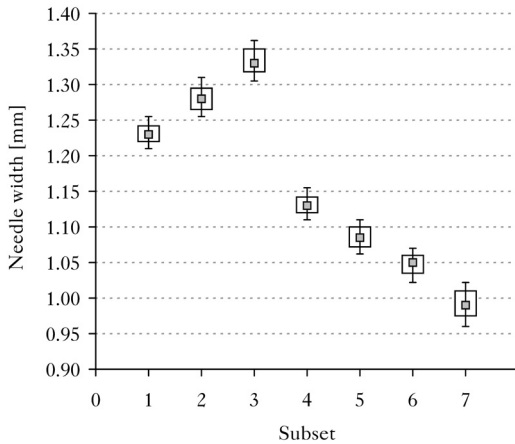


Fig. 7.

Graphical expression of differences between model tree subsets based on their average needle width

of the identified model tree subsets, and the borders of natural forest regions and dendroclimatic regions allowed the division of the country territory into four sections: the northeastern country section (NES), the northwestern country section (NWS), the southwestern country section (SWS) and the southeastern country section (SES). Three of the territories contained one pair each of the model tree subsets, *i.e.* a longer needle model tree subset and a shorter needle model tree subset. Only the southeastern section had one subset consisting of model trees with shorter needles that was dominant over the other subsets. (Fig. 8)

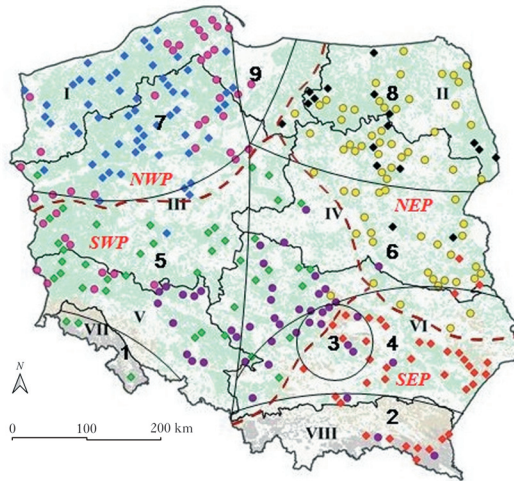


Fig. 8.

I-VIII Natural forest regions (Zielony and Kliczkowska, 2012); 1-9 dendroclimatic regions for Scots pine (Wilczyński *et al.*, 2001); four sections of Poland's territory (NES, NWS, SWS, and SES) in which various specific combinations of the model trees subsets occur

The NES includes two natural forest regions, *i.e.* Masurian-Podlasiian (II) and Mazovian-Podlasiian (IV) as well as two dendroclimatic regions (region 8 and the eastern section of region 6). Two extremely contrasting model tree subsets occur which are the first with the longest needles and the seventh with the shortest and narrowest needles.

The NWS comprises two other natural forest regions, *i.e.* the Baltic (I) and the northern section of Wielkopolska – Pomerania (III) and two dendroclimatic regions (9 and 7). There two model tree subsets (third and fourth subsets) are represented that are relatively similar in terms of needle length but differ considerably in terms of needle width.

The largest of all country territories was the SWS which includes the southern section of the Wielkopolska – Pomeranian (III), Silesian (V), Sudeten (VII) and the western section of the Małopolska (VI) natural forest regions. At the same time, SWS contains dendroclimatic regions 5 and 1 and the western section of region 6. SWS also contains two other model tree subsets, *i.e.* the second and sixth, that represent the longer needle set and shorter needle set, respectively. Few other kinds of model tree subsets could be found within the borders of the SWS.

The last and the smallest country territory was the SES which includes the eastern section of the Małopolska (VI) and Carpathian (VIII) natural forest regions and three dendroclimatic regions (4, 3 and 2). In this section, the fifth model tree subset consisting of shorter-needle model trees, is almost exclusively represented.

Discussion

Changes in the morphological and anatomical structure of pine needles were observed which reflect the diversity of environmental conditions in which they develop and function (Niinemets *et al.*, 2001; Urbaniak *et al.*, 2003). As the morphology and anatomy change, it is obvious that changes in the biometric characteristics of needles will also be observed.

In previous studies on needle biometric traits in Scots pine, the needle length was reported to be highly variable (Pravdin, 1964; Mamaev, 1973; Urbaniak, 1998; Urbaniak *et al.*, 2003; Androsiuk and Urbaniak, 2006; Androsiuk *et al.*, 2011; Lesiczka *et al.*, 2017; Łabiszak *et al.*, 2017) which is largely confirmed in the current study.

Throughout the entire range of Scots pine, within natural populations, it was observed that the length of its needles varies greatly falling into the following ranges: short (<31-45 mm),

medium (45-60 mm) and long (>60 mm) (Novikova and Milyutin, 2006). The average values of this morphological trait in needle samples collected from individual model trees growing in 310 research plots in Poland ranged from 43.58 mm to 100.48 mm with an average needle length for all model trees of 68.68 mm. If the aforementioned ranges are applied to classify the average needle lengths of the model trees studied, then the group with long needles would include as many as 241 or 77.75% of the total number of model trees. Such proportions indicate that the vast majority of sample plots established in Scots pine forests in Poland the model trees have needles in the long needle range (>60 mm).

Short needles characterize Scots pine growing at the periphery of their range (Białobok, 1967; Boratyński, 1991; Urbaniak, 1998; Mátyás *et al.*, 2004; Novikova and Milyutin, 2006) as well as those in higher altitudes (Zajączkowski, 1949; Bobowicz and Radziejewska, 1989; Skrzyżewski, 2004; Androsiuk and Urbaniak, 2006; Urbaniak and Vončina, 2008). In the areas covered by Scots forests in Poland such sites are very rarely represented. Thus, the very high proportion of model trees with needles described as long may indicate that this species is found in optimal growing conditions (Kędzierski and Chojnacki, 1952; Łabiszak *et al.*, 2017).

In some Polish Scots pine provenances and in natural forests, studies have been carried out on needle biometric traits (Bobowicz and Korczyk, 1994; Pawlaczyk *et al.*, 2010; Lesiczka *et al.*, 2017; Łabiszak *et al.*, 2017). In most cases, the average needle lengths of Scots pine calculated for the identified model tree subsets were longer than average needle lengths reported for Scots pine provenances and/or natural forests occurring in the same areas where the sample plots with identified model tree subsets were situated.

On the contrary, the average needle width in all the model tree subsets was smaller than the average needle width presented in the studies mentioned above. In our study needle width varied from 0.86 mm to 1.52 mm over the entire Scots pine range in Poland. Comparing the obtained values of all identified model tree subsets with those from the aforementioned studies, the average needle width was smaller than that shown for the Scots pine trees presented by Bobowicz and Korczyk (1994) and Pawlaczyk *et al.* (2010). This ambiguous situation undoubtedly arose from the use of two different methods to measure this needle trait. In the case of the needles examined in our study, it was determined as the average needle width over the entire needle length, while in other cases it was the maximum needle width measured at the widest part of the needle at the middle of its length. Undoubtedly, comparing the average needle width with the maximum needle width is pointless. On the other hand, our study demonstrated the significant role of needle width in separating model tree subsets into either longer or shorter needle sets (Table 4, Fig. 7).

Comparative studies of Scots pine populations from two earlier IUFRO provenance experiments carried out after 1982 in Kórnik and Supraśl showed that populations from the northern and southern ends of the European Scots pine range are characterized by shorter needles than those from the center (Androsiuk *et al.*, 2011). The results in our study showed that in Poland Scots pine trees with longer needles were found in the northern and western sections of the country, and that needle length decreased southwards.

Understanding the variation in biometric traits of Scots pine needles has some practical applications. For example, needle length, and less often needle width, along with other biometric traits of Scots pine tree crowns have been measured as component data in order to determine the size of the assimilation apparatus of the crowns (*e.g.*, Lemke, 1980). The purpose of these studies was to define the needles' efficiency in the timber volume increment that depended on many factors including: the crown density, its length and width, the tree H and DBH and its

position in the crown canopy of the tree stand as well as the tree stand age class and its stocking. Understanding needle efficiency with respect to the rates of timber volume increment growth in individual trees could be useful in determining the most efficient methods of forest management.

Another example of the practical application of needle length in pine is using it as one of the measures for monitoring changes in environmental conditions. For example, decreasing needle length has been reported in *Pinus contorta* Dougl. and *P. sylvestris* growing around sources of air and soil pollution with a decrease in needle length found to be proportional to the level of pollution concentration (Norgren and Elfving, 1994; Rautio *et al.*, 1998; Klánová *et al.*, 2009; Chudzińska *et al.*, 2014). Moreover, in studies on the effects of NO_x on black pine *Pinus nigra* Arnold needles, a pronounced shortening was observed based on the influence of this factor (Giertych *et al.*, 1999). Further, in studies conducted in Turkey in an area with significantly elevated SO₂ concentrations, the needle length in black pine needles decreased by 30-40% compared to ecologically cleaner areas (Makineci and Sevgi, 2006). The prior examples support the use of needle length as a way to assess the effects of climate change as related to stress conditions (*e.g.*, recurrent, prolonged droughts) and in the relatively greater availability of carbon dioxide required for assimilation. Although there is no data thus far that demonstrate a decrease in needle length in Scots pine as a result of the stress effects of climate change, it has been reported that needle elongation occurs in trees of this species with increased CO₂ concentrations (Lin *et al.*, 2001). However, this issue certainly deserves further study.

Conclusions

- ✦ The variability of biometric traits of Scots pine needles in the north-south gradient of the country and especially the spatial distribution of individual subsets of model trees within the pattern referring to the course of the boundaries of both the dendroclimatic regions and natural-forest regions, is a new contribution to the knowledge of Scots pine ecology in Poland.
- ✦ Since both dendroclimatic regions and natural forest regions have been delineated on the basis of environmental factors differentiating individual sections of the country, it seems obvious that there is a strong relationship between needle biometrical trait variability and regional growing conditions for Scots pine.

Authors' contribution

J.S. and D.P. – conceived the idea, designed the study and set up methodological approach of data processing. J.S. – delivered the needle samples. D.P. – scanned the needles and carried out their measurements. D.P. – conducted the statistical analyses. D.P. and J.L. – wrote the first version of the manuscript. All authors have read and agreed to the published version of the manuscript.

Conflict of interest

Authors declare there is no conflict of interest.

Funding source and acknowledgement

Data collection and research was funded by General Directorate of State Forests in Poland under the project 'Volume increment models for the main forest-forming species of Poland', contract no. EZ.271.3.20.2021, and the project 'Actual and potential site productivity in Poland for the main forest forming tree species', contract no. ER-2717-11/14.

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STRESZCZENIE

Zmienność cech biometrycznych igieł sosny zwyczajnej w Polsce

Sosna zwyczajna *Pinus sylvestris* L. jest jednym z najważniejszych gatunków drzew leśnych na świecie i ma bardzo szerokie rozmieszczenie w Europie i Azji ze względu na wysoki stopień tolerancji ekologicznej (ryc. 1).

Podstawowym celem badań było ustalenie zakresu i rozkładu przestrzennego zmienności długości i szerokości igieł sosny zwyczajnej w Polsce. Materiał badawczy stanowiły igły drugiego rocznika pobierane po 50 sztuk z kilku miejsc 7 okółka, licząc od wierzchołka (ryc. 3), ściętych drzew modelowych wybranych i pomierzonych na 310 powierzchniach badawczych (ryc. 2). Dane biometryczne zostały przetworzone, a na uśrednionych wartościach wykonano statystyki podstawowe (średnią, minimum i maksimum, odchylenie standardowe oraz współczynnik zmienności) i test HSD Tukeya, wykorzystując program Statistica 12.0 (StatSoft). Przestrzenną zmienność cech biometrycznych igieł sosny zwyczajnej w skali kraju badano przy użyciu wielowymiarowych analiz (analiza skupień, PCA), wykorzystując oprogramowanie Orange Data Mining 2.7.

Średnie wartości długości igieł zebranych z poszczególnych drzew modelowych rosnących na powierzchniach próbnych w Polsce wahały się od 43,58 do 100,48 mm, a średnia długość igieł dla wszystkich drzew modelowych wynosiła 68,68 mm (tab. 2). Duża zmienność długości igieł u sosny zwyczajnej uzasadniała wyróżnienie mniejszych jednostek grupujących drzewa modelowe z igłami o podobnej długości. Biorąc pod uwagę długość i szerokość igieł oraz współrzędne geograficzne, wyróżniono za pomocą analizy skupień dwa zbiory drzew modelowych o przewadze igieł o długości większej od średniej (długoigielne) oraz o długości mniejszej od średniej (krótkoigielne) (ryc. 4). Ich rozmieszczenie w Polsce przedstawiono na rycinie 5. Analiza składowych głównych (PCA) wykazała, że pierwsza składowa główna (PC1) wyjaśnia, iż prawie 38% informacji zawierała długość igieł w danych cech biometrycznych igieł, zaś druga składowa (PC2) wyjaśnia nieco ponad 32% informacji i jest dodatnio skorelowana z długością geograficzną (tab. 1). Można zatem stwierdzić, że główną składową różnicującą wyróżnione zbiory drzew modelowych były wartości cech biometrycznych igieł. Wyniki testu HSD Tukeya dla długości igieł oraz ich szerokości potwierdziły zasadność wyróżnionych dwóch wyżej wymienionych zbiorów drzew modelowych (tab. 3, 4; ryc. 6, 7).

Zbiór drzew długoigielnych składał się z trzech podzbiorów, w których średnia szerokość igieł zmniejszała się wraz ze zwiększaniem się ich średniej długości, natomiast zbiór drzew krótkoigielnych składał się z czterech podzbiorów, w których średnia szerokość igieł zmniejszała się wraz ze skracaniem się ich średniej długości (ryc. 5; tab. 2).

Średnia szerokość igieł wynosiła 1,17 mm. Dwa z trzech podzbiorów drzew modelowych, których igły były dłuższe od średniej, a ich szerokość większa od średniej, były rozmieszczone w północnej części kraju, natomiast rozmieszczenie drzew modelowych o zarówno długości, jak i szerokości igieł mniejszych od średnich wartości tych cech nie było równie jednoznaczne, jak w przypadku szerokości igieł ze zbioru drzew modelowych o dłuższych igłach. Rozmieszczenie poszczególnych podzbiorów drzew modelowych stało się podstawą do zidentyfikowania wzorca przestrzennego rozkładu zmienności cech biometrycznych igieł sosny zwyczajnej w Polsce określonego na podstawie obu biometrycznych cech igieł, tj. ich długości i szerokości. Wzorec ten został wyrażony w postaci wydzielenia czterech części kraju (północno-wschodniej, północno-zachodniej, południowo-zachodniej i południowo-wschodniej), zróżnicowanych pod względem wielkości i występujących w nich podzbiorów drzew modelowych (ryc. 8).

W trzech częściach Polski stwierdzono po jednej parze podzbiorów drzew modelowych, podzbiór drzew modelowych o dłuższych igłach i podzbiór drzew modelowych o krótszych igłach. Tylko w południowo-wschodniej części był reprezentowany jeden podzbiór składający się z drzew modelowych krótkoigielnych, który zdecydowanie dominował nad zaledwie kilkoma drzewami modelowymi z jednego z podzbiorów sosen długoigielnych. Przyczyna grupowania się parami podzbiorów drzew modelowych o dłuższych i krótszych igłach w wyróżnionych obszarach pozostaje na razie nieznana.

Rozmieszczenie wyróżnionych podzbiorów w znacznej mierze pokrywało się z granicami zarówno krain przyrodniczo-leśnych, jak i wyróżnionych w Polsce regionów dendroklimatycznych dla sosny zwyczajnej (ryc. 8). Taki rozkład przestrzenny wyróżnionych podzbiorów wskazuje na związek zmienności cech igieł z regionalnymi warunkami wzrostu sosny zwyczajnej w Polsce.