

Nadbitka

ALFRED E. SZMIDT

**Genetic variation among eleven populations of Scots pine
(*Pinus sylvestris* L.) as determined by catalase polymorphism**

INTRODUCTION

Until quite lately our knowledge of the genetic variation of forest trees populations was based on the measurements of various morphological characters, where in most cases a large number of different genes are involved. During the last few years a rapid development of the isoenzyme studies shed quite a new light on this variation. As it has been shown by numerous authors e.g. Bergmann (1974, 1978), Lundkvist (1979), Mejnartowicz (1976), Rudin (1974) a surprisingly great amount of variation has been indicated in populations of various forest trees species. In the previous paper (Szmidt, 1979) it was postulated that the multiple forms of catalase occurring in Scots pine haploid macrogametophyte tissue (endosperm) exhibit a simple Mendelian mode of inheritance according to the one gene two alleles system. This paper reports the preliminary identification of catalase polymorphism in eleven populations of Scots pine originating from Poland.

MATERIALS AND METHODS

Seed material was collected from single trees in 11 populations of Scots pine originating from different parts of Poland. In each of the investigated populations 18 to 28 individuals were analysed with the exception of populations Lubin, Niepołomice and Goleniów where seed samples from only 10, 11 and 14 trees were available respectively. The locations of the investigated populations are presented in Fig. 1. Populations Lubin, Świerklaniec and Niepołomice were established from seeds of unknown origin while the remaining populations are probably indigeneous. The catalase polymorphism was investigated in the haploid endosperm tissue isolated from dormant seeds as described earlier (Szmidt, 1979). In order to evaluate the genetic similarity of the inve-

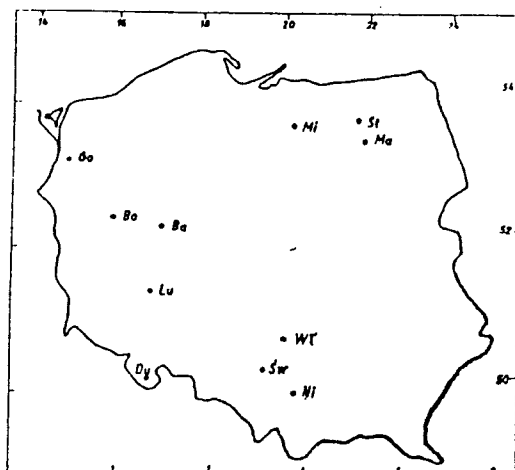


Fig. 1. Locations of 11 investigated populations of Scots pine

stigated populations the genotypic similarity index (I) as proposed by Hedrick (1971) was used, according to the following formula:

$$I_{xy} = \frac{\sum_{j=1}^n P_{jx} \cdot P_{jy}}{1/2 \left(\sum_{j=1}^n P_{jx}^2 + \sum_{j=1}^n P_{jy}^2 \right)},$$

where P_{jx} and P_{jy} are the frequencies of the j -th genotype in populations x and y , and n is the number of genotypes at the locus.

RESULTS

Out of seven catalase variants determined so far (Szmidt, 1979) 3 to 6 occurred in each of the investigated populations (Tab. 1). Variants C-1 and C-5 were the most widespread and occurred in all populations

Table 1

Catalase variants frequencies in 11 populations of Scots pine

Variant Population	C-1	C-2	C-3	C-4	C-5	C-6	C-7
Goleniów (Go)	0.722	0.000	0.000	0.000	0.273	0.000	0.055
Strzałowo (St)	0.525	0.075	0.025	0.000	0.250	0.075	0.050
Maskulińskie (Ma)	0.675	0.075	0.000	0.000	0.200	0.025	0.025
Miomłyn (Mi)	0.444	0.111	0.000	0.000	0.417	0.000	0.028
Bolewice (Bo)	0.481	0.130	0.037	0.000	0.333	0.000	0.019
Babki (Ba)	0.521	0.083	0.000	0.021	0.292	0.000	0.083
Lubin (Lu)	0.645	0.035	0.000	0.035	0.215	0.035	0.035
Świerklaniec (Sw)	0.518	0.054	0.000	0.000	0.357	0.000	0.071
Włoszczowa (Wl)	0.683	0.045	0.000	0.000	0.205	0.022	0.045
Duszniki (Du)	0.750	0.025	0.000	0.000	0.175	0.000	0.050
Niepołomice (Ni)	0.364	0.136	0.000	0.000	0.316	0.091	0.091

Table 2

Catalase genotypes frequencies and heterozygosity in 11 populations of Scots pine

Genotype Population	1 - 1	1 - 2	1 - 3	1 - 4	1 - 5	1 - 6	1 - 7	2 - 2	2 - 5	2 - 7	3 - 5	5 - 5	5 - 7	6 - 6	h_{exp}
Go	0.555	0.000	0.000	0.000	0.334	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.111	0.000	0.445
St	0.300	0.000	0.050	0.000	0.200	0.150	0.050	0.000	0.100	0.050	0.000	0.100	0.000	0.000	0.600
Ma	0.500	0.050	0.000	0.000	0.200	0.050	0.050	0.050	0.000	0.000	0.000	0.100	0.000	0.000	0.450
Mi	0.222	0.056	0.000	0.000	0.388	0.000	0.000	0.056	0.056	0.000	0.000	0.166	0.056	0.000	0.556
Bo	0.296	0.111	0.000	0.000	0.260	0.000	0.000	0.037	0.074	0.000	0.074	0.111	0.037	0.000	0.556
Ba	0.291	0.042	0.000	0.042	0.292	0.000	0.083	0.042	0.000	0.000	0.000	0.083	0.083	0.000	0.584
Lu	0.430	0.071	0.000	0.071	0.215	0.071	0.000	0.000	0.000	0.000	0.000	0.071	0.071	0.000	0.499
Sw	0.357	0.000	0.000	0.000	0.250	0.000	0.071	0.036	0.036	0.000	0.000	0.179	0.071	0.000	0.428
Wl	0.455	0.045	0.000	0.000	0.274	0.045	0.091	0.000	0.045	0.000	0.000	0.045	0.000	0.000	0.500
Du	0.600	0.000	0.000	0.000	0.200	0.000	0.100	0.000	0.050	0.000	0.000	0.050	0.000	0.000	0.350
Ni	0.182	0.091	0.000	0.000	0.272	0.000	0.000	0.091	0.000	0.000	0.000	0.091	0.182	0.091	0.545

Table 3

Genotypic similarity (I) among 11 populations of Scots pine

	Go	St	Ma	Mi	Bo	Ba	Lu	Św	Wl	Du	Ni
Go	—										
St	0.761	—									
Ma	0.927	0.857	—								
Mi	0.771	0.790	0.767	—							
Bo	0.815	0.850	0.750	0.922	—						
Ba	0.851	0.857	0.866	0.927	0.939	—					
Lu	0.924	0.872	0.961	0.802	0.898	0.907	—				
Św	0.863	0.875	0.923	0.769	0.916	0.954	0.915	—			
Wl	0.942	0.887	0.975	0.818	0.890	0.915	0.953	0.925	—		
Du	0.943	0.789	0.964	0.677	0.544	0.808	0.908	0.868	0.955	—	
Ni	0.700	0.667	0.678	0.874	0.842	0.901	0.758	0.817	0.703	0.571	—

with frequencies higher than 0.500 and 0.100 respectively. Variant C-7 also occurred commonly however with a frequency of less than 0.100. The remaining 4 variants occurred in only some of the investigated populations.

The observed frequencies of different catalase genotypes and the observed proportions of heterozygotes are presented in Table 2. The homozygous genotype C-1/C-1 occurred most commonly and had the most pronounced contribution to the observed homozygosity of the investigated populations. Highest frequencies of this genotype as well as the lowest heterozygosity values have been indicated in southern popu-

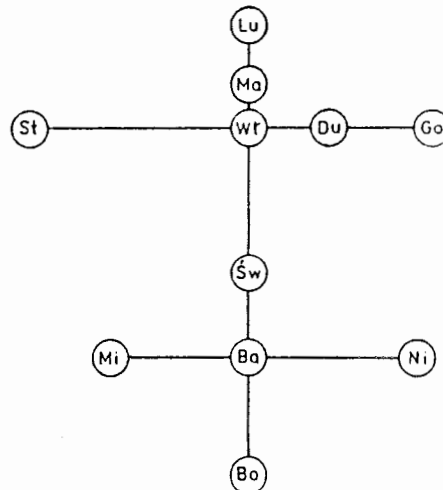


Fig. 2. Genotypic distance between 11 populations of Scots pine

lations Duszniki, Świerklaniec, Lubin and in the northern population Goleniów. On the other hand, populations Strzałowo, Mitomłyn, Bąbki and Bolewice had much higher proportions of heterozygotes. Genotypic similarity (I) values of the investigated populations are presented in

Table 3. The populations genotypically most distinct from all others were Strzałowo and Niepołomice. The values of genotypic similarity (I) were then transformed into values of genotypic distance ($D=1-I$) and expressed as a dendrite (Fig. 2).

DISCUSSION

Many authors pointed out a marked heterogeneity of Polish populations of Scots pine (Giertych, 1970; Przybylski, 1972; Cierniewski and Przybylski, 1978). Also in the present study a considerable variation of the investigated populations has been indicated with regard to the frequency of occurrence of various catalase variants and genotypes. Out of 11 populations studied, the most outstanding one was population Strzałowo located in the north-eastern part of Poland (Masurians). It was characterized by a highest proportion of heterozygotes ($h=0.600$) as well as by the lowest genotypic similarity values in a comparison with all remaining populations studied (Fig. 2). A marked heterozygosity of this population has been reported as well by Mejnartowicz (1979) for three other enzymatic loci. A relatively high proportion of heterozygotes has been also observed in another Masurian population Miłomłyn ($h=0.556$) and in the two western populations Bolewice ($h=0.556$) and Babki ($h=0.584$). It is worth noting, that these populations originate from the areas known as the most abundant in valuable pine stands in Poland. Giertych (1970) postulated, that fairly good adaptive value of Scots pine populations from central Europe could be connected with an increase in their heterozygosity resulting from the postglacial fusion of the eastern and western ranges of this species. The above results could support to some degree this postulation. It must be kept in mind however, that especially in the case of Masurian populations of Scots pine one may expect a considerable variation even among adjacent stands (Przybylski, 1972; Cierniewski and Przybylski, 1978). It was also reflected in a relatively low genotypic similarity of the populations Strzałowo, Maskulińskie and Miłomłyn. Similar differentiation among several Masurian populations has been found by Mejnartowicz (1979) with respect to the frequency of occurrence of leucine aminopeptidase and acid phosphatase isoenzymes. However, since many of populations of Polish Scots pine were established artificially it is impossible to determine whether or not these differences result from the processes of natural genetic differentiation.

On the other hand, there is some evidence from the quantitative studies that Scots pine populations originating from mountains e.g. Kozłina Kłodzka in the deep south of Poland are among the most poorly growing populations in our country (Przybylski, 1972; Cierniew-

ski and Przybylski, 1978). The least heterozygous population found in the present study was population Duszniki ($h=0.350$) which in fact originates from Kotlina Kłodzka.

In general the highest proportions of heterozygotes has been observed in western and Masurian populations. The above differences in heterozygosity were mainly due to the different frequencies of the C-1/C-1 genotype, being the lowest in western populations Bolewice (0.296), Babki (0.291) and in the Masurian populations Strzałowo (0.300) and Miłomłyn (0.222). The frequency of occurrence of this genotype in southern populations was much higher and ranged between 0.357 (Świerk-laniec) and 0.600 (Duszniki). The most striking exception from the above pattern of distribution of the C-1/C-1 genotype was the southern population Niepołomice, which is also one of the most distant population in a comparison with remaining. The distinctiveness of this population has been also pointed out by Mejnartowicz (1979), who suggested its Austrian origin. Since the results presented here concerned the polymorphism of only one genetic locus, the above characterization of variation of the investigated populations cannot be generalized too far. On the other hand however, a general accordance of our data with the results from other quantitative and enzymatic studies underlines the value of such investigations.

SUMMARY

The polymorphism of catalase has been studied in 11 populations of Scots pine (*Pinus sylvestris* L.) using starch gel electrophoresis. Three to six different catalase variants occurred in each of the investigated populations. The observed heterozygosity ranged between 0.350 and 0.600. A highest heterozygosity was observed in populations Strzałowo, Miłomłyn, Bolewice and Babki, originating from the areas known as the most abundant in valuable pine stands in Poland. On the other hand, southern populations considered as the most poorly growing in our country, were in most cases much less heterozygous.

Institute of Dendrology
Kórnik nr. Poznań

LITERATURE

1. Bergmann F. — 1974. Genetische Abstand zwischen Populationen II. Die Bestimmung des genetischen Abstands zwischen europäischen Fichtenpopulationen (*Picea abies*) auf der Basis von Isoenzym-Genhäufigkeiten. *Silvae Genet.* 23: 28 - 31.
2. Bergmann F. — 1978. The allelic distribution at an acid phosphatase locus in Norway Spruce (*Picea abies*) along similar climatic gradients. *Theoret. Appl. Genet.* 52: 57 - 64.

3. Cierniewski M., Przybylski T. — 1978. Zmienność cech wzrostowych 10-letniej sosny zwyczajnej (*Pinus silvestris* L.) polskich proveniencji, Arbor. Kórn. 23: 171 - 183.
4. Giertych M. — 1970. Zagadnienia genetyczne: Sosna zwyczajna. PWN, Warszawa—Poznań, 232 - 261.
5. Hedrick P. W. — 1971. A new approach to measuring genetic similarity. Evolution 25: 276 - 280.
6. Lundkvist K. — 1979. Allozyme frequency distributions in four Swedish populations of Norway spruce (*Picea abies* K.). I Estimations of genetic variation within and among populations, genetic linkage and a mating system parameter, Hereditas 90: 127 - 143.
7. Mejnartowicz L. — 1976. Genetic investigations on Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco.) populations. Arbor. Kórn. 21: 126 - 187.
8. Mejnartowicz L. — 1979. Genetic variation in some isoenzyme loci in Scots pine (*Pinus silvestris* L.) populations. Arbor. Kórn. 24: 91 - 104.
9. Przybylski T. — 1972. Variability of Scots pine (*Pinus silvestris* L.) of polish provenances. Arbor. Kórn. 17: 121 - 167.
10. Rudin D. — 1974. Gene and genotype frequencies in Swedish Scots Pine populations studied by the isozyme technique. Hereditas 78: 325.
11. Szmidt A. E. — 1979. Inheritance of catalase multiple forms in Scots pine (*Pinus silvestris* L.) endosperm. Arbor. Kórn. 24: 105 - 110.

ALFRED E. SZMIDT

Zmienność genetyczna jedenastu populacji sosny zwyczajnej (Pinus sylvestris L.) określona na podstawie polimorfizmu katalazy

Streszczenie

Stosując elektroforezę na żelu skrobiowym, badano polimorfizm katalazy w 11 populacjach sosny zwyczajnej (*Pinus sylvestris* L.). W każdej z badanych populacji występowało od 3 do 6 różnych fenotypów katalazy. Heterozygotyczność badanych populacji wahała się od 0,350 do 0,600. Najbardziej heterozygotyczne były populacje: Strzałowo, Miłomłyn, Bolewice i Babki pochodzące z terenów znanych jako źródło najlepszych polskich proveniencji sosny. Natomiast populacje południowe zaliczane na podstawie badań proveniencyjnych do najsłabiej rosnących charakteryzowały się w większości znacznie niższą heterozygotycznością.

АЛЬФРЕД Э. ШМИДТ

Генетическая изменчивость одиннадцати популяций сосны обыкновенной (Pinus sylvestris L.) определения на основании полиморфизма каталазы

Резюме

С помощью электрофореза на крахмальном геле был исследован полиморфизм каталазы в 11 популяциях сосны обыкновенной (*Pinus sylvestris* L.). Во всех исследуемых популяциях встречалось от 3 до 6 разных фенотипов каталазы. Гетерозиготность исследуемых популяций колебалась от 0,350 до 0,600. Самой большой гетерозиготностью характеризовались популяции Стжалово, Миломлын, Болевнице и Бабки. Вышеуказанные популяции известны как одни из лучших в Польше. Южные популяции, которые на основании провененционных исследований характеризуются худшими показателями роста, имели значительно меньшую степень гетерозиготности.