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Comparison of phenotypic and genetic selections in Scots pine *(Pinus sylvestris* L.) single tree plot half-sib progeny tests

Abstract: The study was carried out in three Scots pine (*Pinus sylvestris* L.) single tree plot half-sib progeny tests planted in 1984–86. Phenotypic selection was done in two ways: F about 0.5% to 1% of the total number of trees were chosen by the author on the basis of their appearance only, and Fbis on the basis of diameters at breast height and heights measurements and observations scored for individual trees. The best trees were selected on the basis of the index value weighing traits by their economic value. Genetic selection was performed based on both family index value (W_f) and tree index value (W_T), weighing traits by heritability and economic value. This was done in four different ways: (A) The best trees were selected only on the basis of their index value (W_T) with no attention paid to the family; (B) About 10 to 12 trees were selected in the best families, (both (W_f) and (W_T) were taken into consideration); (C) The best 30% of the families (W_f) were selected and then equal numbers of best trees were selected (W_T); (D) The same number families (W_f) as in the phenotypic selection were selected and within these families equal numbers of best trees (W_T). The number of trees that were genetically selected was always the same as the number of phenotypically selected ones (selection type F). The selections were compared using a calculated expected genetic gain and the relative loss of effective population size. As expected, phenotypic selection resulted in the lowest genetic gain. Phenotypic selection generally conserved genetic variability, while genetic selection reduced it, especially when genetic gain was maximised. Phenotypic selection type F generally identifies the good families. The agreement of genetic selection with the phenotypic selection is low (0% to 19%) at the individual tree level. This is slightly better with phenotypic selections using measurements data (Fbis). Phenotypic selection is recommended only where information concerning pedigrees is not available. It can provide a simple and cheap way of obtaining material for future selection. Genetic selection method (A) where best trees were selected without any restrictions provided highest genetic gain and cause the greatest loss of genetic diversity.

Additional key words: selection index, heritability, genetic gain, genetic diversity, phenotypic and genotypic selection.

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Introduction

Selection is defined as the "choosing of individuals with desired qualities to serve as parents for the next generation" (Zobel and Talbert 1984). It can be performed using several different methodologies, the choice of which is influenced both by the genetic information available and the time and cost involved.

Phenotypic selection is the oldest method of selection, where the best individuals are selected on the basis of their appearance without any knowledge

about the heritability of the traits of interest and is based on the assumption that a good phenotype is associated with a good genotype. This method is simple, fast and effective, but it has also disadvantages. When we chose parents, we do not know if their offspring will be of interest to us also.

Phenotypic selection can be performed by several methods. The simplest one is when selection is based only on the personal feelings of the breeder (for example, when choosing trees for a silvicultural thinning). In some cases general rules regulating phenotypic selection are defined. For example, seed stands are chosen by a special commission in Poland, on the basis of observations and measurements and, if possible, on information about their origin (Kocięcki 1988). Trees can be selected after measuring their phenotypic features (Giertych 1995). In the tree comparison method (Ledig 1974) some restrictions are imposed on the number of neighbouring trees, which are to be compared to the chosen ones.

Genetic selection requires that individuals have a known pedigree. For the selection to be optimal, all genetic information must be combined into an index. It should take into account the phenotypic value of the family, within–family variations and trait heritabilities. This is known as a combined index. Index selection is always superior to alternative methods in terms of genetic gain (Falconer and Mackay 1996).

The main selection method used in Poland is population selection (Matras 1989). Individual selection is supplemental to the main selection strategy. During individual selection plus trees are selected only on the basis of their phenotypes. Foresters have been interested in a comparison between the effectiveness of phenotypic and genotypic selection (Urbański 1998).

The first comparison between phenotypic and genotypic selection was made by Wei and Lindgren (1991). This study was based only on a theoretical approach. In another paper Wei (1995) obtained results for two practical examples. One is an experiment with half sib families of *Pinus contorta* and the second is an experiment with *Pinus sylvestris* full sibs. Selection revealed that genetic variance depended on heritability and selection intensity. If selection is more intensive, genetic gain is higher, but this results in a greater reduction in genetic diversity. Using phenotypic selection the genetic gain is small but also reduction of genetic diversity is small.

Giertych (1995) compared genetic gain for volume for 14 years old Scots pine selected by genotypic or phenotypic methods in a progeny test. Phenotypic selection in this study was made choosing 50 trees, which had the highest volume, irrespective of their family. Selection was made after measuring the trees. Genetic selection was performed using calculated heritabilities on the provenance, family and individual level. Genetic gain has been expressed as percentages of the mean for the whole trial. It amounted to 58% using genotypic selection and 44% using phenotypic selection. Of the genotypically selected trees 48% were also phenotypically selected.

A similar comparison of phenotypic and genotypic selection methods was made with *Pinus elliottii* (Pswarayi and Barnes 1994). A combined index selection was compared with classical phenotypic selection on a plantation in Zimbabwe for volume after 15 years. Phenotypically about 1% of trees (60 trees) from the population were selected. Selection methods were compared using genetic gain on volume and additive variance reduction. The genetic gain was 52.5% resulting from genetic selection and 46.3% resulting from phenotypic selection. These results are similar to those of Giertych (1995). However, the combined index selection resulted in a greater reduction in the additive genetic variance, down to 50% compared with 83% for phenotypic selection.

In another study on Scots pine full-sib progenies Giertych and Mąka (1994) have shown that phenotypic selection may sometimes assign much importance to a trait with little or no heritability, such as presence of spike knots, which will be of no consequence in genotypic selection.

In other papers phenotypic and genotypic selection were compared on the basis of computer simulations using the Monte Carlo procedure. Generally, they can be divided into those, which examine infinite populations (Wei and Lindgren 1991, 1994, Wei 1995, Wei et al 1998) and finite populations (Cotterill and Jackson 1989, Anderson et al. 1998a, 1998b, 1998c). These studies try to investigate general rules. The general conclusion from these papers indicates that genotypic selection provides higher genetic gain. In some situations this theoretical approach also indicates that phenotypic selection, which is simple and cheap, performs on the same level as genotypic selection.

The comparison of different methods selection methods within Scots pine half sib family seedling seed orchards is the aim of this paper. Results of this study can also provide some guidance on how to compromise between capturing a sufficiently large genetic gain while maintaining genetic diversity in the breeding population.

Materials and methods

Location and design of the experimental areas

The study was carried out on three Scots pine (*Pinus sylvestris L.*) single tree plot half-sib progeny tests planted in 1984–86 as seedling seed orchards (Table 1). Open-pollinated progenies (half–sibs) were planted, which in this paper are referred to as families. While the mothers are plus trees, fathers are

Table 1. Experimental areas locations and their basic characteristics

Forest District. Compartment	Elevation (m) Latitude Longitude	Forest Range	Year of planting	Area [ha]	Number of families	Number of trees
Rosiny, 390	25	Zaporowo	1985	17.42	68	12 825
	54°25'N, 19°51'E					
Smardze, 127a	240	Syców	1984	7.43	39	4 272
	51°12'N, 17°55'E					
Kierz, 40abfg	320	Świdnik	1986	3.05	41	2 807
	51°10'N, 22°17'E					

not known but it is assumed that they are from nearby stands. Each mother tree is numbered to identify the family and identification numbers those are related to used in national register of plus trees (Matras 1996). Trees were randomly planted in 3 × 3 m spacing in a single tree plot distribution.

Phenotypic selection

A phenotypic selection for the purpose of this study was done in each experimental area, choosing the best trees on the basis of theirs appearance only (F). Trees that were straight, not forked and with regular crowns were selected. Unconsciously, trees where primarily selected for traits, which influence wood quality but tree dimensions were also considered. On each area about 0.5% to 1% of the total number of trees were chosen. All the phenotypic selections were made by the author prior to any measurements.

The second phenotypic selection (Fbis) was made on the basis of diameters at breast height and height measurements as well as some assessed quality traits. Simple index values were calculated for each tree (without a genetic component, i.e. $h^2 = 1$ for all traits) and the best trees were selected on the basis of their index value W (equation no 1). Economic weights (Table 2) were employed for the construction of indices in Fbis as was done in genetic selection. They also have been kept in the mind of the breeder when using method F but there is no control over this.

Genetic selection

Index selection was performed using both family index value (W_f) and tree index value (W_t). These indices include a genetic component – trait heritability. The same numbers of trees were selected genetically as using phenotypic selection (F). Genetic selection was done in four different ways:

A. The best trees were selected only on the basis of their index value (W_T), where selection did not pay attention to the family.
B. Selection of about 10 to 12 trees per family starting with the best families. In this selection both (W_f) and (W_T) were taken into consideration.
C. Selection of 30% of the best families (W_f) with an equal number of trees selected (W_T) per family.

D. The same number of families (W_f) were selected as was done in phenotypic selection (F) and then an equal number of the best trees per family were selected (W_T).

This is not an error free genetic selection because of comparison of plus trees or rather their progenies. However, it is permissible because the selection is made within the progenies and not among the plus trees themselves.

Measurements and assessments of all trees (Table 2)

For all trees diameter at breast height (DBH) and height were measured. Also for each tree some quality features were assessed on each area including: stem straightness, crown width, branch diameter, multiple top, branch angle, crown form and basal sweep. Additionally, in the area near Rosiny the occurrence of lateral branches, which compete as multiple leaders, stem forking and occurrence of male and female flowers were assessed. In Smardze additionally, the occurrence of crooked branches on the top whorl and presence of two-year-old cones were assessed. The presence of two-years-old cones and main stem forking were assessed additionally in Kierz (Table 2).

Statistical methods

Analyses were made only for families represented by more than 20 trees. The ANOVA and estimation of variance components for the measured and assessed traits were performed according to the following model:

$Y_{ij} = \mu + F_i + E_{ij}$
μ – total mean
F_i – random effect of family i
E_{ij} – random effect of tree j in family i (random error)

Source of variance	d.f.	Expected mean square	F
Total	N-1		
Families	F-1	$\sigma^2_E + n\sigma^2_F = A$	A/B
Error	N-F	$\sigma^2_E = B$	

N   –   total number of trees

F   –   number of families

$n = (\sum_{i=1}^{F} s_i - \sum_{i=1}^{F} s_i^2 / \sum_{i=1}^{F} s_i)(F - 1)$ –   mean number of trees per family

s_i –   number of trees in family i

σ_E^2 –   variance component for residual

σ_F^2 –   variance component for family

$V_{Ph} = \sigma_E^2 + \sigma_F^2$ –   phenotypic variance

$V_F = \dfrac{\sigma_E^2}{n} + \sigma_F^2$ –   family variance

$h_F^2 = \sigma_F^2 / (\dfrac{\sigma_E^2}{n} + \sigma_F^2) = (A - B) / A$ –   family heritability

$h_S^2 = 4\sigma_F^2 / (\sigma_E^2 + \sigma_F^2) = 4\sigma_F^2 / V_{Ph}$ –   single tree heritability

$h_w^2 = h_s^2 (\dfrac{1 - 0.25}{1 - h_s^2 0.25})$ –   within family heritability (Falconer 1974)

Table 2. Measured and accessed traits

No.	Trait	Mode of measurement			Economical weight
1	DBH	Average of 2 cross measures [1 mm]			1.0
2	Height	Using a ruler bar [1 cm]			1.0
		Traits scored visually on a 3 point subjective scale			
	Trait	Value			
		1	2	3	
3	Stem straightness	straight	medium	crooked	–3.0
4	Crown width	narrow	medium	wide	–0.5
5	Branch diameter	thin	medium	thick	–0.5
6	Multiple tops	one	two or more	absent	–2.0
7	Branch angle	90°–60°	60°–30°	< 30°	–1.0
8	Crown form	full	medium	regular and open	1.0
9	Cones	many	some	few or not present	–0.5
		Traits scored visually on a 2 point scale (present – not present)			
10	Lateral branches which compete with the leader				–0.5
11	Basal sweep				–2.0
12	Stem forking under DBH				–2.0
13	Crooked branches on the top whorl possibly caused by insect or fungal attack				–2.0
14	Male and females flowers				0.25
15	Main stem forking above DBH				–2.0

Calculated mean squares for families and residuals were compared with the expected mean squares and the variance components for the family and the residuals were estimated. Using these variance components, heritabilities for families and for single trees were calculated.

Heritability for binominal traits was transformed according to Falconer and Mackay (1996) and McGuirk (1989) using the formula:

(1) $h_n^2 = h_{0/1}^2 \dfrac{1 - p}{i^2 p}$

where:

p – proportion of individuals with threshold traits

i – mean liability of affected individuals in the population from Appendix, Table A in Falconer and Mackay (1996)

h_n^2 – heritability in normal scale

$h_{0/1}^2$ – heritability in binominal scale

There is a substantial literature dealing with the estimation of heritability from binominal data (Robertson and Lerner 1949, Dempster and Lerner 1950. Van Vleck 1972, Hill and Smith 1977, McGuirk 1989). The theory treats binominal characters as threshold traits, with an underlying normal distribu-

tion of genetic and environmental values, which are not expressed until a certain threshold value is reached on the underlying normal scale. The underlying continuous variable has been called the liability (*i*) in the context of human diseases as threshold characters and this term is used in equation after Falconer and Mackay (1996).

In order to select trees simultaneously allowing for several traits, an index value was calculated for each tree and family using the formulas:

(2) $W = d_1 E_1 + ... + d_k E_k$ – for phenotypic tree index value

where:

d_k – selection differential for trait *k*

$d_k = (x_k - \bar{x}_k) / \sqrt{V_k}$ – selection differential

V_k – trait *k* phenotypic variance

$\bar{x}_k$ – average trait *k* value

x_k – trait value

(3) $W_f = h_{F1}^2 d_{F1} E_1 + ... + h_{Fk}^2 d_{Fk} E_k$ – genotypic family index value (Giertych and Mąka 1994)

where:

h_{F1}^2 – family heritability for trait number 1

d_{F1} – family selection differential for trait number 1

$d_F = (\bar{x}_F - \bar{X}) / \sqrt{V_F}$

$\bar{x}_F$ – mean value of trait x for family (arithmetic average)

$\bar{X}$ – total mean for trait x

V_F – family variance

Genotypic index value for a tree was calculated using a combined selection where account was taken of the genetic value of its family and the genetic value of the tree within its family:

(4) $W_T = W_f + W_t$ – Genotypic value of the tree

were:

(5) $W_T = h_{w1}^2 d_{w1} E_1 + ... + h_{wk}^2 d_{wk} E_k$ – genetic index value of a tree within its family

d_{wk} – selection differential for trait *k*

$d_w = (x - \bar{x}_F) / \sqrt{V_w}$ – selection differential

$V_w = \sigma_E^2 - \sigma_E^2 / n$ – within family variance (Falconer 1974)

X – trait value

The selections A, B, C, D, F and Fbis were compared calculating the genetic gain:

For genetic selections – (6) $DG = h_{F1}^2 d_{F1} + h_{w1}^2 d_{w1} + ... + h_{Fk}^2 d_{Fk} + h_{wl}^2 d_{wk}$

For phenotypic selections – (7) $DG = h_{s1}^2 d_1 + ... + h_{sk}^2 d_k$

In this formula notations are the same as above.

Effective population size N_e was calculated after Robertson (1961):

(8) $N_e = n^2 / \sum n_j^2$

where:

n denotes the number of trees on the area and n_j the number of trees in families.

Also calculated was the loss of genetic diversity (LA) of Wei (1996) following Askew & El–Kassaby (LA = F–N_e) and relative loss (LR) which is expressed in the form

(9) $LR = (F-N_e)/F$

The general project investigation organisation is presented in Figure 1.

Results

Average traits values and their standard deviations as well as phenotypic and family components of variance were presented in table 3.

In the area near Rosiny 8483 trees were evaluated. All the assessed traits, except lateral branches competing for leader shoot, exhibited statistically significant differences between families (Table 3). The highest values of the F statistic were obtained for DBH and height. Male and female flowers had the largest family, within family and single tree heritabilities (0.943,
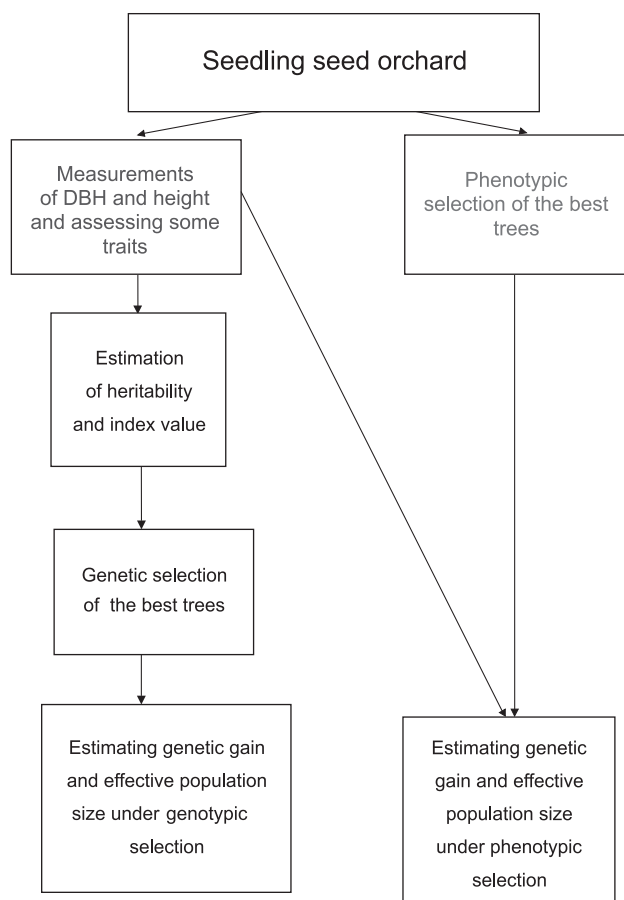
Fig. 1. General project organisation

In the area near Smardze 2659 trees were evaluated. No significant family differences were detected for multiple top leader and crocked branched (Table 3). All remaining traits analysed had significant family effects. The F statistic, was highly significant for branch angle, crown form and DBH. Crooked branches on the top whorl had the highest family, within family and single tree heritabilities (0.937, 0.381, 0.51) respectively. High heritabilities were also obtained for branch angle, crown form, DBH, and height. In Smardze, as in Rosiny, the trait multiple top had the lowest family heritability (Table 4).

In the area near Kierz 1106 trees were evaluated. Only for height, multiple tops and cones were significant family effects detected (Table 3). The highest value of the F statistic was for the trait "cones". This trait is also characterised by highest heritability. Heritability estimates for crown width and branch diameter amounted to 0 (Table. 4).

There is one distinguished family (number 2831) in the Rosiny trial. Its family index value (W_f=16.38) is double of that of the other good families: (2261, 2534, 2571, 1701) with index values W_f of 8.27, 8.14, 7.54 and 7.40 respectively. Distinctly negative index values were obtained for families: 1710, 2535, 2540, 2823, 2830.

In Smardze, there is no single outstanding family. The best families in this area are 799 (W_f = 6.14), 800 (W_f = 5.82) and 2112 (W_f =5.72). The worse index value was obtained for family 2111 (W_f = –4.71).

In Kierz, the best families are 47, 52, 74, 561, 200 and 1071 (W_f = 3.07, 2.77, 2.40, 2.39, 2.25, 2.10 respectively) and the worst families are 44 and 50 (W_f =–5.42, –4.71).

0.198, 0.247). DBH and height were also characterised by high heritabilities. The lowest family heritabilities were for multiple tops and lateral branches competing with the tree leader shoot (Table 4).

Table 3. Trait characteristics in experimental areas Rosiny, Smardze and Kierz

Trait	Area in Rosiny					Area in Smardze					Area in Kierz				
	F	$\bar{x}$	s.d.	V_{Ph}	V_F	F	$\bar{x}$	s.d.	V_{Ph}	V_F	F	$\bar{x}$	s.d.	V_{Ph}	V_F
DBH [cm]	12.90***	13.52	1.79	34.13	2.112	5.17***	13.85	2.13	37.217	2.602	1.25 ns	11.90	2.11	46.10	2.041
Height [m]	13.02***	6.89	0.69	50.42	3.147	3.22***	843.89	109.78	7940.68	36.561	1.68**	6.22	83.81	76.42	4.458
Stem straightness	5.55***	2.00	0.62	0.40	0.011	3.07***	1.86	0.49	0.245	0.011	1.15 ns	2.04	0.44	0.20	0.008
Crown width	3.63***	2.74	0.45	0.20	0.004	2.01***	2.67	0.48	0.224	0.006	0.94 ns	2.74	0.45	0.21	0.007
Branch diameter	7.46***	2.23	0.56	0.32	0.012	1.96***	2.06	0.43	0.163	0.005	0.60 ns	2.14	0.40	0.17	0.004
Multiple tops	1.56*	1.29	0.49	0.24	0.002	1.11 ns	1.11	0.33	0.112	0.002	1.44 *	1.23	0.45	0.21	0.010
Branch angle	6.48***	2.25	0.47	0.23	0.007	6.11***	2.20	0.44	0.203	0.017	1.05 ns	2.21	0.44	0.20	0.007
Crown form	8.49***	2.14	0.72	0.55	0.023	5.52***	2.07	0.63	0.408	0.030	1.51 ns	2.08	0.45	0.21	0.011
Cones	–	–	–	–	–	3.13***	2.56	0.64	0.434	0.019	2.41**	2.70	0.53	0.32	0.026
Lateral branches	1.19 ns	0.07		0.06	0.001	–	–	–	–	–	–	–	–	–	–
Basal sweep	2.16***	0.10		0.09	0.001	2.24***	0.14	–	0.170	0.005	1.11 ns	0.06		0.052	0.002
Stem forking	–	–	–	–	–	–	–		–	–	1.32 ns	0.15		0.127	0.005
Crooked branches	–	–	–	–	–	1.00 ns	0.06		0.091	0.005	–	–	–	–	–
Flowers	5.97***	0.14		0.12	0.004	–	–	–	–	–	–	–	–	–	–
Main stem forking	2.30***	0.12		0.11	0.001	–	–	–	–	–	1.05 ns	0.15		0.126	0.005

*, **, *** – significant at p = 0.05, p=0.01 and p=0.001 respectively, ns – non significant

Table 4. Family heritabilities on the experimental areas in Rosiny, Smardze and Kierz

Trait	Experimental trials		
	Rosiny	Smardze	Kierz
DBH	0.923	0.807	0.232
Height	0.923	0.699	0.425
Stem straightness	0.820	0.675	0.089
Crown width	0.725	0.503	0.000
Branch diameter	0.866	0.494	0.000
Multiple tops	0.357	0.098	0.297
Branch angle	0.846	0.837	0.047
Crown form	0.882	0.680	0.335
Cones	–	0.819	0.591
Lateral branches which compete with the leader shoot	0.548	–	–
Basal sweep	0.773	0.746	0.461
Stem forking under DBH	–	–	0.416
Crooked branches on the top whorl possibly caused by insect or fungal attack	–	0.937	–
Male and females flowers	0.943	–	–
Stem forking	0.789	–	0.058

Results of genetic selection are presented in Figures 2, 3 and 4 and in Table 5.

Rosiny trial

During phenotypic (F) selection 89 trees were chosen. Out of the 68 families, trees from 35 families were selected (Fig. 2). Taking into consideration the number of trees per family, family 2831 is clearly distinguished. In this family 9 trees were chosen, constituting 10.1% of all chosen trees. In 2 families 5 trees were chosen. in 5 families 4, in 8 families 3 trees, in 7 families 2 trees and in 12 families 1 tree. Phenotypic selection based on measurements (Fbis) gave trees from 37 families. In 2 families 8 trees were selected,
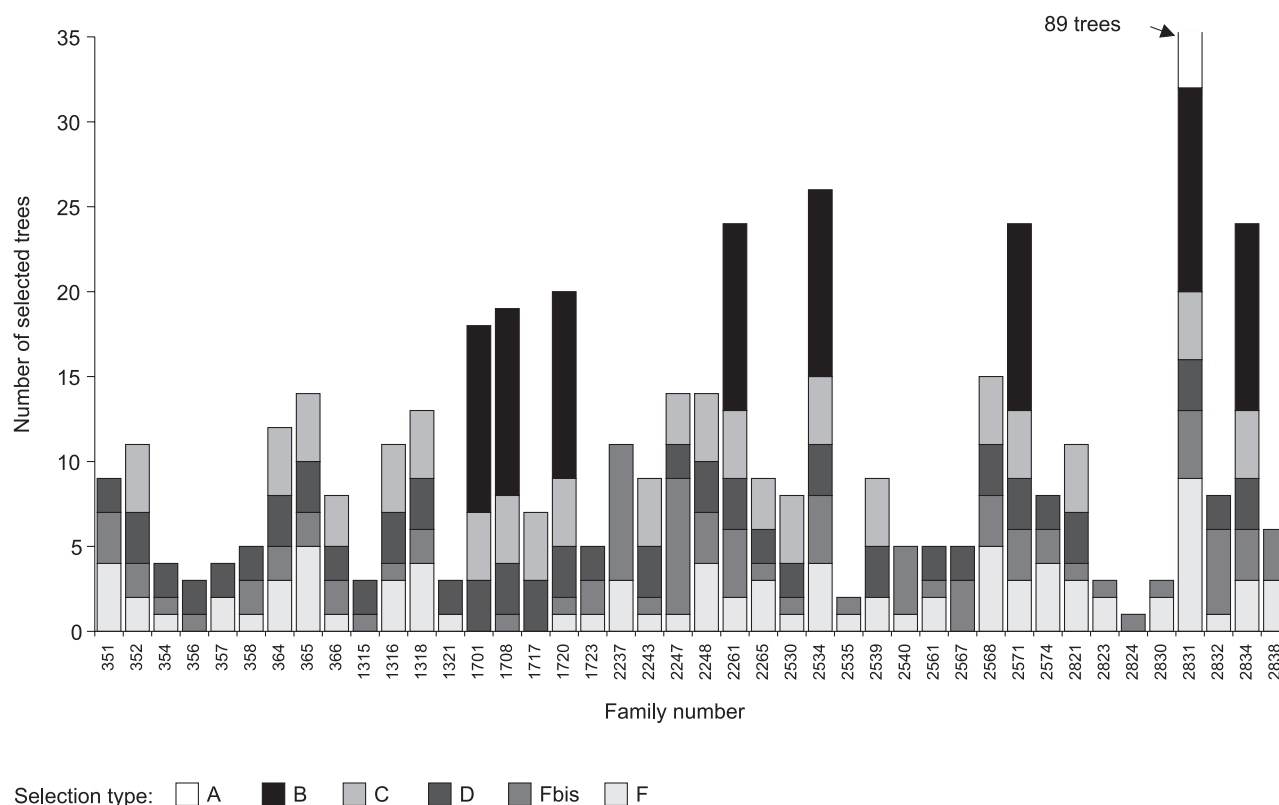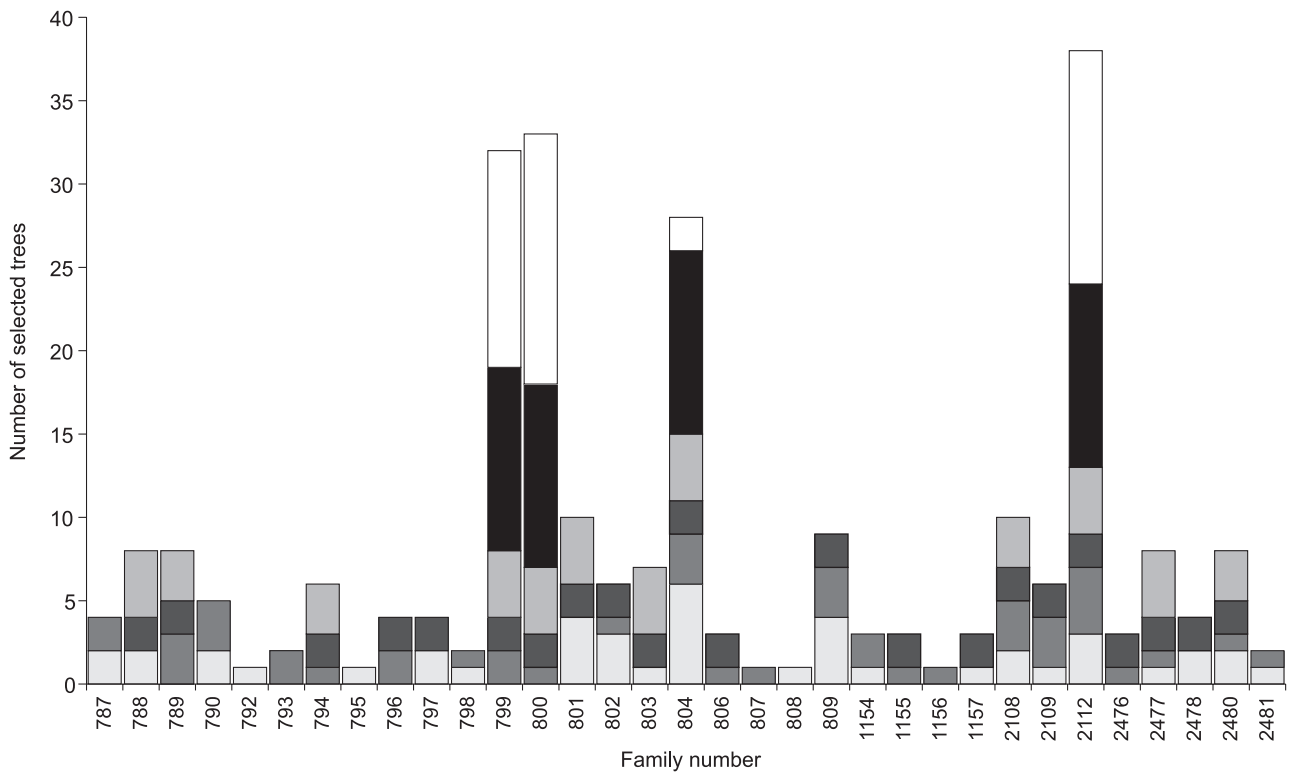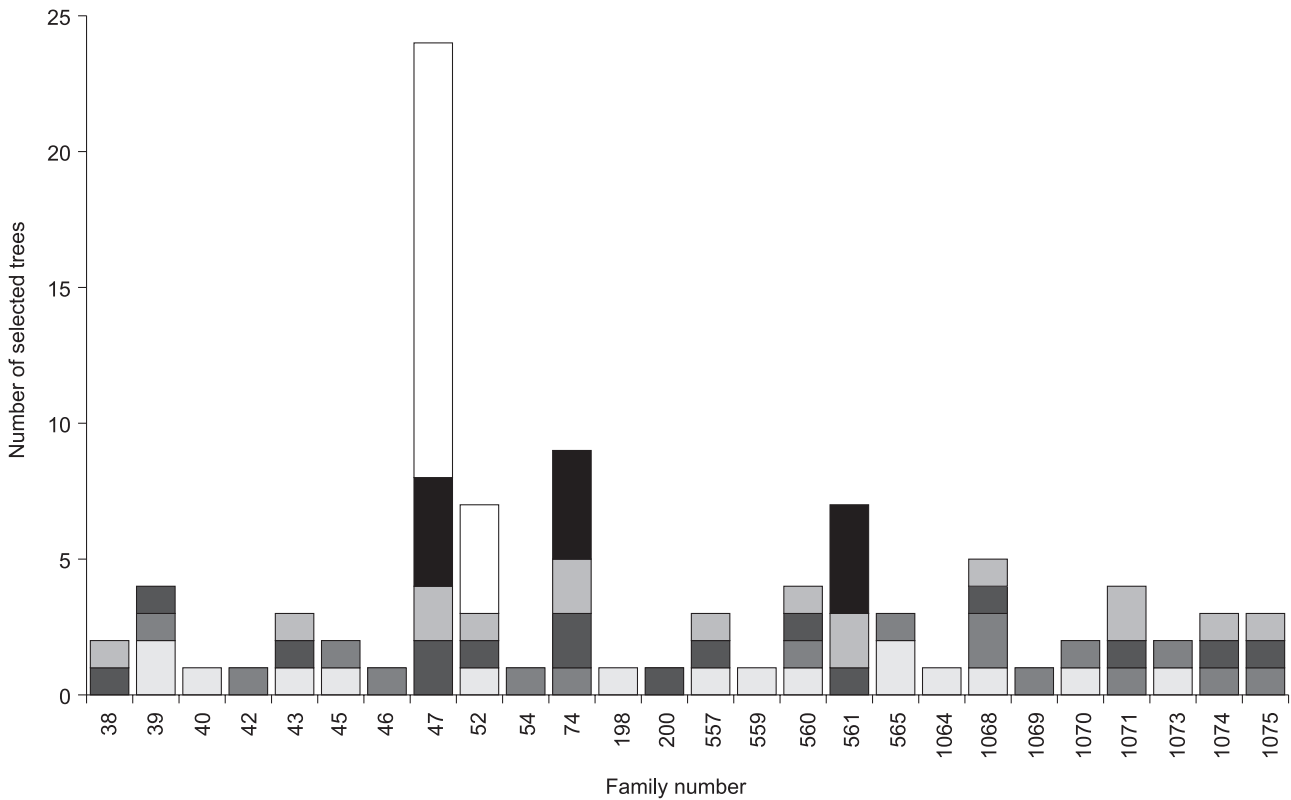

Fig. 2. Number of selected trees in the families in the Rosiny area

Fig. 3. Number of selected trees in the families in the Smardze area

Fig. 4. Number of selected trees in the families in the Kierz area

Table 5. Characteristics of the different selection results on the experimental areas in Rosiny, Smardze and Kierz

Experimental areas	Selection type	Number of selected families	Sum average genetic gain for analysed traits in standard deviation units	Percent of conserved effective population size (*100%–LR*)	Number of trees common with phenotypic selection	Number of trees common with Fbis selection
Rosiny	A	1	17.009	2.6	9 (10.2%)	4 (5.5%)
	B	8	6.912	21.1	6 (6.8%)	12 (13.6%)
	C	23	4.010	57.6	8 (9.0%)	16 (21.9%)
	D	35	2.551	88.8	12 (13.6%)	19 (26.0%)
	F	35	0.178	64.7	–	9 (10.2%)
	Fbis	37	0.062	63.5	9 (10.2%)	–
Smardze	A	4	3.763	7.2	1 (2.3%)	8 (18.2%)
	B	4	3.663	11.3	3 (6.8%)	9 (23.1%)
	C	12	2.760	33.5	7 (15.9%)	8 (18.2%)
	D	22	2.384	62.4	8 (18.2%)	12 (30.8%)
	F	22	0.462	44.3	–	3 (7.7%)
	Fbis	24	1.021	53.8	3 (7.7%)	–
Kierz	A	1	2.229	2.7	0	0
	B	4	1.420	10.6	0	2 (5.3%)
	C	12	1.346	28.4	3 (18.8%)	2 (5.3%)
	D	14	1.314	34.1	3 (18.8%)	3 (18.8%)
	F	14	0.220	34.1	–	3 (18.8%)
	Fbis	15	0.342	37.8	3 (18.8%)	–

in 1 family 5 trees, in 4 families 4 trees each, in 7 families 3 trees, in 8 families 2 trees were selected and in 15 families 1 tree. In this method, 5 families were chosen where no trees were selected phenotypically by mode F.

When using selection method A, where trees were selected only on their index value, irrespective of the number of families to which they belong, only the trees from one family 2831 were chosen. This best family under index selection was also noticed in phenotypic selection. In genotypic selection by mode B 12 trees of family 2831 were chosen and in each of the following 7 best families (2261, 2534, 2571, 1701, 2834, 1702, 1708) 11 trees were chosen. From families 1701 and 1708 not a single tree was phenotypically (mode F) selected. Genotypic selection by mode C selected 23 families, 20 with 4 trees each and 3 with 3 trees each. Three of these were not identified by phenotypic selection. Using genotypic selection by mode D trees were chosen in 35 best families. In 19 families 3 trees were selected and in 16 families 2 trees. Using this method, 6 families were chosen where no trees were selected phenotypically.

Smardze trial

In phenotypic (F) selection 44 trees were chosen. Out of the 39 families planted, trees from 22 families were selected. Taking into consideration the number of trees selected, family 804 is distinguished. In this family 6 trees were chosen, constituting 14% of the total number of chosen trees (Figure 3). Phenotypic selection by mode Fbis selected 24 families, 1 with 4 trees each, 6 with 3 trees, 5 with 2 trees and 12 with 1 tree. In this method, 11 families were chosen which were not selected phenotypically by mode F.

Choosing trees genotypically by mode "A", trees from 4 families (799, 800, 804 and 2112) were selected. The most chosen trees (15) were from family 800. In family 2212 14 trees were selected and in family 799 13 trees. In family 804, identified as best in phenotypic selection, only 2 trees were chosen. In families 800 and 799 no trees were phenotypically selected. In genotypic selection by mode B 11 trees in each of the 4 best families (799, 800, 804 and 2112) were selected. Selection by mode C gave trees from 12 families 4 with 3 trees and 8 with 4 trees each. Of these 4 families were not phenotypically chosen. Using genotypic selection by mode D in each of the 22 the best families 2 trees were chosen. Among these there were 8 families in which no trees were phenotypically selected.

Kierz trial

Sixteen trees were phenotypically chosen by mode F. Out of the 41 families trees from 14 families were selected. In families 39 and 565 two trees were selected and in the other families only 1 tree was selected (Fig. 4). Phenotypic selection by mode Fbis gave trees from 15 families, 1 with 2 trees and 14 with 1 tree each. In this method, 8 families were chosen which were not selected phenotypically by mode F.

Choosing trees genotypically by mode A gave all 16 trees from family 47, which was not phenotypically noticed. In genetic selection by mode B 4 trees from

each of the 4 best families (47, 52, 74 and 561) were selected. Only family 52 was phenotypically (F) chosen from these four families. In genotypic selection by mode C 2 trees were chosen in 4 families and 1 tree in 8. Only 5 of the latter were phenotypically selected. Using genotypic selection by mode D 2 trees were chosen from families 47 and 74 and 1 tree from 12 families. Only 6 of the latter were phenotypically selected.

Comparison of genetic gain with genetic diversity

The average genetic gain for all traits was significantly greater using selection method A than following selection by methods B, C or D in the Rosiny trial (Fig. 5). Genetic gain obtained by method A was not significantly better than when using method B in the other plots, Smardze and Kierz. The significantly greater genetic gain in selection by method A in the Rosiny trial was influenced by the value of the overall means for several traits (flowers, branch diameter, and stem quality) in family 2831 (the only family chosen by selection method A). Of course, when the index value was constructed different traits were given different economic weights (Table 2), which were taken into consideration. For all traits a greater genetic gain was obtained using method A selection compared to selection using methods B, C and D. Phenotypic selection method resulted in the least genetic gain, both by method F and Fbis.

Loss of genetic diversity, expressed as percent of conserved effective population size ($100\% - N_e$), is greatest following selection by method A which pro-

vided the greatest genetic gain (Figure 5). The greatest genetic variability was preserved using selection method D. In Kierz selection method D and phenotypic selection provided the same level of genetic variability. In the other plots D selection was slightly better. This resulted from the fact that trees chosen by method D were more regularly distributed in the number of *a'priori* imposed families.

Value of phenotypic selection where trees were chosen after measurements (Fbis), is not univocal. It proved to be better then method (F) in Smardze and Kierz, conserving more genetic diversity and providing bigger genetic gain. This method gave smaller genetic gain and lost more genetic variability in Rosiny.

As can be seen from Table 5, the number of specific trees selected both in phenotypic selection F and in any of the genotypic selections is rather low (0 to 19%) and similarly in comparison with selection Fbis, though it is generally somewhat higher (0 to 30%).

Discussion

As expected, phenotypic selection produced lower genetic gain, as a consequence of the selection being based only on the phenotypic value of the individuals. Taking into the consideration the effective population size, results are different. Phenotypic selection generally conserved genetic variability and genetic selection reduced it especially when genetic gain is maximized. Breeders when making selections may be placing greater emphasis on genetic gain than on genetic diversity. Obtained results are with agreement with Wei (1995) result, but confirm it for a number of
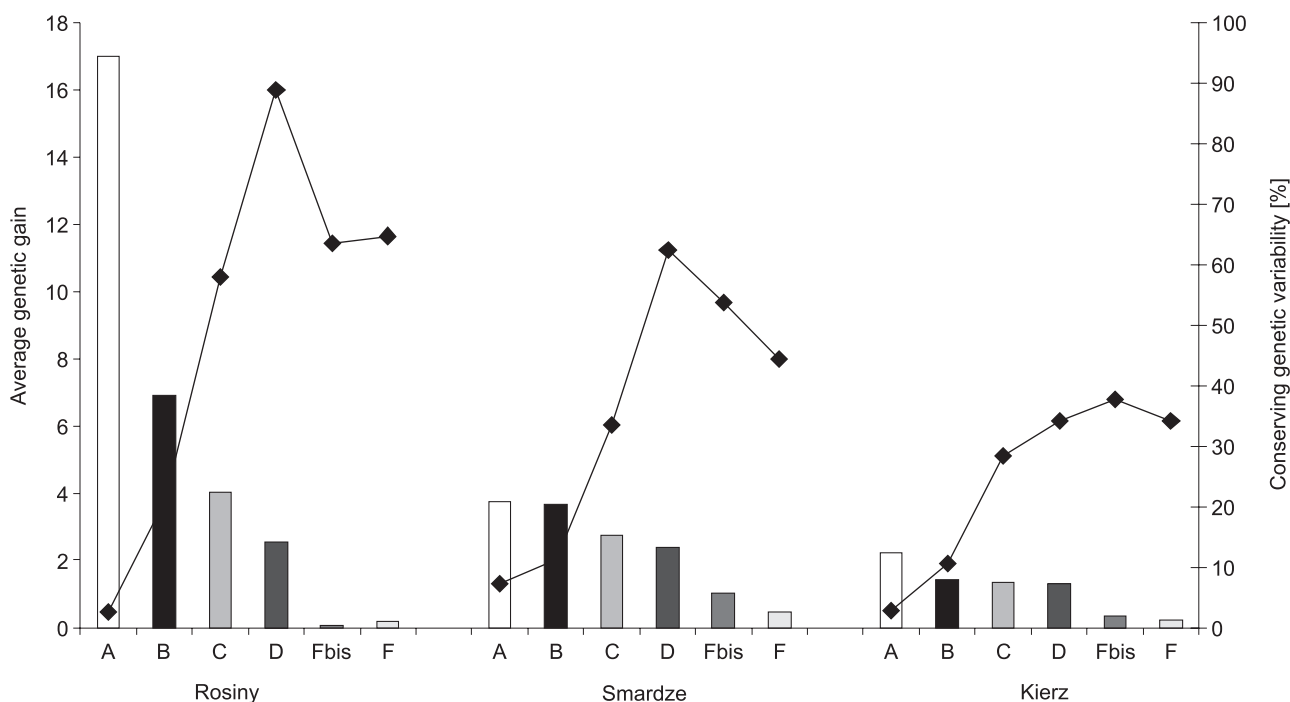

Fig. 5. Comparison between different genotypic and phenotypic selection methods in the three experimental area.

traits. In the present study agreement on individual tree basis is much less then obtained by Giertych (1995) it is probably caused by big differentiation between families on studied experimental plots. Comparing present results with Pswarayi and Barnes (1994) the difference in genetic gain between phenotypic and genotypic selection was much greater.

Phenotypic selection can be used almost everywhere and does not require great scientific support. This is its main advantage. On the basis of this work and the literature, its advantage also includes the fact that it provides large genetic variability.

A disadvantage of this method of selection is the small use of the genetic potential of the material, which is not known. Smaller genetic gain is obtained using this method.

Genotypic selection is performed on the basis of known genetic variability. It provides full control over the traits of interest and the selection level. It permits optimal use of the genetic information, balancing genetic gain and genetic variability loss. However this requires extensive measurement and observations, substantial financial support and complicated statistical calculations.

Large genetic gains are made at the expense of genetic diversity in the selected population (Wei and Lindgren 1991). It is usually difficult or not possible to maximize both. If genetic diversity is the main priority, then selection type (D) where inside families the equal number of trees were selected would be the best method. If both gain and diversity are equal priority then an optimalization strategy such as presented in David at al. (2003) paper will be an effective way to determinate an appropriate selection intensity.

For future selection it is important to conserve large enough diversity in the breeding population (Giertych 1993). When there is lack of variation in a population, successful selection is impossible. Genetic diversity in a breeding population is necessary for adaptation to a changing environment, so diversity in a population is as important as genetic gain.

General conclusions

On the basis of this study, it is possible to formulate conclusions which are independent of the particular circumstances existing in a given progeny tests:

1. Genetic selection method A, where the best trees were selected without any restrictions, requires the most information on the parents, provides highest genetic gain and at the same time leads to the greatest loss of genetic diversity.
2. Phenotypic selection, which does not require information on the parents, provides less genetic gain but maintains a high level of genetic diversity.
3. Agreement between genotypic and phenotypic selection is low (0% to 19%) at the individual tree level.
4. Phenotypic selection utilising measurements is not much different from selection on general appearance only.
5. Phenotypic selection generally identifies the exceptionally good families.
6. Phenotypic selection is recommended only where information concerning pedigrees is not available or at the beginning of a selection programme. It can provide a simple and cheap way of obtaining material for future selection.
7. It is always necessary to adopt a selection method, which will optimise genetic gain with on acceptable predetermined level of genetic variability reduction.

Acknowledgments

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