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БЛОК-ЭФФЕКТ, ВЛИЯЮЩИЙ НА ГЕНЕТИЧЕСКИЕ ПАРАМЕТРЫ, НА ПРИМЕРЕ ИССЛЕДОВАНИЯ 23-ЛЕТНЕГО ПОТОМСТВА *PINUS BRUTIA*

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Многие экологические и биологические факторы могут быть эффективными при оценке генетических параметров в исследованиях потомства. Количество блоков (также называемых репликами) является одним из наиболее важных факторов окружающей среды в этих оценках. Влияние блочных сценариев на генетические параметры было исследовано на основе высоты и диаметра на высоте груди 23-летнего потомства, созданного с помощью 4 блоков семенного стенда и саженцев турецкой красной сосны (*Pinus Brutia* Ten.). Средние значения составили 14,14 м для высоты дерева и 17,69 см для диаметра на высоте груди в исследованных образцах. В результате дисперсионного анализа были обнаружены общезначимые ($p < 0{,}05$) различия между блоками и отличительными родственными признаками. Хотя дисперсия ошибок была одинаковой для обоих признаков, были отмечены большие различия между другими компонентами сценариев. Индивидуальная наследуемость, фенотипический коэффициент вариации, генетический коэффициент вариации и генетический прирост варьировались для отличительных признаков и сценариев блоков. Результаты исследования подчеркивают влияние количества блоков на генетические параметры.

Ключевые слова: разведение, прирост, генетика, рост, наследуемость, изменчивость

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BLOCK EFFECT ON GENETIC PARAMETERS IN A 23-YEAR-OLD PROGENY TRIAL OF *PINUS BRUTIA*

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Abstract

Many environmental and biological factors could be effective on estimation of genetic parameters in progeny trials. Number of blocks (also called as replicate) is one of the most important environmental factors in these estimations. Effect of block scenarios on genetic parameters were investigated based on height and diameter at breast height in a 23-year-old progeny trial established by 4 blocks of seed stand and seed orchard seedlings of Turkish red pine (*Pinus brutia* Ten.) in this study. Averages were 14.14 m for tree height and 17.69 cm for diameter at breast height in polled seed sources. Generally significant ($p<0.05$) differences among blocks, and families for the traits in the scenarios were found by results of analysis of variance. While variance of error was similar for both traits, there were large differences were estimated among other variance components for the scenarios. Individual heritability, phenotypic coefficient of variation, genetic coefficient of variation, and genetic gain varied for the traits and block scenarios. Results of the study emphasized effect of block numbers on genetic parameters.

Keywords: breeding, gain, genetic, growth, heritability, variation

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Introduction

Turkish red pine (*Pinus brutia* Ten.) is classified as one of the most economically important tree species for Turkish forestry and the “National Tree Breeding and Seed Production Programme” [1] because of its valuable commercial wood product and the largest natural distribution by 5.2 million ha which of %26 of total forest area of Turkey [2]. One of the basic aims of tree breeding programme is to estimate genetic parameters such as heritability and genetic gain based on variance components. Progeny trial is the main tool for the estimations, and an important part of the breeding programme. For these purposes, progeny trials were established in the species based on the programme. However, there could be many environmental (e.g., number of blocks, establishment design, aspect, spacing, homogeneity of the site) and biological (e.g., numbers of families and seed sources, distribution of the species) effect on establishment of the trial. Number of block (also called as replicate) is one of the main environmental factors, which can be changed/balanced by establisher. It plays important roles in the estimations from decision on model to statistical methods [3-12], and also, establishment cost and organization of trials.

In this study, some genetic parameters were estimated for tree height, and diameter at breast height based on different block scenarios in a 23-year-old progeny trial of Turkish red pine to contribute establishment and management of the trials.

Material and methods

The progeny trial was established by one-year containerized seedlings grown 27 seed trees selected phenotypic from each seed stand (SS-1… SS-5), and their clonal seed orchards (SO-1…SO-5) (Table 1) consist of 31 (SO-1), 25 (SO-2), 25 (SO-3), 28 (SO-4) and 20 (SO-5) clones selected from the stands.

The seedlings of the seed sources were planted by 3x2 m spacing by four blocks (also replicate) at experiment site from southern part of Turkey (36°57'30" N latitude and 30°36'39" E longitude, 292 m altitude) in 1997. Tree height (**H**), and diameter at breast height (**D**) were measured by 6 trees from each family at each block at 23rd year at end of growth period of 2020.

Data analysis

The data was analyzed at five scenarios based on purpose of the study. They were scenario **0** (**S0**, standard model by four blocks), scenario **1** (**S1**, by 3 blocks except of first block), scenario **2** (**S2**, by 3 blocks except of second block), scenario **3** (**S3**, by 3 blocks except of third block), and scenario **4** (**S4**, by 3 blocks except of fourth block).

The families were compared by following model of multiple analyses of variance (MANOVA) by [13].

$$Y_{ikl} = \mu + B_i + F_k + BF_{ik} + e_{ikl} \qquad (1)$$

Where Y_{ikl} is the observation from the l^{th} tree of i^{th} block/replicate of j^{th} family, μ is overall mean, B_i is the effect of the i^{th} block (I=1…4), F_k is the effect of k^{th} family (k= 1, 2….134), BF_{ik} is the effect of interaction between block and family, e_{ikl} is random error.

Individual (narrow sense) heritability (h_i^2) was estimated as [14]:

$$h_i^2 = \frac{\sigma_A^2}{\sigma_P^2} = \frac{k\sigma_F^2}{\sigma_P^2} \qquad (2)$$

Where σ_A^2 is the additive genetic variance, σ_F^2 is the genetic variance of families, σ_F^2 is the phenotypic variance, k is the covariance coefficient between half-sibs.

Table 1. Geographic details of the seed sources

Seed Sources	Latitude (N)	Longitude (E)	Altitude (m)
SS-1	36°45'00"	31°57'55"	650
SS-2	36°35'30"	30°28'00"	320
SS-3	36°44'34"	29°28'36"	600
SS-4	37°06'20"	29°07'30"	800
SS-5	37°04'30"	29°32'40"	1100
SO-1 (SS-1)*	37°00'40"	30°50'19"	100
SO-2 (SS-2)	36°58'00"	30°40'42"	257
SO-3 (SS-3)	36°40'04"	29°10'39"	240
SO-4 (SS-4)	37°01'13"	30°43'35"	275
SO-5 (SS-5)	36°58'11"	30°32' 42"	260

*; Mother population of the orchard.

Standard error of the heritability (S.E. (h_i^2)) was estimated as [15]:

$$S.E.(h_i^2)=\sqrt{\frac{16Var(\sigma_F^2)}{(\sigma_P^2)^2}} \tag{3}$$

Coefficients of variations of phenotypic (CV$_f$) and genetic (CV_g) were estimated based on phenotypic (σ_f^2), and genetic (σ_F^2) variances and average ($\bar{x}$) of the traits as [16]:

$$CV_f=\left(\frac{\sqrt{\sigma_f^2}}{\bar{x}}\right)x100\text{, }CV_g=\left[\frac{\sqrt{4\sigma_F^2}}{\bar{x}}\right]x100 \tag{4a\&b}$$

Phenotypic Pearson' correlation (r_p) between tree height and diameter at breast height were estimated by [17].

$$r_P=\frac{\sum xy}{\sqrt{\sum x^2\sum y^2}} \tag{5}$$

Where $\sum xy$ is the sum of the factors of the traits x and y, $\sum x^2$ and $\sum y^2$ are phenotypic variances of the traits x and y.

Genetic correlation (r_g) between tree height and diameter at breast height were estimated as [18]:

$$r_g=\frac{COV_{f(x,y)}}{\sqrt{\sigma^2_{f(x)}}\sqrt{\sigma^2_{f(y)}}} \tag{6}$$

Where $COV_{f(xy)}$ is the genetic covariance between traits x and y, $\sigma^2 f(x)$ and $\sigma^2 f(y)$ are the additive genetic variances of traits x and y, respectively.

Standard error of genetic correlation (σ_{rg}) was estimated by [18]:

$$\sigma_{rg}=1-r_g^2\sqrt{\frac{\sigma_{h^2_x}\sigma_{h^2_y}}{h^2_x h^2_y}} \tag{7}$$

Where $\sigma_{h_x^2}$ and $\sigma_{h_y^2}$ are standard error of heritability of traits x and y, $h^2{}_x$ and $h^2{}_y$ are heritability of traits x and y, respectively.

Genetic gain (ΔG %) was estimated as:

$$\Delta G=\frac{(\overline{ID_S}-ID_K)}{MID_K}x100 \tag{8}$$

Where $\overline{ID_S}$ is the average of breeding value estimated by BLUP (Best Linear Unbiased Prediction) of the highest 30 families, ID_K is the breeding value of the control material, and MID_K is the absolute breeding value of the control material.

Results and Discussion

Averages of tree height (**H**), and diameter at breast height (**D**) were 14.14 m and 17.69 cm in polled seed sources, respectively (Table 2). Annual increments were 0.62 m for H and 0.77 cm for H. They were 0.29 m and 0.56 cm in 32-year-old provenance trial of the species [12]. Individuals of seed orchards showed 9% higher growth performance for volume in 14th year result of progeny trial of the species [19].

Table 2. Averages (x̄) and standard deviation (S) of the traits for the seed sources

Seed sources	H (m)		D (cm)	
	x̄	S	x̄	S
SS	14.07	16.50	17.02	3.86
SO	14.15	18.06	17.73	4.20
Total	14.14	18.02	17.69	4.19

Positive and significant (*$p<0.05$*) phenotypic (*$r=0.76$*) and genetic (*$r=0.85\pm0.03$*) relations were found between height and diameter at breast height. Similar relation was also reported in provenance and progeny trials of Turkish red pine [12].

Significant (*$p<0.05$*) differences among blocks, and families for the traits in the scenarios were found based on results of analysis of variance except of among blocks (*$p>0.05$*) in scenarios 1 and 2. Block x family interactions was also significant in the scenarios (Table 3). Significant (*$p<0.05$*) differences among families were also reported for height and diameter in the species in early results of progeny trials of Turkish red pine [20-22]. While homogenous experimental area was expected in progeny trial, it could not be under control because of large number of genotype [23]. It was suggested heterogeneity of the site could be balanced by number of blocks [4].

The variance of error was similar for both traits, while large differences were estimated among other variance components for the scenarios (Table 4). The differences were about three times for the variance among blocks in S2 (1.21 %) and S3 (3.93 %), and the variance among families between S2 (3.97 %) and S1 (10.28 %) for height (Table 4). Variances among blocks were lower than 1% for diameter at breast height (Table 4). Variance of block x family interaction decreased from 19.80% (**S0**, four blocks) to 14.29% (**S1**, three blocks except of block 1) for height (Table 4). It showed heterogeneity of first block. Bian *et al.* [24] reduced 13% and 19% of error variance by missing plot for height and diameter in progeny trial of China fir (C*unninghamia lanceolata* (Lamb.) Hook.). The results emphasized importance of number of blocks, traits and selection of experimental area for accurate estimations.

Large differences were estimated for individual heritability (h_i^2), phenotypic coefficient of variations (CV_f), genetic coefficient of variations (CV_g), and genetic gain (ΔG %) for the traits and scenarios (Table 5). For instance, individual heritability ranged from 0.16 (S2) to 0.42 (S1) for height, and also genetic gain increased from 1.52 (S2) to 5.38 (S1) for the trait (Table 5). It was reported that in a progeny trial of Turkish red pine, the plot error was eliminated, that was, it was reduced to zero, for tree height in interlocked model and for diameter at breast height in twelve blocks model. The accuracy of predicted breeding values in height and diameter were increased significantly [12]. Similar results were also found that genetic parameters could change in different forest tree species based on analysis procedure [5, 7, 8, 24, 25]. For instance, heritability increased 35% and 51% for height and diameter in progeny trial of China fir [24] by different number of plots. Individual heritability, phenotypic and genetic coefficient of variations and genetic gain were generally higher in diameter at breast height than height in scenarios (Table 5). The results emphasized importance of number of blocks, traits and selection of experimental area for accurate estimations. Besides, there could be many environmental and biological factors together with block number. It was reported than heritability of growth traits changed for ages in the species [i.e., 19, 26].

Table 3. Results of analysis of variance

Traits	**Source of variation**	**Scenarios** **S0**	**S1**	**S2**	**S3**	**S4**
Height	Block (B)	p <0.001	p <0.001	p <0.001	p <0.001	p <0.001
	Family (F)	p <0.001	p <0.001	p <0.05	p <0.05	p <0.05
	FxP	p <0.001	p <0.001	p <0.001	p <0.001	p <0.001
Diameter	Block (B)	p <0.05	**p>0.05**	**p>0.05**	p <0.05	p <0.05
	Family (F)	p <0.001	p <0.001	p <0.001	p <0.001	p <0.001
	FxP	p <0.001	p <0.05	p <0.001	p <0.05	p <0.05

Table 4. Variance components of the traits

Variance components*	Scenarios				
	S0	S1	S2	S3	S4
			Height		
σ_B^2	868.2 (2.64 %)	438.5 (1.40 %)	368.2 (1.21 %)	1336.6 (3.93 %)	1332.7 (3.75 %)
σ_F^2	1911.4 (5.82 %)	3224.1 (10.28 %)	1208.6 (3.97 %)	1416.4 (4.16 %)	1795.1 (5.05 %)
σ_{BxF}^2	6505.1 (19.80 %)	4483.1 (14.29 %)	7787.8 (25.58 %)	7118.8 (20.93 %)	6669.8 (18.75 %)
σ_e^2	23561.8 (71.73 %)	23227.8 (74.04 %)	21075.9 (69.24 %)	24144.1 (70.98 %)	25772.0 (72.46 %)
			Diameter		
σ_B^2	5.57 (0.32 %)	2.31 (0.13 %)	2.46 (0.15 %)	9.37 (0.52 %)	8.79 (0.47 %)
σ_F^2	109.98 (6.26 %)	134.52 (7.69 %)	96.40 (5.93 %)	98.81 (5.50 %)	113.07 (6.09 %)
σ_{BxF}^2	72.54 (4.13 %)	60.23 (3.44 %)	98.54 (6.06 %)	69.89 (3.89 %)	62.32 (3.36 %)
σ_e^2	1568.70 (89.29 %)	1551.80 (88.73 %)	1428.40 (87.86 %)	1618.80 (90.09 %)	1673.20 (90.08 %)

*; is the variance among blocks, is the variance among families, is the variances of block x family interaction, is the variance of error.

Table 5. Some parameters for the traits

Parameters	Scenarios				
	S0	S1	S2	S3	S4
			Height		
h_i^2	0.24±0.08	0.42±0.10	0.16±0.09	0.17±0.09	0.21±0.09
CV_g	6.18	7.96	4.96	5.31	5.99
CV_f	12.64	12.32	12.37	12.76	13.08
ΔG %	3.16	5.38	1.52	2.57	2.58
			Diameter		
h_i^2	0.25±0.06	0.31±0.07	0.24±0.07	0.22±0.07	0.24±0.07
CV_g	11.85	13.02	11.17	11.21	12.04
CV_f	23.65	23.46	22.91	23.84	24.35
ΔG %	7.66	9.16	5.29	8.08	6.13

Conclusions

The results of the study showed importance of number of blocks in estimations. However, number of block is a changeable environmental factor by trial managers. Homogenous test area should be selected in establishment stage of trials. Future studies should be carried out for accurate conclusions on the trials based on rotation age of the species. Results of the study could be combined with other progeny trials in the species.

Blocks and their number should be checked during data collection and estimations.

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