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FORESTRY SCIENCE

Predicted genetic gains for growth traits and Genotype x Environment interaction in *Pinus greggii*: new perspectives for genetic improvement in Brazil

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Abstract: *Pinus greggii* has potential for inclusion in temperate zone breeding programs around the world as it is frost resistant and produces high yields for pulp production. This study estimates the genetic parameters for two *P. greggii* progeny tests established in Telêmaco Borba, Paraná, Brazil. We evaluated diameter at breast height (DBH) and total height (H) at seven and nine years of age. The narrow-sense heritability (h_i^2) ranged from 0.225 (H, 7 years) to 0.515 (H, 9 years). The genetic correlation was high for all traits, reaching up to 0.91 between traits and 0.94 between ages. In addition, the results show the presence of Genotype x Environment interaction, and as such, the most productive and stable progeny were identified based on the Harmonic Mean of the Relative Performance of Genetic Values (MHPRVG) values. These population has genetic materials that are superior in terms of both DBH and H compared to the control and to *P. greggii* materials analyzed internationally. Our results contribute to the literature by providing further genetic information on this species, while also demonstrating the implications of thinning for genetic gains and effective population size.

Key words: Effective size, genetic correlation, MHPRVG, tree breeding.

INTRODUCTION

Worldwide, the development of the forestry sector has relied heavily on *Pinus* L. making it one of the most commonly planted exotic genera. The most frequently used *Pinus* species for forestry are *Pinus taeda* L. and *Pinus elliotti* Engelm. However, with the rapid expansion of the industrial sector and increasing demand for new materials, there is a need to diversify the species offered and provide alternatives to meet supply demands with better quality feedstock. This diversification must attend to the needs of industry, including offering better quality wood properties, while also guaranteeing resistance to pests, disease, and adverse conditions. One species that offers such favorable characteristics and requires further study is *Pinus greggii* Engelm (Shimizu 2008).

Locally known as “Pino prieto”, *P. greggii* is a species endemic to Mexico, with light green acicles and height varying from 10 to 25 meters (Perry 1991). The natural geographic distribution of the species is in the Sierra Madre Oriental mountains (between 20°N and 26°N, 98°W and 101°W) at elevations ranging from 1500 to 2500 meters. Commonly, the soils where the species occur are deep and slightly clayey (Poynton 1977). According to Camcore (1988), there are two major *P. greggii* populations in Mexico with distinct characteristics, one in the north and another in the central-eastern region. The northern population experiences greater incidence of frost and is resistant to dry conditions, while the central-eastern population shows a faster growth rate. The distance between these two populations is about 400 kilometers. The average temperature is 16.5 ^{O}C and 18.0 ^{O}C for the northern and central-eastern population, respectively (Donahue 1993).

The wood of *P. greggii* has a pale-yellow color, with low resin content and many knots due to the abundance of branches along the trunk. The wood density ranges from 450 to 510 kg/m^3, depending on tree age (Locia & Manzo 2001). It is widely used for civil construction, as mine props, and as firewood (Perry 1991). The pulp and paper produced from *P. greggii* is favorable, since it has low ash content and the process yield is about 45% for kraft pulp, which is similar to the process yield of *P. taeda* and *P. elliottii* (Dhawan et al. 1990).

In addition to the multiple end uses of its wood, *P. greggii* also stands out for its capacity to resist cold, dry weather and frost, which are convenient characteristics for temperate zone forestry around the world (Martínez-Sifuentes et al. 2020). Despite these advantages, *P. greggii* is still poorly exploited, with few scientific studies on the species and no reports of its commercial use.

With a potential species identified, as is the case with *P. greggii*, breeders must assess the genetic control inherent in the species in order to advance breeding programs; this can be done by estimating genetic parameters. Valuable information can be extracted from genetic parameters, such as the best selection strategies to obtain short- and long-term gains (Walsh & Lynch 2018).

Another important tool for breeding programs is the genetic correlation between traits, since it demonstrates the possibility of conducting indirect selection between two traits (Walsh & Lynch 2018). This tool also allows the breeder to establish the genetic correlation between ages, making early selection possible and reducing the time required for the selection cycle of a generation (Tambarussi et al. 2017). The efficiency and reliability of indirect and early selection is closely related to the existence and magnitude of genetic correlation (Walsh & Lynch 2018).

Understanding the genetic control is essential for breeding programs. However, the individual phenotype is not only decomposed into genetic and environmental factors. There is also an interaction between the two, commonly referred to as Genotype x Environment interaction (GxE) (Braga et al. 2020). This factor is crucial to consider in a breeding program where the genetic materials are tested in different locations, as it is possible to assess the GxE and indicate the best genetic material for each location (Vencovsky & Barriga 1992). Therefore, the GxE analysis aims to predict the productivity of genetic materials in multiple and different environments (Braga et al. 2020). The Harmonic Mean of the Relative Performance of Genetic Values (MHPRVG) analysis is a reliable tool used in breeding programs, as it indicates the most productive and stable (i.e., those that may perform similarly in multiple environments) genetic materials, in addition to permitting analyses with unbalanced data (Resende 2007).

Thus, this study aimed to estimate the genetic parameters, genetic correlation between traits/ages/environments, and the GxE interaction for two *P. greggii* progeny tests. The goal was to identify the best genetic materials for each site, as well as the most stable material, to support the creation of a seed orchard.

MATERIALS AND METHODS

Field experiments

The data were provided by Klabin S.A and consist of two *P. greggii* progeny tests (Table I) established in 2002. Progeny with no degree of breeding were provided by CAMCORE and collected from plus-trees in Querétaro and Hidalgo provenances, Mexico. The evaluated traits were diameter at breast height (DBH, cm) and total height (H, m), at seven and nine years of age. Both tests were established in randomized blocks, with nine replications, six plants per plot, and 3 x 2.5 m spacing. Each test included the same 15 *P. greggii* progeny plus one *P. taeda* control, an improved commercial material used for comparison, for a total of 864 plants in each test.

Table I. Sites of analyzed progeny tests of *Pinus greggii.*

Experiment	Latitude (S)	Longitude (W)	Soil type
PGI	24°12'50''	50°32'13''	Dystrophic Red Latosol, clayey and very clayey texture
PGII	24°11'12''	50°32'14''	Haplic Cambisol, medium texture

Statistical analyses and genetic parameters

All statistical analyses and estimates of genetic parameters were performed in RStudio (R Core Team 2018). The genetic parameters were estimated using the Residual or Restricted Maximum Likelihood/Best Linear Unbiased Prediction (REML/BLUP) mixed model methodology, with the *lme4* package employed to process the mixed models (Bates et al. 2015).

The variance components were estimated according to the following mixed model:

$$y = Xr + Zg + Zp + e$$

where, r is the fixed effect associated with replication; g is the random effect associated with the progenies; p is the random effect associated with the plot; e is the residual effect; and X and Z are the incidence matrices of the fixed and random effects, respectively. Based on this model, the following variance components were generated: σ_g^2: genetic variance; σ_d^2: within progeny variance; σ_e^2: residual variance; and σ_a^2: additive genetic variance (estimated as $\sigma_a^2 = 4\sigma_g^2$).

The significance of the random effects (progeny) was tested by the Likelihood Ratio Test (LRT), which uses a chi-square test with 1 degree of freedom. The heritabilities were estimated at the individual (narrow-sense) level ($h_i^2 = \frac{\sigma_a^2}{\sigma_g^2+\sigma_e^2+\sigma_d^2}$), within progeny level ($h_d^2 = \frac{3\sigma_a^2}{\sigma_d^2}$), and individual among environments level (joint analysis) ($H^2 = \frac{\sigma_g^2}{\sigma_g^2+\sigma_e^2+\sigma_d^2}$). The coefficient of genetic variation ($CV_g(\%) = \frac{\sqrt{\sigma_g^2}}{\overline{m}}100$), coefficient of individual genetic variation ($CV_{gi}(\%) = \frac{\sqrt{\sigma_a^2}}{\overline{m}}100$), coefficient of residual variation ($CV_e(\%) = \frac{\sqrt{\sigma_e^2}}{\overline{m}}100$), and relative coefficient of variation ($\widehat{b} = \frac{CV_g}{CV_e}$) were also estimated, where $\overline{m}$ is the trait mean. In addition, the selection accuracy ($r_{aa} = \sqrt{h_i^2}$) was estimated to verify the reliability of selection.

The Best Linear Unbiased Prediction (BLUP) components were estimated for diameter at breast height (DBH) at nine years of age for both tests to verify the GxE interaction and indicate the best progeny for each site.

Genotypic correlation between traits and ages

The genotypic correlation ($r_{g(x,y)}$) between traits and ages were estimated as: $r_{g(x,y)} = \frac{Cov_{g(x,y)}}{\sqrt{\sigma^2_{gx}\sigma^2_{gy}}}$; where, Cov_g is the genotypic covariance between traits X and Y; σ^2_{gx} is the genotypic variance of trait X; and σ^2_{gy} is the genotypic variance of trait Y.

Productivity, adaptability, and stability

The Genotype x Environment (GxE) interaction was decomposed into simple and complex proportions based on the methodology described by Cruz & Castoldi (1991). For the productivity, adaptability, and stability analysis, we used a joint analysis between the two environments according to the following mixed model:

$$y = Xr + Zg + Zp + Zge + e,$$

where, r is the fixed effect associated with replications; g is the random effect associated with genotypes; p is the random effect associated with plots; ge is the random effect associated with the GxE interaction; *e* is the residual effect; and *X* and *Z* are the incidence matrices of the fixed and random effects, respectively.

The analysis then proceeded according to the methodology described by Resende (2007) to obtain the harmonic mean of genotypic values (MHVG), relative performance of genotypic values (PRVG), and the combined productivity, adaptability, and stability of genotypic values (MHPRVG) for diameter at breast height (DBH) at nine years of age.

Thinning simulation

Based on the objectives of the company, the formation of a seed orchard was simulated for both experiments. As such, the thinning simulation considered maintaining only one individual per plot in each block to avoid crossing between relatives. For selection, the individual BLUP was considered, aiming to select only the best individuals based on genetic values. The selection was based on DBH at nine years of age. Another scenario was considered for the thinning simulation, in which only progeny with positive BLUP values were selected. This scenario reduces the number of progenies within the genetic pool, with the expectation of greater genetic gains.

In addition, the effective number for both populations was obtained before and after the thinning simulation, according to the following equation:

$$N_e = \frac{4N_f\overline{K}_f}{\overline{K}_f + 3 + \left(\frac{\sigma^2_{kf}}{\overline{K}_f}\right)},$$

where, N_e is the effective number; N_f is the number of progenies; $\overline{K}_f$ is the average number of selected individuals per progeny; σ^2_{kf} is the variance of the number of selected individuals per progeny.

The genetic gains with selection were estimated as follows:

$$EGA = ih_i^2\sigma_f,$$

where, *EGA* is the expected genetic advance under selection; *i* is the selection intensity; σ_f^2 is the phenotypic standard deviation; and h_i^2 is the narrow-sense heritability. The genetic advance as a percent of the population mean was also derived as *GAM%=(EGA/mean)100*.

RESULTS

A deviance analysis was performed (Table II) to assess the model's random effects. In site PGI, the progeny effects for all traits and ages were significant at 0.1% probability. In PGII, DBH at seven years showed significance at 1% probability, while the other traits and ages were significant at 0.1% for progeny effect.

Table II. Likelihood ratio test (LRT) of progeny for diameter at breast height (DBH7) and total height (H7) at seven years of age and at nine years of age (DBH9, H9) in two *Pinus greggii* progeny tests established in Telêmaco Borba, PR, Brazil.

Experiments		DBH7	H7	DBH9	H9
PGI	LRT Progeny	26.07**	20.65**	25.85**	31.96**
PGII	LRT Progeny	24.79*	12.53**	29.45**	16.88**

LRT Progeny: progeny likelihood ratio test; LRT Plot: plot likelihood ratio test; **: significant at 0.1% probability; *significant at 1% probability.

In general, PGI showed higher narrow-sense heritability (h_i^2) than PGII (Table III). In PGI, the h_i^2 values ranged from 0.317 (DBH7) to 0.515 (H9), while in PGII the values ranged from 0.225 (H7) to 0.351 (DBH9). The heritability within progeny (h_d^2) were also higher in PGI. Among environments, the narrow-sense heritability (H^2) ranged from 0.212 (DBH7) to 0.263 (H7) and from 0.328 (DBH9) to 0.386 (H9).

The genetic coefficient of variation ($CV_g(\%)$) values were very similar in both sites, ranging from 6.6% (H9) to 7.7% (DBH9) in PGI and from 5.4% (H9) to 9.6% (DBH9) in PGII. The residual coefficient of variation ($CV_e(\%)$) ranged from 16.4% to 30.8%. The CV_{gi}/CV_g ratio was equal to 2.0 for all traits in both sites. As for the relative coefficient of variation ($\widehat{b}$), it was inferior to 1.0 for all traits in both sites. The breeding values (BLUPs) were estimated for DBH at nine years of age (Table IV) to rank the best progeny within each test based on genetic performance.

The progeny with the best performance for PGI and PGII were 192 and 30, respectively (mean of 17.60 and 16.36 cm, respectively). It is important to note that there were several *P. greggii* progeny that showed better performance than the *P. taeda* control. The mean DBH of progeny 192 in PGI was 8.24% higher than the *P. taeda* control. On other hand, the mean DBH of progeny 30 in PGII reached a performance 3.34% greater than the *P. taeda* control.

The genetic correlation between traits, ages, and environments were estimated (Table V), and we found statistical significance at 5% for all results. The genetic correlation between DBH and total

Table III. Genetic parameters of two *Pinus greggii* progeny tests established in Telêmaco Borba, PR, Brazil, for DBH (cm) and height (m) at seven and nine years of age.

	7 years				9 years			
	PGI		PGII		PGI		PGII	
	DBH	H	DBH	H	DBH	H	DBH	H
h_i^2(SE)	0.317 (0.11)	0.500 (0.12)	0.311 (0.06)	0.225 (0.09)	0.350 (0.11)	0.515 (0.12)	0.351 (0.07)	0.320 (0.08)
h_d^2	0.277	0.498	0.251	0.192	0.311	0.498	0.290	0.280
h_m^2	0.790	0.821	0.822	0.738	0.821	0.850	0.846	0.774
H^2	0.212	0.263	0.266	0.217	0.328	0.381	0.324	0.386
$CV_g(\%)$	6.7	7.0	8.2	7.0	7.7	6.6	9.6	5.4
$CV_{gi}(\%)$	13.3	13.9	16.3	13.9	15.4	13.2	19.1	10.7
$CV_e(\%)$	22.1	17.1	28.1	28.0	24.5	16.4	30.8	17.6
$\widehat{b}$	0.30	0.41	0.29	0.25	0.31	0.40	0.29	0.31
CV_{gi}/CV_g	2.00	2.00	2.00	2.00	2.00	2.00	2.00	2.00
r_{aa}	0.56	0.70	0.50	0.47	0.59	0.72	0.59	0.56
Mean	14.1	12.5	12.8	12.0	15.6	13.5	14.3	12.9

SE: standard error. h_i^2: narrow-sense heritability; h_d^2: heritability within progeny; h_m^2: heritability at progeny mean level; H^2: narrow-sense heritability among environments; $CV_g(\%)$: genetic coefficient of variation; $CV_{gi}(\%)$: individual genetic coefficient of variation; $CV_e(\%)$: residual coefficient of variation; $\widehat{b}$: relative coefficient of variation; r_{aa}: selection accuracy.

height at seven years reached 0.866 and 0.905, respectively, for PGI and PGII; the correlation for the same traits at nine years of age reached 0.905 and 0.674 for PGI and PGII.

As for the genetic correlation between ages, in PGI it reached 0.781 and 0.810 for DBH and H, respectively, while in PGII it was 0.94 and 0.66 for the same traits. The genetic correlation between environments was inferior to 0.565 for all traits and ages, verifying the difference found for the BLUP ranking of progeny.

The GxE interaction was decomposed, resulting in 65.15% complex and only 34.85% simple. These results confirm the influence of the interaction effect, corroborating the low genetic correlation between environments. All 16 progeny were ranked jointly and sorted by productivity, adaptability, and stability of genetic values (MHPRVG) for DBH9 (Table VI). Progeny 35 is both the most productive and the most stable. Progeny 192 and 187 also stood out, as they performed better and are more stable than the *P. taeda* control.

In order to support the creation of a seed orchard, a thinning simulation was conducted (Table VII) leaving only one plant per plot within each block to avoid mating between relatives. In addition, another scenario was considered in which only the progeny with positive BLUPs were selected to achieve greater genetic gains. The original effective number (N_e) for PGI and PGII were 59.82 and 59.84, respectively.

After thinning simulation for a seed orchard, the N_e decreased to 48 for both sites and the expected genetic advance was 12.49% and 15.03% for PGI and PGII, respectively. On other hand,

Table IV. Ranking of the best progeny in two (PGI and PGII) *Pinus greggii* progeny tests established in Telêmaco Borba, PR, Brazil, for diameter at breast height (DBH, cm) at nine years of age.

	PGI			PGII		
Rank	Progeny	BLUP	New Mean	Progeny	BLUP	New Mean
1	192	1.5914	17.60	30	1.7319	16.36
2	194	1.4456	17.06	35	1.5391	15.81
3	35	0.9574	16.58	*P. taeda*	1.2870	15.55
4	187	0.7994	16.42	187	1.2107	15.48
5	193	0.6001	16.22	192	0.7941	15.06
6	172	0.5404	16.16	33	0.4002	14.67
7	*P. taeda*	0.5240	16.14	194	0.3581	14.63
8	173	0.4084	16.03	172	0.0602	14.33
9	184	-0.0549	15.56	193	0.0600	14.33
10	33	-0.1404	15.48	173	0.0335	14.30
11	30	-0.1874	15.43	190	-0.0268	14.24
12	185	-0.4781	15.14	185	-0.6415	13.63
13	190	-0.7214	14.90	184	-1.0570	13.21
14	186	-1.7267	13.89	186	-1.2845	12.98
15	24	-1.7516	13.87	183	-1.9605	12.31
16	183	-1.8064	13.81	24	-2.5045	11.76

P. taeda: control.

Table V. Genetic correlation (r_g) between ages and traits of *Pinus greggii* for site PGI (upper diagonal), PGII (lower diagonal), and between environments (main diagonal) in Telêmaco Borba, PR, Brazil.

Traits	DBH7	H7	DBH9	H9
DBH7	**0.30***	0.87*	0.78*	0.67*
H7	0.91*	**0.33***	0.80*	0.81*
DBH9	0.94*	0.88*	**0.42***	0.91*
H9	0.59*	0.66*	0.67*	**0.56***

DBH7: diameter at breast height at seven years; DBH9: diameter at breast height at nine years; H7: total height at seven years; H9: total height at nine years; *: significant at 5% probability. Bold numbers indicate the genetic correlation between environments.

Table VI. Ranking of the best progeny of two *Pinus greggii* progeny tests sorted by MHPRVG values for diameter at breast height (DBH, cm) at nine years of age.

Rank	Progeny	MHVG	PRVG	MHPRVG
1	35	16.30	16.33	16.33
2	192	16.24	16.28	16.28
3	187	16.03	16.06	16.06
4	*P. taeda*	15.91	15.94	15.94
5	194	15.90	15.94	15.94
6	30	15.74	15.77	15.77
7	193	15.28	15.32	15.32
8	172	15.25	15.29	15.29
9	173	15.16	15.20	15.20
10	33	15.06	15.09	15.09
11	190	14.52	14.55	14.55
12	184	14.29	14.33	14.33
13	185	14.29	14.33	14.33
14	186	13.26	13.29	13.29
15	183	12.83	12.87	12.87
16	24	12.52	12.56	12.56

P. taeda: control.

Table VII. Thinning simulations based on diameter at breast height (DBH, cm) at nine years of age for two *Pinus greggii* progeny tests in Telêmaco Borba, PR, Brazil.

	PGI			PGII		
	Mean	N_e	*GAM%*	Mean	N_e	*GAM%*
Original	15.62	59.82	-	14.27	59.84	-
Seed Orchard	20.00	48.00	12.49	19.33	48.00	15.03
Positive BLUPs	21.04	24.00	15.93	20.18	30.00	19.18

N_e: effective number; $_{GAM\%}$: genetic advance of the population mean.

selecting the progeny with positive BLUPs greatly reduced the N_e, but provided better genetic advances (15.93% and 19.18%).

DISCUSSION

Both experiments showed significance at 5% between progeny according to the LRT test, indicating substantial differences in genotype performance, which facilitates the selection process. Based on the classification by Resende (2007), the narrow-sense heritability (h_i^2) values are considered high magnitude for total height in PGI (both ages) and medium magnitude for DBH in both sites at seven and nine years of age. These results indicate considerable genetic control of the evaluated traits. Braga et al. (2020), evaluating *P. taeda* at 11 years of age in the same region as the present study, found slightly higher h_i^2 values, ranging from 0.438 (DBH) to 0.582 (total height). However, Aguiar et al. (2010), studying *P. greggii* progeny of the same provenances used herein, found h_i^2 values of 0.23 and 0.30 for DBH and total height, respectively, at 13 years of age. Hodge & Dvorak (2012) reported a value of 0.23 for volume at eight years of age for progeny collected from 13 provenances, including those used in the present study.

High values for heritability, such as those encountered in this study, are extremely important for a breeding program. The higher the heritability values the greater the reliability of selection, since heritability shows the proportion of the population's variance that might be attributed to genetic factors. When heritability values are low, there is a greater chance that the breeder will select individuals that performed well due to environmental factors, such as better luminosity, low-levels of competition and better soil quality, thus overlooking the additive genetic factors. On the other hand, high heritability values indicate that an individual's performance is mostly influenced by genetic factors, which can be exploited.

The coefficient of genetic variation ($CV_g(\%)$) values were superior to those found by Aguiar et al. (2010), who reported 2.20% for total height and 5.7% for DBH at 13 years of age. In the present study, both traits showed high levels of genetic diversity, since the values were near 7%, which is crucial in a breeding program. Low genetic diversity might result in the end of a breeding program after few selection cycles, as it narrows the genetic pool and causes problems related to inbreeding (Sebbenn et al. 2008). For all traits in both sites, the coefficients of residual variation ($CV_e(\%)$) were lower than 31.0% and are therefore considered acceptable for forestry experiments (Pimentel-Gomes & Garcia 2002). According to Mora & Arriagada (2016), growth traits tend to present higher $CV_e(\%)$ values. Nevertheless, the values encountered in this study are considered medium to high magnitude for DBH and high to very high for total height.

Accuracy is defined as the correlation between true and estimated genetic parameters (Walsh & Lynch 2018). Within breeding programs, high values of selection accuracy are extremely important since they are related to selection reliability. Thus, if the values are low there is a greater chance that the breeder selects individuals influenced by environmental factors. The values for selection accuracy (r_{aa}) ranged from 0.56 (DBH7) to 0.72 (H9), with little variation between r_{aa} for traits, ages, or environments, and are similar to the accuracy levels reported in other studies on forestry species (Resende 2007).

The relative coefficient of variation ($\widehat{b}$) values were lower than 1.0 for all results. According to Vencovsky & Barriga (1992), it is favorable for values of this parameter to be higher than 1.0. Nevertheless, it is still possible to obtain genetic gains by selection with greater selection intensity. To improve $\widehat{b}$, the inclusion of new genetic material in the test is recommended, which would increase the genetic variance and, consequently, the $CV_g(\%)$.

For all traits, the CV_{gi}/CV_g ratio values were equal to 2.0. This is a very positive result, considering that values equal to or lower than 1.0 mean that the additive variance is null. Sebbenn et al. (2008) found values of 1.75 for DBH and total height in their analysis of *Pinus elliotti* at 25 years of age.

The high genetic correlation (r_g) values between traits and ages can be attributed to the association already identified between DBH and height and the limited age difference between the two analyses. When the r_g values are high, the breeder can perform indirect selection between traits. In the present case, DBH and total height can be improved simultaneously by selecting only individuals for DBH values, data that is much easier to collect. The r_g between DBH and total height found herein was slightly inferior to the value found by Hodge & Dvorak (2000) of 0.910 for *P. greggii* at five and eight years of age. Our results for r_g indicate good reliability in indirect selection between DBH and total height, since the values were generally higher than 0.85 (Resende 2015). In relation to early selection, the r_g between ages show that it is possible and effective to conduct selection at seven years with the goal of obtaining gains at nine years (Resende 2015). Considering that forests have long rotation cycles, early selection can anticipate the identification of individuals for selection and save years between cycles (Wu 1998).

For all cases, the genetic correlation between environments was inferior to 0.56, indicating the presence of GxE interaction. Therefore, the most stable genotypes, or those that can perform equally in both sites, must be identified (Braga et al. 2020). The low r_g between environments means that the best genotypes for one site may not be the best for the other, which is consistent with the BLUP estimates. Given this situation, all 16 progeny were simultaneously sorted by their productivity, adaptability, and stability (MHPRVG values) and the three superior progeny were identified as 35, 192, and 187. In addition, these three progeny obtained better performance than the *P. taeda* control, indicating significant potential for exploitation within the *P. greggii* population.

Hodge & Dvorak (2012) identified at eight years of age a mean DBH of 14.4 cm and 10.2 for two *P. greggii* progeny tests established in South Africa and Chile, respectively. However, their database included provenances from the North and Central-East of Mexico, while the present study included only southern provenances, which are known for their higher growth rate (Donahue & López-Upton 1999).

The values for effective number (N_e) were 59.82 and 59.84 for PGI and PGII, respectively, and both decreased to 48 after seed orchard thinning simulation. On other hand, the N_e was greatly reduced in the scenario with only positive BLUP values, which can be attributed to the reduction in the number of progeny in both experiments. Necessarily, the greater the number of progeny in the population, the higher the N_e. On the other hand, if the number of plants per progeny is increased (even tending to infinity) the maximum contribution for the effective number in allogamous species will be four ($N_e = 4$) (Vencovsky & Crossa 2003). This explains why the seed orchard simulation reduced the N_e only by about 11.00 since all progeny were maintained, while the positive BLUP scenario reduced the N_e by about 30.00.

Moderate genetic gains were obtained with the seed orchard simulation (12.49% and 15.03%); however, the thinning methodology aimed not only to obtain genetic gains at all costs, but also create a seed orchard that would avoid crossing between relatives. The positive BLUP scenario obtained higher genetic gains (15.93% and 19.18%); however, the N_e was drastically reduced, which could generate problems related to endogamy (Vencovsky & Crossa 2003). In practical terms, both scenarios could be used simultaneously, so that the breeder can obtain greater genetic gains with high selection intensity while also improving favorable allele frequencies without significantly reducing the effective population size (N_e). In other words, genetic gains can be obtained for both the short and long term.

CONCLUSIONS AND CONSIDERATIONS FOR THE BREEDER

The *P. greggii* progeny tests established in Telêmaco Borba, Paraná, Brazil, showed enough genetic diversity for the development of a breeding program, although new genetic material is needed to further increase the genetic variance. The heritability values vary from moderate to high indicating that the evaluated traits have high levels of genetic control, which reflects reliability in the selection process. Based on the BLUP ranking for each site and the genetic correlation between sites, we found GxE interaction. Therefore, the most stable and productive progeny (35, 192 and 187) were identified by their MHPRVG values. The genetic correlation between DBH and total height is possible and reliable. Thus, early selection between seven and nine years of age may also be effective. Nevertheless, it is highly recommended that future studies analyze the genetic correlation at older ages. Although the genetic gains after thinning were moderate, the main objective is to create a seed orchard without substantially reducing the effective number while also avoiding crossing between relatives. Thus, the thinning simulation showed slight gains for the creation of a seed orchard and significant gains based on a scenario with higher selection intensity.

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