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Genetics/ Original Article

Genetic parameters, selection gains and associations between characters of *Carya illinoinensis* using mixed models

Abstract – The objective of this work was to estimate the genetic parameters of pecan (*Carya illinoinensis*) cultivars through mixed model analyses of data on vegetative growth, fruit production, and fruit quality traits. The study was conducted from 2021 to 2023, using the Barton, Desirable, Elliot, Mohawk, Jackson, Shoshoni, Stuart, and Success pecan cultivars, in the municipality of Santana do Livramento, in the state of Rio Grande do Sul, Brazil. The experimental design was completely randomized. Each replicate was composed of ten plants, totaling 80 plots. Nut vegetative growth, production, and quality were evaluated. The influence of the genotype x environment interaction on production traits and nut quality was confirmed. However, these effects were not observed on vegetative growth. Production per plant and productivity per hectare exhibited positive correlations with production efficiency in relation to canopy volume. For the vegetative and production traits, broad-sense individual heritability is low, suggesting a strong environmental influence. However, for the fruit quality traits, heritability is medium to high, indicating a greater genetic contribution and, therefore, a greater potential for response to selection.

Index terms: genetic correlation, pecan, productivity, selection.

Parâmetros genéticos, ganhos de seleção e associações entre caracteres de *Carya illinoinensis* com uso de modelos mistos

Resumo – O objetivo deste trabalho foi estimar os parâmetros genéticos de cultivares de nogueira-pecã (*Carya illinoinensis*) por meio de análises com modelos mistos dos dados de características de crescimento vegetativo, produ**ção de frutos** e qualidade de frutos. O estudo foi conduzido de 2021 a 2023, tendo-se utilizado as cultivares de nogueira-pecã Barton, Desirable, Elliot, Mohawk, Jackson, Shoshoni, Stuart e Success, no município de Santana do Livramento, no estado do Rio Grande do Sul, Brasil. O delineamento experimental foi inteiramente casualizado. Cada repetição foi composta por dez plantas, tendo totalizado 80 parcelas. Foram avaliados o crescimento vegetativo, a produção e a qualidade das nozes. Confirmou-se a influência da interação genótipo x ambiente para os caracteres produtivos e de qualidade das nozes. No entanto, esses efeitos não foram observados no crescimento vegetativo. A produção por planta e a produtividade por hectare apresentaram correlações positivas com a eficiência produtiva em relação ao volume de copa. Para os caracteres vegetativos e de produção, a herdabilidade individual no sentido amplo mostra-se baixa, o que sugere forte influência ambiental. No entanto, para os caracteres de qualidade dos frutos, a herdabilidade é média a alta, o que indica maior contribuição genética e, portanto, maior potencial de resposta à seleção.

Termos para indexação: correlações genéticas, nogueira-pecã, produtividade, seleção.

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Introduction

Pecan [*Carya illinoinensis* (Wangenh) K. Koch], belonging to the Juglandaceae family, is native to the United States and Mexico (Wells, 2017) and is well known for its nuts, whose consumption has increased due to the benefits to human health and the price paid in the market (Casagranda et al., 2023). For this reason, pecan cultivars were brought from Mexico and the United States to Brazil, where some of them did not adapt well and were eliminated from the orchards (Poletto et al., 2020).

Currently, in Brazil, Ministério da Agricultura, Pecuária e Abastecimento (Brasil, 2024) allowed of the use of 34 pecan cultivars for the production and commercialization of seedlings and seeds. These cultivars can be used in breeding programs to meet market demands, as well as to improve resistance to diseases or adaptation to new production areas. The selection of superior genotypes depends on genetic parameters such as genetic variability, heritability, and genetic correlations of characters of interest (Silveira et al., 2024).

A common technique used to estimate genetic parameters is the mixed model. This technique uses the restricted maximum likelihood (REML) approach and the best linear unbiased prediction (BLUP). REML estimates the components of variance, while BLUP predicts genetic values (Resende, 2002). The advantages of the use of both techniques, in a complementary way, are the possibility of the simultaneous correction of environmental effects and the capacity of comparing individuals or varieties over time and space (Silva et al., 2017). Regarding perennial plants, REML/BLUP has been considered the standard for genotype selection (Silveira et al., 2022), particularly in species as sweet orange (*Citrus sinensis* Pers.) and papaya (*Carica papaya* L.) in the studies of Capistrano et al. (2021) and Ramos et al. (2014), respectively.

The objective of this work was to estimate the genetic parameters of pecan cultivars through mixed model analyses of data on vegetative growth, fruit production, and fruit quality traits.

Materials and Methods

The experiment was carried out from 2021 to 2023 at the Vila Palomas farm, in the municipality of Santana do Livramento, in the state of Rio Grande do Sul, Brazil. The orchard was implanted in 2001 using a spacing between rows of 9 m and between plants of 6 m. Plant density was 185 plants per hectare.

The following eight cultivars were used in the study: Barton, Desirable, Elliot, Jackson, Mohawk, Shoshoni, Stuart, and Success. The experimental design was completely randomized. Each replicate was composed of ten plants, totaling 80 plots. Although the crop treatments were determined by the farm owner and not by the researchers, all plants were subjected to the same fertilization, pruning, and weed and phytosanitary control.

The evaluated variables were: plant height (m); lateral width (m); transverse width (m); trunk diameter (cm), measured at 1.3 m from the ground level using a measuring tape; canopy volume (m^3); trunk circumference (cm); trunk radius (cm); trunk cross-sectional area (cm^2); production efficiency in relation to trunk cross-sectional area (PETCSA, kg cm^{-2}); production efficiency in relation to canopy volume (PECV, kg m^{-3}); productivity per hectare (Mg ha^{-1}); production per plant (kilogram per plant); number of fruit attached to the capsule after harvest (NFAC); number of nuts per kilogram; nut yield (%), calculated as kernel mass divided by total fruit mass; total mass (g), calculated as the sum of kernel mass and husk mass; kernel length (mm); nut length (mm); kernel mass (g); husk mass (g); husk thickness (mm); kernel width (mm); nut width (mm); color to the capsule, visually determined by comparing the layer color to a four-color standard. Nut length, husk thickness, kernel width, and nut width were determined using a pachymeter.

Canopy volume was obtained using the following equation:

$$\mathrm{CV} = \frac{1}{3} \times \pi \times (\mathrm{RAD} \times 100)^2 \times \mathrm{H}$$

where CV is canopy volume, RAD is trunk radius (cm), and H is plant height (m).

In the statistical analysis, estimates of components of variance and the prediction of genetic values were carried out by REML/BLUP. The significance of random effects was obtained through the deviance analysis using the REML method, and significance was tested using the likelihood ratio test. The deviances were determined as described by Resende (2016), using the model with and without the respective effects. The deviance obtained in the complete model was subtracted from the model without the effects and compared with the chi-square value with one degree of freedom. Once the fixed effects were considered, the block factor was tested using Snedecor's F-test.

For the completely randomized experimental design, the following statistical model was used: $y = X_r + Z_a + W_p + T_i + e$, where y represents the data vector; r is the vector of replicate effects added to the general average; a is the vector of individual additive genetic effects (random); p is the vector of the effects of the graphs; i represents the vector of the effects of the genotype x environment (GxE) interaction; e is the vector of errors or residues; and X, Z, W, and T are the matrices of incidence for r, a, p, and i, respectively.

The equations of the mixed model correspond to:

$$\begin{bmatrix} X'X & X'Z & X'W & X'T \\ Z'X & Z'Z+I^{-1}\lambda_1 & Z'W & Z'T \\ W'X & W'Z & W'W+I^{-1}\lambda_2 & W'T \\ T'X & T'Z & T'W & T'T+I^{-1}\lambda_3 \end{bmatrix} \begin{bmatrix} \tilde{m} \\ \tilde{g} \\ \tilde{p} \\ i \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ T'y \end{bmatrix}$$

where $\lambda_1 = \frac{1-p}{h^2} = \frac{\hat{\sigma}_e^2}{\hat{\sigma}_g^2}; \lambda_2 = \frac{1-\rho}{c^2} = \frac{\hat{\sigma}_e^2}{\hat{\sigma}_c^2}; \lambda_3 = \frac{1-\rho}{p^2} = \frac{\hat{\sigma}_e^2}{\hat{\sigma}_p^2}$, with $\hat{\sigma}_e^2, \hat{\sigma}_g^2, \hat{\sigma}_c^2$, and $\hat{\sigma}_p^2$ representing the residual, genetic, common environmental, and phenotypic variances, respectively. In this case, broad-sense individual heritability within the block is given by $h^2 = \hat{\sigma}_g^2 / \hat{\sigma}_g^2 + \hat{\sigma}_c^2 + \hat{\sigma}_p^2 + \hat{\sigma}_e^2$, individual repeatability in the block is given by $\rho = \hat{\sigma}_g^2 + \hat{\sigma}_c^2 + \hat{\sigma}_p^2 / \hat{\sigma}_g^2 + \hat{\sigma}_c^2 + \hat{\sigma}_p^2 + \hat{\sigma}_e^2$, the common environmental correlation between plots is given by $c^2 = \hat{\sigma}_c^2 / \hat{\sigma}_g^2 + \hat{\sigma}_c^2 + \hat{\sigma}_p^2 + \hat{\sigma}_e^2$, and the coefficient of determination of the permanent effects of the plot is given by $p^2 = \hat{\sigma}_p^2 / \hat{\sigma}_g^2 + \hat{\sigma}_c^2 + \hat{\sigma}_p^2 + \hat{\sigma}_e^2$. The iterative estimators of the variance components in REML were obtained using the expectation-maximization algorithm (Dempster et al., 1977). In this case:

$$\hat{\sigma}_e^2 = \left[y'y - \hat{m}'X'y - \hat{g}'Z'y - \hat{p}'W'y - \hat{I}'T'y\right] / \left[N - r(X)\right],$$
$$\hat{\sigma}_g^2 = \left[g'^{I^{-1}} g + \hat{\sigma}_e^2 \mathrm{tr}(I^{-1}C^{22}\right] \Big/ q, \hat{\sigma}_p^2 = \left[\hat{p}'p + \hat{\sigma}_e^2 \mathrm{tr}C^{44}\right] / s,$$
$$\hat{\sigma}_i^2 = \left[\hat{I}'i + \hat{\sigma}_e^2 \mathrm{tr}C^{44}\right] / q,$$

where N is the total number of data, r(X) is the rank of matrix X, C is the matrix of coefficients of the mixed model equations, tr is the matrix trace operator, q is the number of individuals, and s is the number of genotype x harvests. C^{22}, C^{33}, and C^{44} come from:

$$C^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} & C_{14} \\ C_{21} & C_{22} & C_{23} & C_{24} \\ C_{31} & C_{32} & C_{33} & C_{34} \\ C_{41} & C_{42} & C_{43} & C_{44} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} & C^{13} & C^{14} \\ C^{21} & C^{22} & C^{23} & C^{24} \\ C^{31} & C^{32} & C^{33} & C^{34} \\ C^{41} & C^{42} & C^{43} & C^{44} \end{bmatrix}$$

The variance components associated with the model effects correspond to: $\hat{h}_g^2 = \hat{\sigma}_g^2 / \hat{\sigma}_f^2$, the heritability of individual plots in the broad sense, i.e., total genotypic effects; C_p^2, the coefficient of determination of plot effects; $C_{gm}^2 = \hat{\sigma}_{int}^2 / \hat{\sigma}_f^2$, the coefficient for determining the effects of the genotypes x measurements interaction; $r_{gmed} = \hat{\sigma}_g^2 / \hat{\sigma}_g^2 + \hat{\sigma}_{int}^2$, the genotypic correlation through measurements; $h_{mg}^2 = \hat{\sigma}_g^2 \Big/ \hat{\sigma}_g^2 + \left(\frac{\hat{\sigma}_e^2}{b}\right) + \left(\frac{\hat{\sigma}_c^2}{nb}\right)$ genotype mean heritability; n, number of plots; b, number of blocks; $\hat{r}_{gg} = \sqrt{h_{mg}^2}$, accuracy in genotype selection; $CV_g(\%) = \left(\sqrt{\hat{\sigma}_g^2} / \mu\right) \times 100$, coefficient of genotypic variation; $CV_e(\%) = \left(\sqrt{\hat{\sigma}_c^2} / \mu\right) \times 100$, coefficient of environmental variation; and $CV_r = CV_g / CV_e$, relative coefficient of variation.

The association among characters was estimated through the genetic correlation of the genotypic values, i.e., averages of the cultivars estimated by BLUP. The correlation coefficients between variables were also estimated, and significance was evaluated using Student's t-test, at 1 and 5% probability. The magnitudes of correlation were classified according to Silveira et al. (2021). A correlation network was used to express the functional relationship of the correlation estimates between the studied characteristics (Figure 1). The proximity between the features was proportional to the absolute value between their correlations. The thickness of the edges was controlled by applying a cut-off value of 0.40, where only ≥ 0.40 edges were highlighted. The positive correlations were represented in green, whereas the negative ones were represented in red. All analyses were carried out using the SELEGEN-REML/BLUP (Resende, 2016) and Rbio (Bhering, 2017) software.

Results and Discussion

Based on the analysis of deviance, most characters had significant genotypic effects (Tables 1, 2, and 3), meaning there was selection feasibility due to a greater genetic variability among cultivars. Therefore, vegetative, production, and quality characters may be used either individually or in combination with each other to determine diversity patterns, characterize cultivars, and identify plants that have commercial potential, considering edaphoclimatic conditions. In this case, the exceptions were trunk diameter, PECV, and PETCSA, for which no significant genotypic effect was observed, despite a significant GxE interaction.

The GxE interaction influenced nut production and quality characters but not the vegetative ones ($p<0.05$) (Tables 1, 2, and 3). In a study on sweet oranges, Capistrano et al. (2021) considered such interaction undesirable for genetic improvement due to the difficulty in predicting the behavior of genotypes regarding changes in the environment, which may result in a different performance in production cycles.

Vegetative characters, such as plant height, trunk circumference, trunk diameter, radius, and trunk cross-sectional area were not influenced by any GxE interaction, but by the year effect (Table 1). However, since the GxE interaction refers to the relative behavior of a genotype by comparison with others when grown in different settings (Borém et al., 2021), climate

Table 1. Verisimilitude values (LRT) of the deviance analysis and estimates of genetic parameters (individual restricted maximum likelihood) of eight pecan (*Carya illinoinensis*) cultivars for the vegetative characters plant height (PH), transverse width (TW), lateral width (LW), canopy volume (CV), trunk circumference (TC), trunk diameter (TD), radius (RAD), and trunk cross-sectional area (TCSA)(1).

Effect	Variable							
	PH	TW	LW	CV	TC	TD	RAD	TCSA
Complete	42.26	-79.94	-70.85	1301.2	634.5	112.6	-202,9	1467.8
Genetic	47.13	-77.76	-61.50	1310.0	646.5	124.7	-190.8	1480.5
Environment	132.1	-13.56	-20.37	1364.3	1051.1	529.2	213.1	1953.3
GxE(2) interaction	42.28	-75.69	-64.72	1303.5	634.5	112.7	-202.8	1468.0
$LRT_{genotype}$	4.87*	2.18 ns	9.35*	8.74*	12.08*	12.08*	12.09*	12.6*
$LRT_{measurement}$	89.84*	66.38*	50.48*	63.09*	416.6*	416.5*	416.0*	485.4*
LRT_{GxE}	0.02^{ns}	4.25*	6.13*	2.26^{ns}	0.07^{ns}	0.08^{ns}	0.07^{ns}	0.160^{ns}
σ^2_g	0.082	0.029	0.086	44.53	11.68	1.184	0.296	692.4
σ^2_p	0.363	0.171	0.145	97.04	29.82	3.023	0.756	1700.9
σ^2_{gm}	0.001	0.013	0.018	5.805	0.016	0.002	0.000	0.742
σ^2_e	0.194	0.115	0.124	72.28	1.109	0.112	0.028	37.67
σ^2_g	0.641	0.328	0.373	219.6	42.64	4.321	1.080	2.431
h^2_g	0.128	0.089	0.232	0.203	0.274	0.274	0.274	0.28
r	0.695	0.611	0.620	0.644	0.974	0.974	0.974	0.98
C^2_p	0.567	0.522	0.389	0.442	0.700	0.700	0.699	0.69
C^2_{gm}	0.002	0.040	0.047	0.026	0.000	0.000	0.000	0.00
r_{gmed}	0.986	0.692	0.831	0.885	0.999	0.999	0.999	0.99
h^2_{mg}	0.608	0.485	0.738	0.716	0.791	0.791	0.791	0.80
$\hat{r}_{gg}$	8.304	6.937	6.485	98.48	47.25	15.04	7.521	180.7
CV_e (%)	5.307	4.881	5.429	8.633	2.228	2.229	2.233	3.39
CV_g (%)	3.450	2.461	4.534	6.776	7.234	7.234	7.235	14.5
CV_r	0.650	0.504	0.835	0.785	3.247	3.246	3.240	4.28

(1) $\hat{\sigma}^2_g$, genotypic variance; $\hat{\sigma}^2_p$, phenotypic variance; $\hat{\sigma}^2_{gm}$, variance of the genotypes x measurements interaction; $\hat{\sigma}^2_e$, residual variance; h^2_g, broad-sense individual heritability; r, repeatability at the plot level, given by $(\hat{\sigma}^2_g + \hat{\sigma}^2_{ep})/\hat{\sigma}^2_p$; C^2_p, coefficient for determining the effects of the permanent environment; C^2_{gm}, coefficient for determining the effects of the genotypes x measurements interaction; r_{gmed}, genotypic correlation through measurements; h^2_{mg}, average heritability of the genotype (range); $\hat{r}_{gg}$, selective accuracy; CV_e, coefficient of experimental variation; CV_g, coefficient genetic variation; and CV_r, coefficient of relative variation. (2)Genotype x environment. *Significant by the Chi-square test, at $p<0.05$, with 1 degree freedom. ^{ns}Nonsignificant.

conditions still directly influence the vegetative development of pecan trees. An example is rain intensity in critical periods, such as flowering, which may harm pollination and, consequently, productivity if it occurs close to kernel-filling stages (Casagranda et al., 2023).

Production per plant, plant productivity per hectare, and number of fruits attached to the capsule did not exhibit any significant effect related to year, which shows their strong genetic influence (Table 2). These data are in alignment with those found by Casagranda et al. (2023), who identified significant differences in the production of different pecan cultivars.

The environment exerted a strong influence on nut quality characters (Table 3). In the literature, the quality and morphological characteristics of nuts have been shown to depend on where the pecan trees are grown. For instance, differences were observed between cultivars grown in Brazil (Poletto et al., 2020) and China (Hou et al., 2014). Poletto et al. (2018) added that, when choosing cultivars for Southern Brazil, it is important to consider kernel yield, kernel mass, and nut size.

The CV_e ranged from 2.23 to 31.91% for radius and NFAC, respectively (Tables 1 and 2). Furthermore, CV_g, which shows the genetic variability of every character in a given population (Santos et al., 2018), ranged from 2.26 to 19.01% for nut yield and husk mass, respectively (Tables 2 and 3). Regarding CV_r, trunk circumference, trunk diameter, and radius

Table 2. Verisimilitude values (LRT) of the deviance analysis and estimates of genetic parameters (individual REML) of eight pecan (*Carya illinoinensis*) cultivars for the production characters production efficiency in relation to the trunk cross-sectional area (PETCSA), production efficiency in relation to the canopy volume (PECV), production per plant (PP), nut yield (NY), productivity per hectare (PRODT), number of fruits attached to the capsule (NFAC), and number of nuts per kilogram (NN)(1).

Effect	Variable						
	PECV	PETCSA	PP	NY	PRODT	NFAC	NN
Complete	-1,432.1	-1,713.5	565.7	601.7	-208.0	1,586.7	1,299.2
Genetic	-1,429.6	-1,710.2	573.2	612.8	-199.9	1,597.8	1,309.9
Environment	-1,430.1	-1,687.9	566.2	613.6	-207.6	1,586.8	1,299.3
GxE(2) interaction	-1,425.8	-1,704.04	570.0	631.8	-204.1	1,587.0	1,465.1
$LRT_{genotype}$	2.57^{ns}	3.25^{ns}	7.520*	11.100*	8.120*	11.07*	10.69*
$LRT_{measurement}$	2.07^{ns}	25.52*	0.550^{ns}	11.880*	0.350^{ns}	0.04^{ns}	0.10^{ns}
LRT_{GxE}	6.30	9.46*	4.290*	30.140*	3.860*	0.30^{ns}	165.8*
σ^2_g	0.000	0.000	1.076	1.231	0.038	114.54	402.8
σ^2_p	0.000	0.000	0.178	0.642	0.005	5.838	1.476
σ^2_{gm}	0.000	0.000	0.356	1.349	0.011	9.272	167.1
σ^2_e	0.000	0.000	3.204	3.621	0.107	359.51	63.72
σ^2_g	0.000	0.000	4.814	6.842	0.160	489.16	635.2
h^2_g	0.111	0.129	0.224	0.180	0.235	0.234	0.634
r	0.193	0.419	0.260	0.274	0.264	0.246	0.637
C^2_p	0.081	0.290	0.037	0.094	0.029	0.012	0.002
C^2_{gm}	0.107	0.093	0.074	0.197	0.069	0.019	0.263
r_{gmed}	0.509	0.582	0.751	0.477	0.772	0.925	0.707
h^2_{mg}	0.522	0.562	0.727	0.601	0.742	0.773	0.868
$\hat{r}_{gg}$	0.067	0.038	6.509	48.88	1.196	59.41	119.03
CV_e (%)	26.88	26.66	27.50	3.892	27.30	31.91	6.706
CV_g (%)	10.68	13.71	15.93	2.269	16.19	18.01	16.86
CV_r	0.397	0.514	0.580	0.583	0.593	0.564	2.514

(1) σ^2_g, genotypic variance; $\hat{\sigma}^2_p$, phenotypic variance; $\hat{\sigma}^2_{gm}$, variance of the genotypes x measurements interaction; $\hat{\sigma}^2_e$, residual variance; h^2_g, broad-sense individual heritability; r, repeatability at the plot level, given by $(\hat{\sigma}^2_g + \hat{\sigma}^2_{ep})/\hat{\sigma}^2_p$; C^2_p, coefficient for determining the effects of the permanent environment; C^2_{gm}, coefficient for determining the effects of the genotypes x measurements interaction; r_{gmed}, genotypic correlation through measurements; h^2_{mg}, average heritability of the genotype (range); $\hat{r}_{gg}$, selective accuracy; CV_e, coefficient of experimental variation; CV_g, coefficient genetic variation; and CV_r, coefficient of relative variation. (2)Genotype x environment. *Significant by the Chi-square test, at $p<0.05$, with 1 degree freedom. ^{ns}Nonsignificant.

were the characters that exhibited a higher CV_g than CV_e (Table 1). These results are an indicative that genetic effects are high for these characters, which can be used for genetic gains through selection among cultivars.

After the components of variance were obtained, other parameters were estimated, such as broad-sense heritability, which ranged from 0.08 to 0.75 for transverse width and husk thickness, respectively (Table 3). According to Brogin at al. (2003), values of broad-sense heritability are considered: low, when below 0.30; intermediate, between 0.30 and 0.60, enabling genetic gains through selection; and high, above 0.60. Santos et al. (2018) concluded that high heritability values show that methods of simple selection may lead to significant gains, supposing that the environment exerts little influence.

Repeatability at the plot level ranged from 0.19 to 0.98 for PECV and trunk cross-sectional area, respectively (Table 2). Low repeatability values show the need for a large number of replicates to reach a satisfactory coefficient of determination (Pereira et al., 2013). Knowledge about coefficients of repeatability of characteristics of interest allows of evaluating the time required for an accurate selection of genetically superior individuals (Bruna et al., 2012).

Production per plant and productivity per hectare showed a positive correlation with PECV, as follows: r = 0.99 ($p<0.01$) and r = 0.87 ($p<0.01$), respectively (Table 5). To estimate productivity, the amount

Table 3. Verisimilitude values (LRT) of the deviance analysis and estimates of genetic parameters (individual REML) of eight pecan (*Carya illinoinensis*) cultivars for the quality characters nut length (NL), nut width (NW), kernel length (KL), kernel mass (KM), husk thickness (HT), kernel width (KW), husk mass (HM), total mass (TM), and color to the capsule (Color)(1).

Effect	Variable								
	NL	NW	KL	KM	HT	KM	HM	TM	Color
Complete	859.9	209.3	684.5	191.0	-991.6	24.9	25.20	319.1	-130.5
Genetic	877.6	224.3	700.1	203.9	-969.0	33.7	39.99	330.5	-94.00
Environment	859.9	217.9	684.6	195.4	-989.2	26.0	25.67	319.3	-130.5
GxE(2) interaction	880.8	299.0	705.0	313.9	-950.1	78.190	80.28	392.3	-130.5
$LRT_{genotype}$	17.6*	15.01*	15.62*	12.89*	22.66*	8.88*	14.79*	11.41*	36.55*
$LRT_{measurement}$	0.04^{ns}	8.55*	0.12^{ns}	4.39*	2.41^{ns}	1.15^{ns}	0.47^{ns}	0.16^{ns}	0.01^{ns}
LRT_{GxE}	20.8*	89.6*	20.52*	122.8*	41.4*	53.28*	55.08*	73.20*	0.01^{ns}
σ^2_g	22.7	2.84	11.00	2.879	0.014	0.435	0.845	2.728	0.338
σ^2_p	0.153	0.131	0.141	0.081	0.000	0.022	0.013	0.028	0.002
σ^2_{gm}	3.656	0.713	2.150	0.918	0.002	0.205	0.207	0.983	0.001
σ^2_e	11.022	0.477	5.620	0.451	0.003	0.250	0.253	0.943	0.153
σ^2_g	37.599	4.167	18.912	4.329	0.019	0.912	1.318	4.683	0.494
h^2_g	0.606	0.683	0.582	0.665	0.754	0.478	0.641	0.583	0.683
r	0.610	0.714	0.589	0.684	0.771	0.501	0.651	0.589	0.688
C^2_p	0.004	0.031	0.007	0.019	0.018	0.024	0.010	0.006	0.004
C^2_{gm}	0.097	0.171	0.114	0.212	0.088	0.224	0.157	0.210	0.002
r_{gmed}	0.862	0.800	0.836	0.758	0.896	0.680	0.803	0.735	0.997
h^2_{mg}	0.914	0.907	0.902	0.891	0.946	0.827	0.902	0.870	0.962
$\hat{r}_{gg}$	43.02	24.12	33.89	19.31	1.040	4.491	4.784	9.365	3.814
CV_e (%)	7.716	2.864	6.994	3.477	4.973	11.13	10.52	10.37	10.26
CV_g (%)	11.09	6.994	9.785	8.783	11.50	14.69	19.21	17.63	15.23
CV_r	1.437	2.442	1.399	2.526	2.313	1.320	1.826	1.701	1.484

(1) $\hat{\sigma}^2_g$, genotypic variance; $\hat{\sigma}^2_p$, phenotypic variance; $\hat{\sigma}^2_{gm}$, variance of the genotypes x measurements interaction; $\hat{\sigma}^2_e$, residual variance; h^2_g, broad-sense individual heritability; r, repeatability at the plot level, given by $(\hat{\sigma}^2_g + \hat{\sigma}^2_{ep})/\hat{\sigma}^2_p$; C^2_p, coefficient for determining the effects of the permanent environment; C^2_{gm}, coefficient for determining the effects of the genotypes x measurements interaction; r_{gmed}, genotypic correlation through measurements; h^2_{mg}, average heritability of the genotype (range); $\hat{r}_{gg}$, selective accuracy; CV_e, coefficient of experimental variation; CV_g, coefficient genetic variation; and CV_r, coefficient of relative variation. (2)Genotype x environment. *Significant by the Chi-square test, at $p<0.05$, with 1 degree freedom. ^{ns}Nonsignificant.

harvested in kilogram was multiplied by the number of plants per hectare. PECV suggests that, the smaller the canopy, the higher the fruit production. According to Brugnara & Sabião (2020), some characters, as canopy volume, are affected by edaphoclimatic differences, resulting in distinct developments in each setting, which shows the importance of carrying out studies in each region.

Although production per plant presented a nonsignificant correlation with most characters, it was correlated to nut yield ($r = 0.33$, $p<0.01$) and number of nuts per kilogram ($r = 0.44$, $p<0.01$). In addition, production per plant led to a good kernel filling and, consequently, a good nut yield. However, an excessive number of fruits per plant may result in small and poorly filled fruit, explaining the reasonable number of nuts per kilogram.

Nut yield had significant negative correlations with NFAC ($r = -0.75$), husk thickness ($r = -0.98$), and color to the capsule ($r = -0.81$). Regarding husk thickness, farmers value fruit with thin husk since it is easier to process (Poletto et al., 2020). As to the color character, it does not have any direct relation to yield since it does not exert any direct influence on kernel filling.

Selection based on the estimates of genetic gains predicted by BLUP enabled the prediction of the three best genotypes, which account for about 37.5% of the genotypes under evaluation (Table 4). In the case of production per plant, genetic gains ranged from 0.17 to 1.48 g per plant, with cultivar Barton increasing the new average in 79.9%. Regarding nut yield, genetic gains ranged from 0.19 to 1.39 g per plant. Once again, the Barton cultivar was highlighted, increasing the new average in 50.2%. Productivity exhibited genetic gains between 0.03 and 0.28 g per plant. These results are in alignment with those found by Casagranda et al. (2023), who reported the superiority of cultivar Barton due to its high production values. Moreover, cultivars Barton, Elliot, and Shoshoni were selected due to their high production per plant. This result is an indicative that the Elliot and Shoshoni cultivars may replace Barton when the aim is gain in production, whereas Elliot and Success may replace Barton when gain in productivity is the target.

Nut yield was higher for cultivars Shoshoni and Jackson, in addition to Barton, which showed the best performance. Shoshoni exhibited a genetic gain of 1.14 g per plant and increased the average in 50%, while Jackson, whose gain was 0.86 g per plant, increased the average in 49.7%. Therefore, these cultivars may be selected to increase gains related to nut yield.

Considering the increase in pecan-producing areas in Southern Brazil (Bilharva et al., 2018), the need to find cultivars with characteristics of commercial interest supports the conservation of the morphological, chemical, and genetic variability of the species (Poletto et al., 2020).

Table 4. Estimates of predicted genetic gains by best linear unbiased prediction for production per plant (PP), productivity (PRODT), and nut yield (NY) of pecan (*Carya illinoinensis*) cultivars, considering their average performance in the experimental cycles.

Trait	Cultivar	Estimates of predict genetic gains(1)				
		g	u+g	Gain	$\bar{X}_{new}$	u+g+gem
PP (kg per plant)	Barton	1.477	7.99	1.477	79.9	8.157
	Elliot	1.133	7.646	1.305	78.1	7.775
	Shoshoni	0.017	6.495	0.864	73.7	6.493
PRODT (Mg ha^{-1})	Barton	0.281	1.477	0.281	14.77	1.504
	Elliot	0.213	1.409	0.247	14.43	1.430
	Success	0.0097	1.205	0.168	13.64	1.206
NY (%)	Barton	1.396	5.028	1.396	50.2	5.079
	Shoshoni	0.885	4.978	1.140	50.0	5.002
	Jackson	0.302	4.918	0.861	49.7	4.929

(1)g, genotypic effects; u+g, predicted genotypic values, free from all interaction with cycles; $\bar{X}_{new}$, new average; and u+g+gem, average genotypic value in the cycles under study and overall average interaction.

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Table 5. Genetic correlations between pecan (*Carya illinoinensis*) traits.

Trait(1)	PH	LW	TW	CV	PECV	TC	DT	RAD	TCSA	PETCSA	PP	Yield	PROD	NFAC	NN	NL	NW	KL	KM	HT	KM	HM	TM
PH	1.00																						
LW	0.27	1.00																					
TW	-0.04	-0.10	1.00																				
CV	0.59	0.59	0.58	1.00																			
PECV	0.27	-0.02	-0.05	0.03	1.00																		
TC	0.80*	0.31	0.16	0.71*	0.06	1.00																	
TD	0.80*	0.31	0.16	0.71*	0.06	1.00**	1.00																
RAD	0.80*	0.31	0.16	0.71*	0.06	1.00**	1.00**	1.00															
TCSA	0.80*	0.28	0.14	0.69	0.07	1.00**	1.00**	1.00**	1.00														
PETCSA	-0.19	-0.02	0.04	-0.15	0.84*	-0.42	-0.42	-0.42	-0.41	1.00													
PP	0.53	0.28	0.22	0.50	0.87*	0.43	0.43	0.43	0.44	0.61	1.00												
Yield	0.42	-0.34	0.37	0.29	0.18	0.38	0.38	0.38	0.41	-0.04	0.33	1.00											
PROD	0.51	0.25	0.25	0.50	0.87*	0.43	0.43	0.43	0.44	0.61	1.00**	0.33	1.00										
NFAC	-0.57	0.12	-0.68	-0.64	-0.05	-0.44	-0.44	-0.44	-0.44	0.11	-0.34	-0.75*	-0.34	1.00									
NN	0.55	0.11	0.62	0.80*	0.10	0.71*	0.71*	0.71*	0.70	-0.11	0.44	0.53	0.45	-0.73*	1.00								
NL	-0.05	-0.47	-0.39	-0.52	-0.34	-0.03	-0.03	-0.03	0.01	-0.50	-0.45	0.28	-0.45	0.13	-0.45	1.00							
NW	-0.62	0.09	-0.37	-0.59	0.13	-0.78*	-0.78	-0.78*	-0.79*	0.45	-0.18	-0.69	-0.18	0.70	-0.87**	-0.03	1.00						
KL	0.01	-0.44	-0.44	-0.52	-0.22	-0.02	-0.02	-0.02	0.02	-0.40	-0.35	0.31	-0.35	0.13	-0.47	0.99**	0.01	1.00					
KM	-0.49	0.17	-0.41	-0.52	0.11	-0.73*	-0.73*	-0.73*	-0.73*	0.40	-0.14	-0.53	-0.15	0.59	-0.88**	0.09	0.95**	0.14	1.00				
HT	-0.42	0.35	-0.30	-0.25	-0.14	-0.33	-0.33	-0.33	-0.36	0.04	-0.26	-0.98**	-0.25	0.74*	-0.54	-0.24	0.72*	-0.26	0.57	1.00			
KM	-0.37	-0.13	-0.47	-0.65	-0.02	-0.55	-0.55	-0.55	-0.53	0.08	-0.27	-0.27	-0.27	0.49	-0.92**	0.59	0.75*	0.64	0.84**	0.34	1.00		
HM	-0.49	-0.03	-0.42	-0.62	-0.10	-0.61	-0.61	-0.61	-0.60	0.08	-0.33	-0.49	-0.33	0.60	-0.94**	0.44	0.86**	0.46	0.90**	0.56	0.96**	1.00	
TM	-0.48	-0.09	-0.40	-0.62	-0.10	-0.60	-0.60	-0.60	-0.59	0.06	-0.33	-0.37	-0.33	0.53	-0.93**	0.52	0.81*	0.54	0.87**	0.45	0.98**	0.99**	1.00
Color	-0.67	-0.01	-0.09	-0.43	-0.45	-0.63	-0.63	-0.63	-0.66	-0.10	-0.62	-0.81*	-0.60	0.54	-0.64	-0.02	0.73*	-0.08	0.60	0.82*	0.47	0.66	0.60

(1)PH, plant height; LW, lateral width; TW, transverse width; CV, canopy volume; PECV, production efficiency in relation to canopy volume; TC, trunk circumference; TD, trunk diameter; RAD, radius; TCSA, trunk cross-sectional area; PETCSA, production efficiency in relation to trunk cross-sectional area; PP, production per plant; PROD, productivity; NFAC, number of fruit attached to the capsule; NN, number of nuts per kilogram; NL, nut length; NW, nut width; KL, kernel length; KM, kernel mass; HT, husk thickness; KW, kernel width; HM, husk mass; TM, total mass; and Color, color to the capsule. ** and *Significant by the t-test, at α = 0.01 and α = 0.05, respectively.

Conclusions

1. Broad-sense individual heritability is low for pecan (*Carya illinoinensis*) vegetative and production traits, suggesting a strong environmental influence.
2. For quality traits, heritability is medium to high, indicating a greater genetic contribution and, therefore, a greater potential for response to selection.
3. Production and nut quality characters are subject to the effects of the genotype x environment interaction.
4. Production, productivity, and production efficiency in relation to canopy volume show correlation and a strong interaction with each other.
5. Cultivars Shoshoni and Jackson may be selected to increase pecan nut yield.

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