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Seedling emergence capacity and morphological traits are under strong genetic control in the resin tree *Pinus oocarpa*

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***Pinus oocarpa* is a widely distributed species essential for resin production in Mexico, where demand surpasses supply. This study aimed to identify differences and variation levels of seedling emergence capacity and morphological traits in resin-producing high-yield *P. oocarpa* trees and estimate their genetic control. Seeds from 72 open-pollinated families were planted using a randomized complete block experimental design. Differences between families were determined and pooled using cluster analysis. We recorded wide differences in seed emergence capacity and morphological traits (cotyledon number and length, and hypocotyl length), allowing to establish three family groups. We also calculated the contribution of the variation sources to the total variance and genetic parameters involved. Our data evidenced high genetic control for all tested variables. We found a moderate and positive genetic correlation between cotyledon length, cotyledon number, and hypocotyl length. We also found a high negative genetic correlation between emergence capacity and hypocotyl length. At the phenotypic level, we found a high and significant correlation between cotyledon length and number. Grouping *P. oocarpa* into families should aid decision-making for sexual propagation since a high propagation capacity of the high-yield trees is essential for genetic improvement programs. Moreover, we demonstrate that the heritability of the emergence capacity and other morphological traits is high; these traits can be useful for the early selection of high-yield families.**

Keywords: Egg-cone pine, Cotyledons, Genetic Control, Genetic Correlation, Genetic Variation, Heritability

Introduction

Pinus oocarpa Schiede ex Schltdl. (egg-cone pine) is naturally distributed along 3,100 km from Sonora, Mexico, through Belize, Guatemala, El Salvador, Honduras, and Nicaragua, between 29° to 12° N latitude (OFI-CATIE 2003). Outside its natural distribution, this species is grown in Brazil, Colombia, Honduras, Mexico, Venezuela, Asia, Africa, the Caribbean, and Oceania, especially Australia (Greaves 1982, Dvorak et al. 2000). *P. oocarpa* is widely used in the forest industry in Mexico; its wood is used for manufacturing posts, beams, packaging, sheets, plywood, toys, doors, sawmills, toothpicks, pulp for paper, and firewood. The tree also has medicinal and ornamental uses. In Mexico, *P. oocarpa* is the main resin-producing species, from which turpentine (a liquid substance) and tar (a solid substance) are obtained through an industrial process. These two raw materials are used to manufacture adhesives, tires, paint, rubber, soap, varnish, perfume, and pharmaceutical products (CONAFOR 2013).

Resin is the second most important non-timber forest product in Mexico, representing 39%-44% of national annual non-timber forest profits (SEMARNAT 2021). The demand for pine resin in Mexico has increased in recent years, exceeding the national production, while its production has decreased in the last two decades. The demand has thus been mainly supplied by Venezuela, Honduras, China, and Cuba (CONAFOR 2013). The deficit in resin production in Mexico is partly due to the lack of research focused on generating methods and integrative technological strategies to increase its production. A genetic improvement program should be implemented to address supply problems and increase resin production, starting with selecting pine species with the highest resin production.

In Mexico, *P. oocarpa* has been studied for the magnitude of its wood density variation (Gutiérrez & Flores 2019) and the genetic control of seedling growth (Viveros et al. 2005). In Michoacán, incipient initiatives for genetically improving *P. oocarpa* to increase its wood and resin production are ongoing (Fabián et al. 2020, Fabián et al. 2021). In 2019, such initiatives were included in a broader research program (Romero et al. 2022). Evaluating the reproductive potential (seed production and germination) of the selected resin trees and estimating the genetic variation, heritability, and genetic correlation between the traits of their progenies is essential for such purpose (Romero et al. 2022).

In Mexico, the forest genetic improvement program begins with the phenotypic selection of superior trees in natural stands. These trees are evaluated through genetic testing, and seed orchards are established. However, no attention has been paid to the reproductive capacity of the selected superior trees, a crucial aspect for forest genetic improvement programs (Zobel & Talbert 1984, White et al. 2007).

Information on the physical and physiological qualities of seeds from *Pinus* trees

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subjected to intensive resin production is insufficient. In *P. pseudostrobus* Lindl. resin trees, although the germination rate is high, the germination speed indicates wide variation among trees (Muñoz-Flores et al. 2023). In contrast, in the Burseraceae family, resin and exudate extraction negatively affects the species' reproductive success and particularly decreases the seeds' viability and germination rate (Eshete et al. 2012, Abad-Fitz et al. 2022). Therefore, since the selected *P. oocarpa* resinous trees (Romero et al. 2022) constitute the base population for the forest genetic improvement program and the seed resources to cover urgent needs in reforestation programs and forest plantations (Zobel & Talbert 1984, White et al. 2007), it is essential to know the differences between families in seedling emergence. This information will allow decisions to be made to continue the cycle of genetic improvement; that is, the study of the emergence capacity of *P. oocarpa* resin trees will allow the selection of families without reproductive problems to establish seed orchards in the future. Likewise, gaining insight into the variation level and genetic control of the emergence and morphological characteristics of *P. oocarpa* seedlings is crucial; if a high level of genetic control is found in these characteristics, the selection of phenotypes with high reproductive capacity will be facilitated (Zobel & Talbert 1984, White et al. 2007). In turn, this will facilitate the study of the genetic relationships between emergence and morphological characteristics (Falconer 2017, Escobar-Sandoval et al. 2018).

The objectives of this study are to: (i) determine the differences between *P. oocarpa* families in seedling emergence capacity and morphological characteristics; (ii) determine the level of contribution of families to the total variance of selector characteristics; and (iii) estimate the genetic control of the emergence capacity and morphological characteristics of seedlings through heritability and genetic/phenotypic correlations. Our hypotheses are: (a) the differences between families are large and allow the integration of the high-yield trees into several groups; (b) the contribution of *P. oocarpa* families to the total variance will be low due to the reduced geographical interval where the high-yield trees were selected; and (c) the characteristics that we evaluated have high genetic control and present a high genetic correlation between them since they depend on the embryo's viability.

Materials and methods

Tree selection and cone collection

High-yield *P. oocarpa* trees were selected from the natural forest properties of "Bienes Comunales de San Gabriel Cuentla" in San Simón de Guerrero, Mexico (Fig. 1). The 100 trees with the highest resin production were chosen. Cones from these trees were collected in November-December 2019, and the seeds were cleaned, preserving the trees' identity. Due to seed availability, only 72 trees were selected for seed emergence trials (Fig. 1). The percentage of vain seeds from these trees was below 18%. The selected trees are distributed at elevations of 1661-1825 m a.s.l. The mean annual temperature in the collecting site varies from 19.2 to 21.5 °C and mean annual precipitations from 1.055 to 1.093 mm (Crookston 2006). The soil types were luvisol, cambisol, and regosol (INEGI 2007).

Seed planting

To separate seeds with reserves (full seeds) from vain seeds by flotation, a sample of 300 seeds per tree was soaked in distilled water for 24 h. Sixty full seeds were taken from each tree and sown in pairs in 280 ml tubes. Each tube was labelled with a key number (tree number selected in the field and consecutive seed number) that was kept until the end of the trial. The substrate was a mixture of peatmoss®, perlita®, and vermiculita® (60:20:20). Additionally, 5 g·l⁻¹ of Multicote® brand-controlled release fertilizer (06-18-12 + Em) was added. During the first month, samples were irrigated three times a week. Captan WP (1 g·l⁻¹) was applied once a week to avoid fungal attack. All these experiments were conducted in a greenhouse in *La Protectora de Bosques* (PROBOSQUE), Mexico. The average temperature in the greenhouse was 19.5 °C, with minimum and maximum temperatures of 10 and 35 °C, respectively.

Experimental design and evaluated variables

The experimental design was randomized complete blocks with six repetitions (blocks) per family. The experimental unit comprised ten seeds. All germinated seeds from the same tree were considered as a half-sibs family (Zobel & Talbert 1984, Falconer & Mackay 1996).

To determine the emergence capacity (*EC*), the number of seeds that emerged 30 days after sowing was recorded, using the following equation (eqn. 1):

$$EC(\%)=\left(\frac{S_{em}}{S_{tot}}\right)\cdot 100 \qquad (1)$$

where S_{em} is the number of emerging seeds and S_{tot} is the total number of seed tested. Forty-five days after sowing, the number of cotyledons was counted, and hypocotyl length and cotyledon length were measured with a ruler.

Statistical analysis

Differences and grouping of families

Compliance with the assumption of normality and homogeneity of variances of all tested variables (emergence capacity, cotyledon number, hypocotyl length, and cotyledon length) was verified using the Kolmogorov-Smirnov and Levene tests, respectively. None of the variables met any of the assumptions ($p < 0.01$); therefore, to identify differences between *P. oocarpa* families, non-parametric RT4 variance analyses and comparisons of range means were performed (Conover 2012). To establish groups of *P. oocarpa* families, cluster analysis was performed based on Euclidean distances using Ward's grouping (Núñez & Escobedo 2011).

Estimation of variance components

The variance components associated with each variation source were determined with the VARCOMP procedure using the Restricted Maximum Likelihood method of

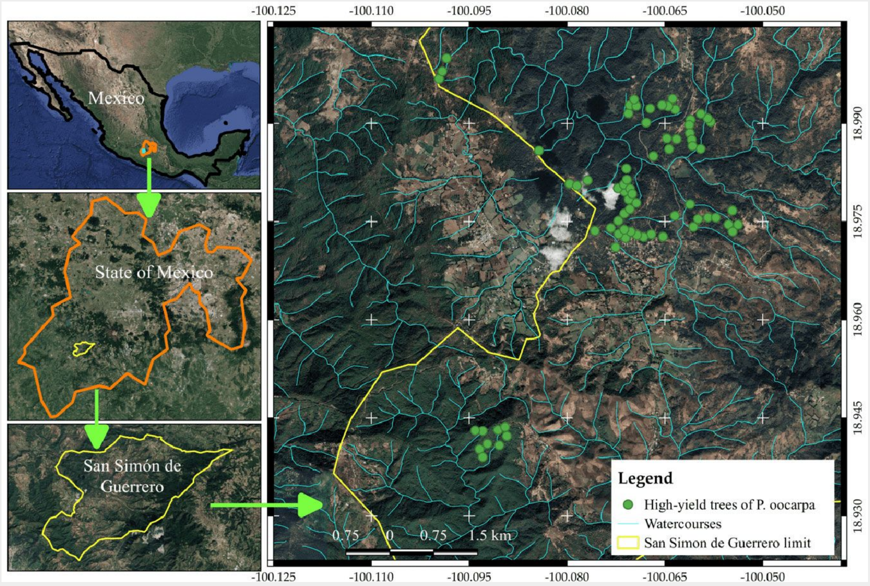

Fig. 1 - Location of superior resin trees of *Pinus oocarpa* in San Gabriel Cuentla, Mexico.

Tab. 1 - Overall mean, minimum, and maximum averages of traits evaluated by family groups of resin-producing high-yield trees of *P. oocarpa*.

Variables	Overall mean	Family averages					
		Group 1		Group 2		Group 3	
		Min	Max	Min	Max	Min	Max
Emergence capacity (%)	80.0	66.7	98.3	25.0	85.0	68.3	98.3
Number of cotyledons	5.97	5.75	6.93	4.97	6.48	5.40	6.28
Cotyledon length (cm)	3.29	2.94	4.17	2.09	3.40	2.70	3.60
Hypocotyl length (cm)	0.77	0.64	1.08	0.55	0.88	0.65	0.88

the statistical package SAS® ver. 9.4 (SAS Institute 2016), using the following statistical model (eqn. 2):

$$Y_{ijk} = \mu + B_i + F_j + B_i \cdot F_j + \varepsilon_{ijk} \qquad (2)$$

where Y_{ijk} is the observed value, μ is the overall mean, B_i is the effect of the i-th block, F_j is the effect of the j-th family, $B_i \times F_j$ is the effect of the interaction of the i-th block with the j-th family and ε_{ijk} is the experimental error.

Genetic parameters and correlations

To calculate the genetic parameters and establish correlations, the variance and covariance components were obtained with the same statistical model as above; the block was considered as a fixed effect, the family was a random effect, and interaction block by family was not considered (Escobar-Sandoval et al. 2018, Reyes et al. 2022). The individual heritability (h_i^2) and family means (h_f^2) were determined with the following equations (Falconer 2017 – eqn. 3, eqn. 4):

$$h_i^2 = \frac{3\sigma_f^2}{\sigma_f^2 + \sigma_e^2} \qquad (3)$$

$$h_f^2 = \frac{\frac{3}{4}\sigma_f^2}{\sigma_f^2 + \frac{\sigma_2^2}{b}} \qquad (4)$$

where σ_f^2 is the family variance, σ_e^2 is the error variance, b is the harmonic mean of the number of seedlings per family.

To avoid overestimating heritability, the additive variance ($\sigma_A = 3\sigma_f^2$) was calculated with the coefficient of genetic determination 3, since *P. oocarpa* families come from open pollination and are composed of a mixture of half-sibs and full-sibs (Escobar-Sandoval et al. 2018, Reyes et al. 2022). The standard error of individual heritability ($EE(h_i^2)$) and the coefficient of genetic variation (CVg) were calculated using the following equations (Falconer 2017 – eqn. 5, eqn. 6):

$$EE(h_i^2) = \frac{[2(1+(nf-1)h^2)]^2 \cdot (1-h^2)^2}{na(na-1)(nf-1)} \qquad (5)$$

$$CV_g = (\sigma_A^2 / \bar{X}) \cdot 100 \qquad (6)$$

where na is the number of seedlings per family, nf is the number of families, σ_A^2 is the additive variance, $\bar{X}$ is the general mean.

The phenotypic correlation coefficient between pairs of variables was obtained with the Pearson's correlation coefficient and the genetic correlation coefficients were estimated using the Falconer (2017) equation (eqn. 7):

$$r_{g(XY)} = \frac{COV_{f(X,Y)}}{\sqrt{\sigma_{f(X)}^2 \cdot \sigma_{f(Y)}^2}} \qquad (7)$$

where $\sigma_{f(X)}^2$ and $\sigma_{f(Y)}^2$ are the variances of families X and Y, respectively; $COV_{f(X,Y)}$ is the family covariance of those variables, obtained using the following formula (White & Hodge 1989 – eqn. 8):

$$COV_{X,Y} = \frac{\sigma_{f(X+Y)}^2 - (\sigma_{f(X)}^2 + \sigma_{f(Y)}^2)}{2} \qquad (8)$$

where $\sigma_{f(X+Y)}^2$ is the covariance of families of the variable $X + Y$. The standard error of the genetic correlation was obtained with the following equation (Falconer & Mackay 1996 – eqn. 9):

$$EE(r_g) = (1 - r_g^2)\sqrt{\frac{EE(h_{iX}^2)EE(h_{iY}^2)}{2h_{iX}^2 h_{iY}^2}} \qquad (9)$$

Results

Differences between morphological traits and grouping into families

The general average emergence capacity was 80%, the average cotyledon number was 5.97, the average cotyledon length was 3.29 cm, and the average hypocotyl length was 0.77 cm. All the variables presented significant differences between *P. oocarpa* families ($p < 0.0001$). The mean emergence capacity per family ranged from 25% (family 21) to 98% (families 7, 43, and 87). The mean cotyledon number per family ranged from 4.97 cm (family 85) to 6.93 cm (family 34). The mean cotyledon length per family ranged from 2.09 cm (family 21) to 4.17 cm (family 65), and the mean hypocotyl length per family ranged from 0.55 cm (family 84) to 1.08 cm (family 56 – Tab. 1).

Our multivariate analysis divided *P. oocarpa* families into three groups: the first comprises 25 families, the second includes 18 families, and the third group has 29 families (Fig. 2). Generally, for all the variables, *P. oocarpa* families of groups 1 and 2 presented high and low mean values, respectively. Group 3 families presented intermediate mean values (Tab. 1).

Variation

On average, the contribution of *P. oocarpa* families to the total variance was 15.8%. The average contribution of the block, block interaction per family, and error were 7.6%, 12.3%, and 64.4%, respectively. For all the variables, the contribution of the error to the total variance was higher than the contribution of the family, block, and block by family (Tab. 2). The highest contribution of *P. oocarpa* families to the total variance corresponded to the cotyledon number, while the lowest contribution was that of hypocotyl length (Tab. 2).

Genetic control

The individual heritability values (h_i^2) of

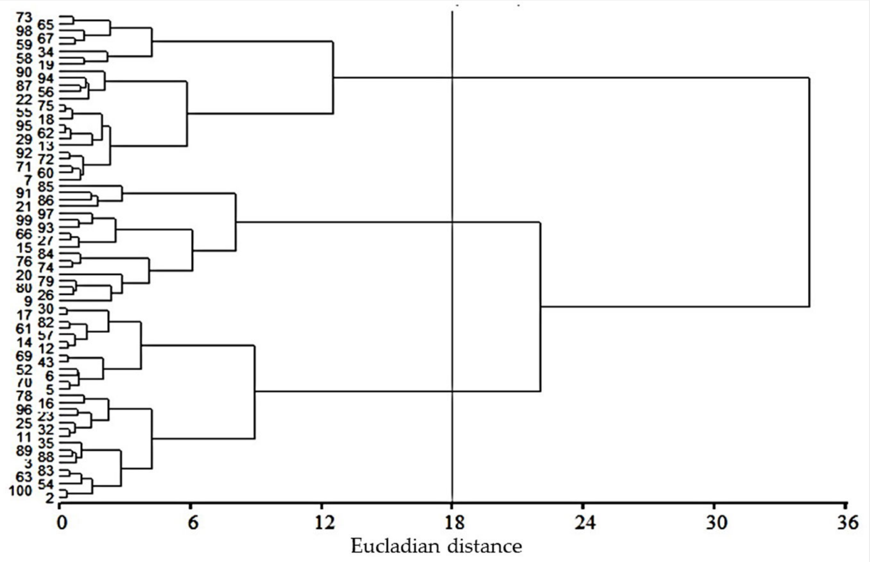

Fig. 2 - Grouping of families of highest resin production of *Pinus oocarpa*.

Tab. 2 - Contribution of variance of seedlings morphological variables and emergence of families of resin-producing high-yield trees of *Pinus oocarpa*.

Variable	Variance components (%)				Total Variance
	Block	Family	Block× Family	Error	
Emergence capacity	0.7	15.64	11.48	72.18	0.16
Number of cotyledons	0.01	19.12	1.21	79.66	0.66
Cotyledon lenght	11.43	17.9	21.27	49.4	0.79
Hypocotyl lenght	18.28	10.38	15.16	56.19	0.1
Mean	7.6	15.76	12.28	64.36	-

Tab. 3 - Coefficient of additive genetic variation (*CVga*), individual heritability (h_i^2), standard error ($EE(h_i^2)$) and heritability of family means (h_f^2) of morphological variables of seedling and emergence of families of resin-producing high-yield trees of *Pinus oocarpa*.

Variables	CVga (%)	h_i^2	$EE(h_i^2)$	h_f^2
Emergence capacity	36.45	0.53	0.05	0.7
Number of cotyledons	10.32	0.58	0.07	0.69
Cotyledon lenght	20.52	0.7	0.06	0.7
Hypocotyl lenght	24.06	0.46	0.07	0.67

the evaluated traits ranged from 0.46 (hypocotyl length) to 0.70 (cotyledon length), while the heritability value of the family means (h_f^2) varied from 0.67 (hypocotyl length) to 0.70 (cotyledon length). The additive genetic variation coefficient ranged from 10.3% (number of cotyledons) to 36.5% (emergence capacity – Tab. 3).

Genetic correlations between the number of cotyledons, hypocotyl length, and cotyledon length were positive, while the genetic correlation between these variables and the emergence capacity was negative. Half of the genetic correlations between variables were low; cotyledon length moderately correlated with hypocotyl length and cotyledon number. Only cotyledon length had a high genetic correlation with emergence capacity, but it was negative (Tab. 4). On the other hand, only the phenotypic correlation between cotyledon length and number was high and significant; the rest of the phenotypic correlation values between variables were low (Tab. 4).

Discussion

Differences and grouping of families

Our first objective was to determine the differences between *P. oocarpa* families' seedling emergence capacity and morphological characteristics. The wide differences observed in seed emergence capacity and seedling morphological traits of *P. oocarpa* trees with the highest resin yields allowed us to establish three groups. This grouping provides important guidelines for the sexual propagation of these trees. A high propagation capacity is essential for the selection of high-yield trees. According to our data, *P. oocarpa* families of groups 1 and 3 are better than families of group 2 in terms of emergence.

In our study, the average seed emergence capacity of high-yield resin-bearing *P. oocarpa* trees was higher than that previously reported for the same species (Rivera 2012) and *P. pseudostrobus* Lindl. (78% germination – Aragón et al. 2020). However, in our study the emergence capacity was similar to other species, such as *P. leiophylla* Schiede ex Schltdl. & Cham. and *P. ayacahuite* var. *veitchii* (Roezl) Shaw (Gómez et al. 2010, López et al. 2018). Likewise, the overall average emergence capacity was lower than the germination rate of *P. pseudostrobus* resin trees in Michoacán, Mexico (Muñoz-Flores et al. 2023).

Notably, the average emergence capacity of group 2 *P. oocarpa* families was lower than in other pine species (Gómez et al. 2010, López et al. 2018, Aragón et al. 2020), which may result from deficient pollination and a possible inbreeding effect (Castilleja et al. 2016, Capilla et al. 2021). Intensive resination might also decrease the physiological quality and, consequently, the viability of these families' seeds (Eshete et al. 2012, Abad-Fitz et al. 2022), warranting further investigations.

A previous study reported that the differences in the number and length of *P. oocarpa* cotyledons are under strong genetic control (Viveros et al. 2005). This information is evidenced by comparing our data with reports on other species. For instance, in our study, the average cotyledon number was the same as that reported for *P. oocarpa* species in Michoacán (Viveros et al. 2005). Also, the general and group average number of *P. oocarpa* cotyledons was lower than the average number of *P. sylvestris* L. cotyledons (Ulusan & Bilir 2008). The cotyledon number was lower in groups 2 and 3 than in group 1, which had more cotyledons than the mean value reported for *P. oocarpa* trees (Viveros et al. 2005). Additionally, the average (general and by groups) cotyledon length was lower than that of *P. oocarpa* trees in Michoacán (Viveros et al. 2005). Regarding hypocotyl length, group 2 families presented lower values than groups 1 and 3.

The differentiation between families by emergence capacity and seedling morphological traits (*e.g.*, hypocotyl and cotyledon length) has implications for plant production due to a positive relationship between these variables and survival and initial growth in the nursery phase (Juárez et al. 2006). Moreover, hypocotyls are considered an early selection trait because they represent the initial growth vigor of the seedlings and an indicator of morphological variation (Juárez et al. 2006, Ulusan & Bilir 2008). Thus, our grouping of *P. oocarpa* trees into families differentiated by emergence capacity, hypocotyl, and cotyledon length may represent a methodological advantage for future studies.

Variation

The family's contribution to the total variance indicates a high genetic control for the traits studied here; therefore, selecting between and within families to obtain genetic gains should be feasible. In our study, the variance of cotyledon number and length was similar to that of another population of *P. oocarpa* (Viveros et al. 2005). On the other hand, the family's contribution to the total variance of emergence capacity

Tab. 4 - Genetic correlations (with standard error, right of diagonal) and phenotypic correlations (with p-values, left of diagonal) between the characteristics evaluated in *Pinus oocarpa*.

Variables	Number of cotyledons	Cotyledon length	Hypocotyl length	Emergence capacity
Number of cotyledons	-	0.414 ± 0.046	0.169 ± 0.108	-0.235 ± 0.120
Cotyledon length	0.539 ± 0.001	-	0.544 ± 0.046	-0.211 ± 0.091
Hypocotyl length	-0.045 ± 0.794	-0.134 ± 0.435	-	-0.774 ± 0.221
Emergence capacity	-0.254 ± 0.135	0.091 ± 0.599	-0.06 ± 0.73	-

was lower than that of *P. greggii* Engelm. (López et al. 2000) and *P. leiophylla* Schiede ex Schltdl. & Cham. (Gómez et al. 2010). The high contribution of the error to the total variance indicated greater variation between plants within the same family, which agrees with reports on *P. oocarpa* and *P. leiophylla* (Viveros et al. 2005. Gómez et al. 2010). The contribution of the block to the total variance indicated a moderate environmental effect for cotyledon and hypocotyl length. However, the block had a very low effect on emergence capacity and cotyledon number since these traits depend on the embryo's viability and are independent of the environmental effect of the experiment (Sáenz et al. 2004, Ulusan & Bilir 2008). Notably, the cotyledon number is not affected by the age of the parent trees (Ulusan & Bilir 2008).

Genetic control and correlation between variables

In previous reports (Stanfield 1971, Cornelius 1994), the heritability values of emergence capacity, number of cotyledons, and cotyledon length have been regarded as "high"; for instance, these variables have heritability values higher than those of growth traits, shape, wood quality, and morphology in forest species (Cornelius 1994, Escobar-Sandoval et al. 2018, Fabián et al. 2020, Reyes et al. 2022). High heritability values indicate a strong genetic control on the emergence and seedling characteristics of *P. oocarpa*. These characteristics can thus be useful for the early selection of families (López et al. 2000).

In our study, the individual heritability values of cotyledon number and length were similar to those of other *P. oocarpa* populations (0.89 and 0.84 – Viveros et al. 2005). In contrast, the heritability of the mean cotyledon number and length of families with the same characteristics was slightly lower than the values reported for another *P. oocarpa* population (0.90 and 0.84 – Viveros et al. 2005). Similarly, we found that the heritability of cotyledon number and length was lower than the reported heritability in the broad sense in *P. sylvestris* (0.983 and 0. 956 – Ulusan & Bilir 2008). In contrast, the heritability values of the cotyledon number in *P. oocarpa* were higher than the broad sense heritability (0.503) in *Pinus wallichiana* A. B. Jack (Rawat & Bakshi 2011). Additionally, we found that the individual and family mean heritability values of emergence capacity in *P. oocarpa* were lower than the broad sense heritability mean of the germinative capacity of *P. wallichiana* (0.80 – Kaur et al. 2022) and *Picea sitchensis* (Bong.) Car. (0.78 – Chaisurisri et al. 1992). However, the final germination rate of *P. wallichiana* had a lower broad sense heritability (0.665 – Rawat & Bakshi 2011) than the heritability value of family means obtained for emergence capacity in the present study.

In our study, the additive genetic variability of emergence capacity and hypocotyl and cotyledon length was higher than the mean additive genetic variability reported for other forest trees (14.7% – Cornelius 1994). Our high values of the coefficient of additive genetic variation indicate a high genetic variability between families of *P. oocarpa* trees relative to the population mean, reflecting a high genetic variability of these traits. We found a moderate positive correlation between cotyledon and hypocotyl length and cotyledon length and number. Moreover, the genetic correlation between cotyledon number and length reported here is very similar to that obtained (0.44) for other *P. oocarpa* populations from Michoacán (Viveros et al. 2005).

We also found a high negative correlation between hypocotyl length and emergence capacity, possibly due to common genes affecting these traits and the linkage effect between nearby genes (Falconer 2017). From the point of view of plant selection, this correlation is unfavorable; although it is desirable to select families with high emergence capacity, a negative genetic correlation with hypocotyl length could negatively influence plant growth in the nursery phase. This observation suggests that the genetic correlation between seedling morphological traits and growth in the nursery phase should be further investigated in *P. oocarpa* families selected for high resin production. For instance, an important genetic correlation has been reported between cotyledon length, growth, and height in the rearing phase (Viveros et al. 2005). In our study, the significant phenotypic correlation between cotyledon number and length was consistent with their genotypic correlation. The value of the phenotypic correlation between cotyledon number and length was higher than the value reported for another population of the same species (0.036 – Viveros et al. 2005).

We did not find a phenotypic correlation between cotyledons number and hypocotyl length, consistent with previous reports for *P. oocarpa* (Viveros et al. 2005) and *P. sylvestris* (Ulusan & Bilir 2008). The low and non-significant phenotypic correlation between cotyledon length and emergence capacity is possible because the genetic component, environmental effect, and interaction between these factors do not favor the genetic response in these variables. However, even without a strong correlation between all the variables, some seedling traits could have an important phenotypic correlation with height and diameter growth in the nursery phase. For instance, in *P. oocarpa* and *P. sylvestris*, a significant phenotypic correlation between cotyledon length and number on one hand and seedling height and diameter on the other hand was observed in the nursery stage (Viveros et al. 2005, Ulusan & Bilir 2008). These observations illustrate the importance of studying the phenotypic relationship between seedling traits, height and diameter growth, and other variables of high-yield resin-producing *P. oocarpa* trees. Grouping *P. oocarpa* into families, as illustrated here, should aid decision-making for sexual propagation because a high propagation capacity of high-yield trees is essential to any genetic improvement program. In addition, we demonstrate here that the heritability of emergence and other seedling traits is high; therefore, these traits could be useful for selecting superior trees with high sexual reproductive capacity.

Conclusions

Seed emergence capacity and seedling characteristics of *P. oocarpa* differ widely, allowing the grouping of families into three groups, one of which presents emergence problems. The family's contribution to the total variance of the evaluated characteristics was moderate and lower than the contribution of the error; therefore, there is a larger variation between seedlings and seeds within families than between families. However, the variation levels indicated the possibility of selecting high-yield *P. oocarpa* trees between and within families.

A strong genetic control was detected for the emergence and other seedling traits. There was a high and negative genetic correlation between hypocotyl length and emergence capacity that is unfavorable because hypocotyl length influences early growth, and families with high germination capacity and growth are required.

The differences, the grouping, the variation levels between families, and the heritability will allow identifying high-yield individuals in seedling emergence capacity and morphological traits, key aspects for forest genetic improvement programs.

Author Contributions

Conceptualization, M.V.V.-G. and L.M.-G; methodology, M.V.V.-G. and L.M.-G; formal analysis, M.V.V.-G.; investigation, M.V.V.-G. and L.M.-G; resources, M.V.V.-G.; data curation, L.M.-G and G.M.-C.; writing – original draft preparation, M.V.V.-G. and L.M.-G; writing – review and editing, L.M.-G and G.M.-C.; project administration, M.V.V.-G. All authors have read and agreed to the published version of the manuscript.

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Data Availability Statement

The data present in this study are available upon request to the corresponding author. The data are not publicly available due to privacy.

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Conflicts of Interest

The authors declare no conflict of interest.

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