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Evaluating breeding strategies in lima bean for northeastern Brazil[1]

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ABSTRACT

Lima bean (*Phaseolus lunatus* L.) is a socioeconomically significant crop in the Northeast region of Brazil, providing income and food security. This study aimed to evaluate the breeding strategy of the lima bean breeding program at the Universidade Federal do Piauí by estimating genetic parameters, analyzing agronomic trait relationships and predicting genetic gains. Six breeding populations were assessed, and 13 agronomic traits were evaluated. The estimated heritabilities (h^2) were high, indicating favorable conditions for selection. The correlation coefficients indicated strong associations among most traits, particularly those related to pods and seeds. These findings indicate that the simultaneous improvement of multiple traits is unfeasible under the current breeding framework, as with any other breeding program. Thus, it is essential to prioritize selection targets such as cycle and quality of pods and seed. The H01 population was notable because of its short cycle and white-seeded phenotype, both being desirable traits for breeding. The H81 and H94 populations also showed potential, exhibiting commercially relevant traits such as large seed size and high 100-seed weight.

KEYWORDS: *Phaseolus lunatus* L., plant breeding, agronomic evaluation.

RESUMO

Avaliação de estratégias de melhoramento de feijão-fava para o Nordeste brasileiro

O feijão-fava (*Phaseolus lunatus* L.) é uma cultura de relevância socioeconômica para o Nordeste brasileiro, proporcionando segurança alimentar e renda. Objetivou-se avaliar a estratégia adotada pelo programa de melhoramento de feijão-fava da Universidade Federal do Piauí, estimando parâmetros genéticos, análise das relações entre características agronômicas e predição de ganhos genéticos. Seis populações de melhoramento foram avaliadas, sendo analisadas 13 características agronômicas. As herdabilidades (h^2) estimadas foram elevadas, indicando condições favoráveis à seleção. Os coeficientes de correlação evidenciaram fortes associações entre a maioria das características, sobretudo aquelas relacionadas a vagens e sementes. Estes resultados indicam que o aprimoramento simultâneo de múltiplas características é impraticável na estrutura atual do programa, assim como em qualquer outro programa de melhoramento, sendo, portanto, essencial a priorização de alvos de seleção, como ciclo e qualidade de vagens e sementes. A população H01 destacou-se pelo ciclo reduzido e sementes brancas, ambas características desejáveis para o melhoramento. As populações H81 e H94 também demonstraram potencial, exibindo características de interesse comercial como elevado tamanho de sementes e peso de 100 sementes.

PALAVRAS-CHAVE: *Phaseolus lunatus* L., melhoramento genético, avaliação agronômica.

INTRODUCTION

Lima bean (*Phaseolus lunatus* L.) is considered the second most important species of the genus after the common bean (*Phaseolus vulgaris* L.) (Agostini-Costa et al. 2015), and is cultivated across tropical and subtropical regions of North and South America, Europe, Africa and southwest Asia (Bria et al. 2019).

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Owing to its broad adaptability and moderate salinity tolerance, it represents a promising protein source under various climate change scenarios (Arteaga et al. 2018, Garcia et al. 2021). Its agronomic traits, such as drought resilience, make it suitable for cultivation in arid regions (Oliveira et al. 2004, Medina et al. 2017).

The lima bean production in Brazil is concentrated in the Northeast region, primarily in the states of Ceará and Paraíba (IBGE 2024), where it serves as a critical subsistence crop and socioeconomic pillar for local communities. Farmers predominantly rely on traditional landraces propagated from their own harvests, a practice that perpetuates low yields and compromises seed quality owing to the absence of advanced production technologies (Penha et al. 2017). Despite these constraints, the national production exceeded 10,000 tons by 2023 (IBGE 2024), underscoring its role in food security and income generation (Lopes et al. 2015). The adoption of improved cultivars could enhance yield stability and seed traits, advancing cultivation expansion and socioeconomic benefits, such as job creation and income diversification (Lopes et al. 2015), particularly in climate-vulnerable regions dependent on rainfed agriculture.

The lima bean breeding program at the Universidade Federal do Piauí (UFPI, Brazil) has been conducting research on the characterization of genotypes and diversity of species (Penha et al. 2017, Silva et al. 2017, Nascimento et al. 2018, Gonçalves et al. 2019, Silva et al. 2019, Brito et al. 2020, Carvalho et al. 2020, Almeida et al. 2021, Machado et al. 2022, Melo et al. 2022, Pires et al. 2022, Silva et al. 2022), establishment of a core collection (Gomes et al. 2020), selection of landrace varieties to family farmers (Sousa et al. 2020, Assunção Filho et al. 2022, Assunção Neto et al. 2022) and studies with breeding populations (Carvalho et al. 2022, Costa et al. 2022).

In this context, this study aimed to evaluate the breeding strategies used by the breeding program by estimating genetic parameters, analyzing agronomic trait relationships and predicting genetic gains across breeding populations. Additionally, the genetic variability was assessed, and key traits to prioritize future improvement efforts for this species were identified.

MATERIAL AND METHODS

The F_3 and F_4 generations of six lima bean populations derived from biparental crosses were evaluated as part of the UFPI's Lima Bean Breeding Program (Table 1). These populations were developed using artificial hybridization (Sousa et al. 2022), and F_1 hybrids were confirmed using SSR and morphological markers at the University of California (UC Davis, USA). The applied molecular markers were BM149 (Gaitán-Solís et al. 2002) and g118 (McConnell et al. 2010), using the following PCR conditions: 94 ºC for 2 min (initial denaturation); 30 cycles of 94 ºC for 15 s, 56 ºC for 15 s and 72 ºC for 15 s, and 72 ºC for 10 min (final extension). The morphological markers were hypocotyl color, pigmentation of the main stem, growth habit, flower color, seed pattern and color. Populations were advanced using the bulk method in a covered area (50 % of shade) to obtain the F_2 and F_3 seeds.

Field trials were conducted in 2019 and 2020, at the Universidade Federal do Piauí, in Teresina, Piauí state, Brazil (05º05'21"S, 42º48'07"W and 72 m of altitude), characterized by Aw-type climate (Kottek et al. 2006) and silty loam soil. Both experiments used the same site.

Table 1. Identification of the lima bean (*Phaseolus lunatus* L.) populations obtained from biparental crossings and their respective seed colors, parents and origins, sourced from the Active Germplasm Bank of *Phaseolus* of the Universidade Federal do Piauí.

Population	Seed color	Female parent	Origin	Male parent	Origin
H01	White	G25236	Argentina	UC 92	United States
H25	Light brown	UFPI 628	Brazil	G25236	Argentina
H46	Cream	UFPI 728	Brazil	UC HASKELL	United States
H50	Light brown	UFPI 628	Brazil	UFPI 728	Brazil
H81	Dark brown	UC 92	United States	UFPI 628	Brazil
H86	Light brown	UFPI 728	Brazil	UFPI 628	Brazil
H94	Light brown	UC 92	United States	UFPI 728	Brazil

The experimental designs differed between the years due to seed availability constraints. A randomized block design, with five replicates, using smaller plots (0.5 × 1.0 m spacing; 10 plants plot^{-1}), was implemented in 2019. Increased seed availability permitted larger plots (0.7 × 1.0 m spacing; 40 plants plot^{-1}) with three replicates in 2020, to enhance heritability estimation accuracy (Lin et al. 1993). All plants were evaluated per plot, and standard cultivation practices were applied throughout the study period (Lopes et al. 2015).

The traits were measured using the following descriptors for *P. lunatus* L. (Biodiversity International 2007): number of days to the beginning of flowering, number of days to maturity, plant height (cm), number of pods per plant, pod length (mm), pod width (mm), pod thickness (mm), number of locules per pod, number of seeds per pod, seed length (mm), seed width (mm), seed thickness (mm) and 100-seed weight (g). The values were simple average measures of ten random pods (pod length, pod width, pod thickness, number of locules per pod and number of seeds per pod) or seeds (seed length, width and thickness) from each plant.

The data were analyzed using a mixed model framework implemented in the *sommer* package (Covarrubias-Pazaran 2016) in R, with replications and populations treated as random effects using the model: $Y = X\beta + Z_1u_1 + Z_2u_2 + \varepsilon$, where Y is the matrix of multivariate responses, $X\beta$ the fixed effect, Z_1u_1 the random effect of repetition, with $u_1 \sim N(0, \sigma^2_B)$, Z_2u_2 the random effect of population, with $u_2 \sim N(0, \sigma^2_G)$, and ε the multivariate residual error, with $\varepsilon \sim N(0, \sigma^2_E)$. The following variance components were estimated: genetic variance (σ^2_G), block variance (σ^2_B) and residual variance (σ^2_E). Broad-sense heritability (h^2) was calculated as: $h^2 = (\sigma^2_G)/[\sigma^2_G + (\sigma^2_B/n_{rep}) + (\sigma^2_E/n_{rep})]$. The genetic gain ($\Delta G$) was evaluated using the best linear unbiased predictor (BLUP) estimated with 10 % of selection intensity. The heritability values were classified as low ($0.01 \leq h^2 \leq 0.15$), medium ($0.15 < h^2 < 0.50$) or high ($h^2 \geq 0.50$), based on their magnitude (Resende 2015).

Genetic, environmental and phenotypic correlations from the model were determined to evaluate the relationship among traits. Significance was tested via the LRT test at 5 % using the *sommer* package in R. The values were obtained using the following equation: $r_{XY} = Cov(X,Y)/\sqrt{V(X).V(Y)}$, where r_{XY} is the correlation coefficient for variables X (response) and Y (explanatory), Cov(X,Y) the covariance between X and Y, and V(X) and V(Y) are the variances of X and Y, respectively.

RESULTS AND DISCUSSION

The crosses used to generate the H01 and H86 populations were confirmed using SSR markers (Figure 1), whereas those used to generate the H25, H46, H50, H81 and H94 populations were confirmed using morphological markers (hypocotyl color, growth habit, flower color, seed color and seed coat pattern). The H50 and H86 populations were grouped because of their reciprocal cross origins.

Table 2 summarizes the BLUP means for each trait across the populations in F_3 and F_4, where positive values denote trait performance above the overall mean and negative values indicate below-average performance. A marked difference in the cycle duration was observed between the generations, with F_4 requiring a longer maturation period.

Notably, the H01 population exhibited negative BLUP values for cycle-related traits, indicating an early maturation phenotype. This is a critical attribute, given the prolonged growth cycle of the species, which can reach up to 5 months from sowing to harvest (Carvalho et al. 2022, Melo et al. 2022). The H81 population displayed below-average values for these traits. H01 and H81 showed a significant breeding value, as prioritizing reduced maturation time enhances agronomic resilience and yield in lima bean, particularly in regions prone to abiotic stressors, such as northeastern Brazil (Lopes et al. 2015).

Comparative analysis revealed that the H01 population had significantly fewer days to flowering

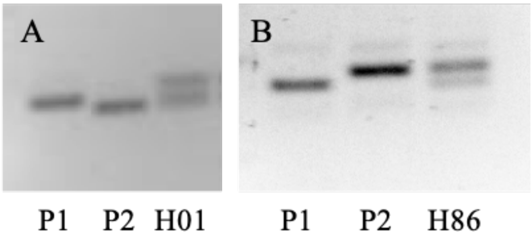

Figure 1. Genomic DNA amplification pattern in *Phaseolus lunatus* L. crossings using the markers BM149 (A) and g118 (B) in agarose gel 2 %. P1 is the female parent and P2 the male parent. The two bands indicate the crossing between parents.

Table 2. Estimates of best linear unbiased predictor (BLUP) for the traits evaluated in six lima bean populations in the F_3 and F_4 generations, in Teresina (Piauí state, Brazil).

Traits	F_3							F_4						
	Mean	H1	H25	H46	H81	H94	H5086	Mean	H1	H25	H46	H81	H94	H5086
NDF	38.08	-6.49	2.91	6.51	-5.11	-0.83	3.01	58.54	-9.46	-1.01	16.64	-7.01	-0.11	0.95
NDM	114.36	-27.48	9.89	10.62	-10.85	14.42	3.38	178.68	-29.06	3.81	9.81	4.44	2.12	8.87
NPP	27.77	-18.79	3.76	7.11	-12.62	-3.34	23.88	23.38	1.74	1.09	-2.71	-0.17	0.91	-0.85
PH	27.01	-1.88	-1.80	7.50	-2.91	-2.35	1.46	34.10	-0.45	-0.79	2.94	-1.36	1.06	-1.39
PL	58.82	-0.33	-3.39	0.88	5.35	0.65	-3.17	55.99	-0.17	-0.02	1.82	3.84	-2.74	-2.72
PW	15.30	0.28	-1.81	0.23	1.80	1.18	-1.68	15.26	-0.16	-0.44	0.89	1.05	-0.64	-0.69
PT	8.08	0.01	-0.01	-0.01	-0.01	0.04	-0.04	7.58	-0.05	-0.16	0.17	0.05	0.01	-0.01
NLP	2.45	-0.06	0.13	0.02	-0.11	-0.09	0.11	2.56	-0.01	-0.01	0.05	0.11	-0.07	-0.07
NSP	2.02	-0.21	0.24	0.21	-0.17	-0.26	0.21	1.69	-0.13	0.12	0.16	-0.06	-0.11	0.02
SL	11.75	0.86	-0.99	-0.76	0.69	1.03	-0.82	10.83	0.57	-0.31	-0.46	0.34	0.16	-0.31
SW	8.01	0.38	-0.44	-0.34	0.31	0.45	-0.36	7.72	0.19	-0.14	-0.18	0.10	0.09	-0.06
ST	5.03	-0.62	-0.06	0.35	0.19	0.12	0.02	5.35	0.17	-0.46	-0.45	0.34	0.45	-0.06
100SW	31.08	-1.10	-4.86	-2.50	5.31	7.56	-4.40	26.52	-0.02	0.21	0.35	-0.14	-0.27	-0.11

NDF: number of days to the beginning of flowering; NDM: number of days to maturity; PH: plant height; NPP: number of pods per plant; PL: pod length; PW: pod width; PT: pod thickness; NLP: number of locules per pod; NSP: number of seeds per pod; SL: seed length; SW: seed width; ST: seed thickness; 100SW: 100-seed weight.

and days to maturity than the landraces evaluated by Assunção Neto et al. (2022) and the genotypes studied by Silva et al. (2015). Furthermore, the values for days to flowering in the present study were markedly lower than those reported by Melo et al. (2022), underscoring the potential of these populations for early-cycle breeding. These findings supported targeted selection to reduce cycle duration, because early maturing cultivars enable earlier harvests, mitigate exposure to drought and align with the farmers' preferences (Lopes et al. 2015).

When the average values for pod traits obtained in the present study were compared to those in the literature, the populations had lower values than the varieties evaluated by Assunção Neto et al. (2022), Melo et al. (2022) and Silva et al. (2015). However, this finding does not diminish their suitability as valuable resources for breeding. Notably, the H46 and H81 populations exhibited a superior pod architecture, with the highest values of pod length, width and thickness, thus positioning them as promising genetic resources. Selection gains in pod traits are desirable for lima bean breeding because large pods facilitate manual harvesting by family farmers (Carvalho et al. 2022). Additionally, they were positively correlated with grain yield, what is commercially important and relevant in breeding programs for this species.

The analysis of genetic parameters (Table 3) highlighted contrasting heritability patterns between the F_3 and F_4 generations. In the F_3 generation, pod thickness exhibited low heritability, whereas the number of pods per plant was moderate. Conversely, the number of pods, pod thickness and seed thickness displayed low heritability estimates in the F_4 generation, whereas plant height and number of locules per pod demonstrated moderate values. All the remaining traits in both generations exhibited high heritability, highlighting a strong genetic influence on the phenotype. Notably, days to flowering and days to maturity demonstrated exceptionally high heritability estimates (89 and 96 % in F_3 and 81 and 68 % in F_4, respectively).

The heritability values reported by Carvalho et al. (2022) were markedly lower for days to flowering and maturity (0.01 and 0.20 %, respectively), and were substantially lower than those identified in the current study. These results underscored the pronounced environmental influence on trait expression, which poses significant challenges to breeding. Such low heritability found in the number of pods per plant, pod thickness, number of locules per pod and seed thickness suggests that phenotypic selection alone may be insufficient, needing complementary approaches to achieve meaningful genetic progress (Parker et al. 2022).

Significant genetic gains were observed in both generations, in terms of days to flowering, days to maturity, pod length, pod width, pod thickness and 100-seed weight. These traits are critical breeding priorities in this species, as they directly contribute to the development of an ideotype characterized by early

Table 3. Estimates of genetic parameters for the traits evaluated in six lima bean populations in the F_3 and F_4 generations, in Teresina (Piauí state, Brazil).

Traits	F_3					F_4				
	σ^2_G	σ^2_B	σ^2_E	h^2	ΔG	σ^2_G	σ^2_B	σ^2_E	h^2	ΔG
NDF	26.14	1.30	15.55	0.89	-7.97	86.33	1.41	56.01	0.81	-98.87
NDM	261.70	8.63	40.84	0.96	-27.43	226.13	7.76	309.65	0.68	-133.18
NPP	165.23	0.00	1,006.03	0.45	10.20	0.47	0.00	110.37	0.01	0.11
PH	18.48	18.50	72.07	0.51	3.82	6.17	1.97	48.03	0.27	8.73
PL	40.49	0.00	22.52	0.69	29.47	6.33	0.00	17.50	0.52	17.04
PW	2.16	0.00	0.51	0.95	18.24	0.71	0.00	0.41	0.83	9.09
PT	0.02	0.06	0.66	0.14	0.28	0.02	0.00	0.39	0.14	0.27
NLP	0.02	0.01	0.06	0.61	1.21	0.01	0.00	0.06	0.36	0.51
NSP	0.05	0.00	0.07	0.78	2.32	0.02	0.00	0.07	0.51	1.11
SL	0.62	0.00	0.45	0.87	8.93	0.14	0.01	0.07	0.81	4.24
SW	0.13	0.01	0.17	0.78	3.83	0.02	0.00	0.03	0.61	1.16
ST	0.11	0.01	0.08	0.85	3.83	0.01	0.00	0.08	0.10	0.08
100SW	26.11	4.93	15.51	0.86	57.43	5.55	0.00	3.46	0.82	25.36

NDF: number of days to the beginning of flowering; NDM: number of days to maturity; PH: plant height; NPP: number of pods per plant; PL: pod length; PW: pod width; PT: pod thickness; NLP: number of locules per pod; NSP: number of seeds per pod; SL: seed length; SW: seed width; ST: seed thickness; 100SW: 100-seed weight; σ^2_G: genetic variance; σ^2_B : block variance; σ^2_E: error variance; h^2: heritability in the broad sense; ΔG: genetic gain.

maturity, enhanced pod architecture and improved seed yield. High heritability estimates for these traits suggested a strong genetic influence, enabling an efficient selection. Prioritizing these traits aligns with breeding objectives to reduce the crop cycle duration, optimize mechanized harvest efficiency and meet market demands, which are key drivers of economic viability in lima bean production systems (Lopes et al. 2015).

Most traits exhibited significant positive correlations ($p < 0.05$) (Tables 4 and 5), with particularly robust associations observed among the pod traits: pod length and pod width (*r*G of 0.99 in F_3 and 0.77 in F_4), and number of locules per pod and number of seeds per pod (*r*G of 0.96 in F_3 and 0.92 in F_4). The seed traits also showed strong interdependencies: seed length and seed width (*r*G of 0.99 in F_3 and 0.86 in F_4); seed thickness with seed width (*r*G of -0.70 in F_3); 100-seed weight with seed length (*r*G of 0.94 in F_3 and 0.96 in F_4) and seed width (*r*G of 0.95 in F_3 and 0.96 in F_4). Notably, days to flowering and days to maturity were highly correlated with the number of pods per plant (*r*G of 0.98 in F_3 and 0.54 in F_4, and 0.76 in F_3 and 0.62 in F_4, respectively) and plant height (*r*G of 0.76 in F_3 and 0.99 in F_4, respectively).

The negative genetic correlations between days to flowering and seed length and days to maturity and seed width (-0.91 and -0.93 in F_3 and -0.73 and -0.77 in F_4, respectively) suggested that early-flowering genotypes may produce larger seeds, a dual advantage for breeding programs targeting both precocity and improved seed quality. Furthermore, strong positive correlations between the pod and seed traits facilitated the selection of commercially important traits. For instance, prioritizing pod architecture could concurrently enhance seed traits, streamlining the development of ideotypes with market-aligned seed profiles, while reducing phenotyping costs.

The trait correlations identified in this study were significantly stronger than those reported in previous studies on lima bean populations (Costa et al. 2022, Assunção Filho et al. 2022). Strong correlations highlighted the direct relationship between pod architecture and seed morphology. This has also been reported in other bean species (Ambachew et al. 2015, Asfaw et al. 2017), providing insights for trait prioritization in breeding programs. Understanding these relationships can guide selection strategies, particularly for the indirect selection of economically critical traits, thereby minimizing resource allocation to maximize genetic gain.

The positive and significant correlation observed between pod and seed traits in the current study, corroborating Assunção Filho et al. (2022), provides a practical tool for breeders to select superior pod and seed types concurrently. Increases in seed traits are particularly appealing because, according to Dobert & Blevins (1993), seed size in lima bean is a

Table 4. Estimates of genetic (*r*G), environmental (*r*E) and phenotypic (*r*P) correlations for the traits evaluated in six lima bean populations in the F_3 generation, in Teresina (Piauí state, Brazil).

Traits	*r*	NDM	NPP	PH	PL	PW	PT	NLP	NSP	SL	SW	ST	100SW
NDF	*r*G	0.76*	0.98*	0.76*	-0.64*	-0.59*	-0.06	0.94*	0.93*	-0.91*	-0.93*	0.66*	-0.55*
	*r*E	-0.16	-0.15	0.09	-0.10	0.35*	-0.16	-0.16	-0.13	0.07	0.08	-0.01	0.87*
	*r*P	0.51*	0.20	0.31*	-0.36*	-0.41*	-0.06	0.40*	0.32*	-0.59*	-0.45*	0.32*	-0.21
NDM	*r*G		0.76*	0.36*	-0.32*	-0.25*	0.42*	0.73	0.55*	-0.51*	-0.51*	0.85*	-0.11
	*r*E		-0.05	0.12	0.05	-0.03	-0.24	-0.03	-0.03	-0.12	-0.29	-0.40*	-0.24
	*r*P		0.24	0.18	-0.16	-0.22	0.04	0.24	0.25	-0.37*	-0.30	0.27*	-0.11
NPP	*r*G			0.83*	-0.68*	-0.60*	-0.08	0.85*	0.98*	-0.98*	-0.99*	0.56*	-0.68*
	*r*E			0.29	0.26	-0.07	0.15	0.22	0.77*	0.14	0.73	0.30*	0.08
	*r*P			0.37*	0.01	-0.26	0.12	0.32	0.75*	-0.26	-0.32*	0.36*	-0.16
PH	*r*G				-0.18	-0.13	-0.21	0.49*	0.61*	-0.59*	-0.66*	0.52*	-0.50*
	*r*E				0.47*	0.37*	-0.06	0.19	0.19	0.24	0.15	-0.11	-0.13
	*r*P				0.29*	0.11	-0.07	0.24	0.28	-0.08	-0.08	0.06	-0.28*
PL	*r*G					0.99*	-0.03	-0.72*	-0.82*	0.70*	0.77*	0.17	0.93*
	*r*E					0.98*	0.41*	0.64*	-0.82*	0.51*	0.47*	0.14	0.24
	*r*P					0.88*	0.34*	0.34	0.20	0.56*	0.57*	0.15	0.58*
PW	*r*G						0.05	-0.73*	-0.82*	0.78*	0.78*	0.16	0.88*
	*r*E						0.34*	0.56*	-0.82*	0.62*	0.47*	0.01	0.50*
	*r*P						0.18	0.04	-0.12	0.72*	0.62*	0.08	0.73*
PT	*r*G							-0.19	-0.08	0.26*	0.19	-0.28*	0.23
	*r*E							0.28	-0.08	0.61*	0.66*	0.81*	0.61*
	*r*P							0.23	0.19	0.42*	0.52*	0.62*	0.43*
NLP	*r*G								0.96*	-0.02	0.01	0.14	-0.21
	*r*E								0.95*	-0.47*	-0.32	0.28*	-0.20
	*r*P								0.92*	-0.83*	-0.99*	0.36*	-0.87*
NSP	*r*G									-0.99*	-0.99*	0.35*	-0.65*
	*r*E									-0.24	-0.22	-0.06	-0.14
	*r*P									-0.67*	-0.53*	0.12	-0.40*
SL	*r*G										0.99*	-0.39*	0.94*
	*r*E										0.98*	0.52*	0.78*
	*r*P										0.95*	0.35*	0.86*
SW	*r*G											-0.38*	0.95*
	*r*E											0.52*	0.75*
	*r*P											0.25*	0.82*
ST	*r*G												0.16
	*r*E												0.51*
	*r*P												0.33*

NDF: number of days to the beginning of flowering; NDM: number of days to maturity; PH: plant height; NPP: number of pods per plant; PL: pod length; PW: pod width; PT: pod thickness; NLP: number of locules per pod; NSP: number of seeds per pod; SL: seed length; SW: seed width; ST: seed thickness; 100SW: 100-seed weight. * Significant at 5 %.

key trait related to its physiological development, in which larger seeds typically yield more nodules and dry matter. Considering the gain values, the selection of these features should be performed in the direction of the ideal seed type, with large and flattened seeds being the commercial type.

Despite its socioeconomic importance in northeastern Brazil, lima bean remains genetically underexplored, with few breeding studies published. This research gap perpetuates the reliance on low-yielding landraces among smallholder farmers, exacerbating their vulnerability to climate variability and food insecurity.

This study established a foundational framework for targeted breeding strategies by quantifying genetic parameters and genetic correlations and predicting selection gains. These insights enable the resource-efficient prioritization of traits and methodologies, addressing both agronomic and market demands. In the context of rising global food demand and climatic instability, advancing lima bean breeding is an alternative for resilience in tropical agriculture.

Table 5. Estimates of genetic (*r*G), environmental (*r*E) and phenotypic (*r*P) correlations for the traits evaluated in six lima bean populations in the F_4 generation, in Teresina (Piauí state, Brazil).

Traits	*r*	NDM	NPP	PH	PL	PW	PT	NLP	NSP	SL	SW	ST	100SW
	*r*G	0.58*	0.54*	0.99*	0.28	0.71*	0.91*	0.78*	0.53*	-0.73*	-0.77*	0.58*	-0.65*
NDF	*r*E	-0.12	0.64*	0.90*	0.72*	0.81*	0.39*	0.43*	0.31*	0.29*	0.28*	0.39*	-0.35*
	*r*P	0.23	0.81*	0.76*	0.29*	0.59*	0.36*	0.25	0.26	-0.37*	-0.20	0.16	-0.43*
	*r*G		0.62*	0.86*	0.01	0.31*	-0.03	0.62*	0.31*	-0.96*	-0.74*	-0.55*	-0.60*
NDM	*r*E		0.58*	0.09	0.93*	0.77*	0.89*	0.52*	0.56*	0.59*	0.75*	0.59*	0.41*
	*r*P		0.86*	0.28*	0.29*	0.41*	0.28*	0.35*	0.25*	-0.21	0.01	0.01	-0.09
	*r*G			-0.75*	-0.50*	-0.65*	-0.91*	-0.35*	0.06	-0.88*	-0.82*	-0.70*	0.79*
NPP	*r*E			0.93*	0.99*	0.93*	0.90*	0.81*	0.81*	0.87*	0.82*	0.82*	0.98*
	*r*P			0.69*	0.85*	0.49*	0.64*	0.69*	0.75*	0.68*	0.72*	0.73*	0.64*
	*r*G				0.29*	0.11	-0.07	0.24	0.28*	-0.08	-0.08	0.06	-0.28*
PH	*r*E				0.41*	0.79*	0.89*	0.82*	0.58*	-0.79*	-0.85*	0.66*	-0.51*
	*r*P				0.90*	0.87*	0.57*	0.42*	0.32*	0.60*	0.75*	0.55*	0.68*
	*r*G					0.77*	0.17*	0.52*	0.62*	0.06	-0.42*	0.96*	-0.08
PL	*r*E					0.95*	0.73*	0.90*	0.92*	0.94*	0.88*	0.84*	0.73*
	*r*P					0.87*	0.56*	0.62*	0.66*	0.54*	0.41*	0.64*	0.33*
	*r*G						0.74*	0.47*	0.33	-0.13	-0.34*	0.98*	0.01
PW	*r*E						0.64*	0.65*	0.70*	0.91*	0.90*	0.85*	0.48*
	*r*P						0.61*	0.42*	0.42*	0.24*	0.26*	0.54*	0.26*
	*r*G							0.43*	0.20	-0.46*	-0.60*	0.81*	-0.31*
PT	*r*E							0.44*	0.64*	0.97*	0.99*	0.96*	0.96*
	*r*P							0.44*	0.53*	0.65*	0.79*	0.94*	0.61*
	*r*G								0.92*	-0.83*	-0.99*	0.36*	-0.87*
NLP	*r*E								0.97*	0.51*	0.41*	0.44*	-0.82*
	*r*P								0.95*	0.28	0.29*	0.43*	-0.74*
	*r*G									-0.71*	-0.94*	-0.29*	-0.88*
NSP	*r*E									0.64*	0.57*	0.98*	0.61*
	*r*P									0.09	0.11	0.39*	-0.36*
	*r*G										0.86*	-0.29*	0.96*
SL	*r*E										0.98*	0.99*	0.98*
	*r*P										0.96*	0.91*	0.85*
	*r*G											-0.70*	0.96*
SW	*r*E											0.98*	0.97*
	*r*P											0.94*	0.77*
	*r*G												0.33*
ST	*r*E												-0.48*
	*r*P												0.98*

NDF: number of days to the beginning of flowering; NDM: number of days to maturity; PH: plant height; NPP: number of pods per plant; PL: pod length; PW: pod width; PT: pod thickness; NLP: number of locules per pod; NSP: number of seeds per pod; SL: seed length; SW: seed width; ST: seed thickness; 100SW: 100-seed weight. * Significant at 5 %.

CONCLUSIONS

1. Given the acquired genetic gains, lima bean breeding programs cannot simultaneously improve multiple traits. Therefore, prioritizing traits, such as cycle traits and pod and seed qualities, is critical;
2. Among the evaluated populations, H01 emerged as a promising candidate owing to its short cycle, large seed size, white seed color, attributes aligned with consumer preferences, and high market value. Similarly, H81 and H94 exhibited exceptional seed traits, including superior size and weight, which are critical to commercial competitiveness.

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