Special Supplement: Pulses

Selection of early lima bean lines for grain yield[1]

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ABSTRACT

The scarcity of improved lima bean (*Phaseolus lunatus* L.) cultivars in Brazil has made it difficult to reach new production levels. This study aimed to select early and high-yielding lima bean lines with commercially desirable seed traits. Forty $F_{6:8}$ generation lines from the Breeding Program of the Universidade Federal do Piauí were evaluated in Tianguá (Ceará state) and Teresina (Piauí state), in Brazil. Variance components, genetic parameters and the Mulamba & Mock selection index were estimated for the statistical analyses. The more prominent traits, in terms of genetic gains, were number of days to flowering, number of pods per plot, grain yield and plant height, indicating favorable conditions for selection. The lines exhibited genetic variability regarding number of days to flowering, reinforcing the potential for selecting early lines. In the simultaneous selection of desirable agronomic traits, the lines H81-32, H25-59, H25-56, H25-66, H25-57 and H81-34 exhibited a superior performance in Tianguá, whereas H50/86-35, H25-64, H81-34, H25-66, H25-54, H25-60, H50/86-36, H25-58, H50/86-38 and H50/86-37 were highlighted in Teresina. H81-34 and H25-66 were promising in both environments, whereas H25-56 was notable for its white seed coat, a desirable trait for the consumer market.

KEYWORDS: *Phaseolus lunatus*, genetic parameters, genetic variability.

RESUMO

Seleção de linhagens precoces de feijão-fava para rendimento de grãos

A escassez de cultivares de feijão-fava (*Phaseolus lunatus* L.) melhoradas no Brasil tem dificultado a obtenção de novos patamares produtivos. Objetivou-se selecionar linhagens de feijão-fava precoces e produtivas, com sementes de padrão comercial. Quarenta linhagens da geração $F_{6:8}$, pertencentes ao Programa de Melhoramento Genético da Universidade Federal do Piauí, foram avaliadas em Tianguá (CE) e Teresina (PI). Nas análises estatísticas, foram estimados os componentes de variância, parâmetros genéticos e índice de seleção Mulamba & Mock. Em relação aos ganhos genéticos, sobressaíram-se o número de dias para início da floração, número de vagens por parcela, produtividade de grãos e altura da planta, indicando a possibilidade de seleção para estes caracteres. As linhagens apresentaram variabilidade genética para o número de dias para o início da floração, com possibilidade de seleção de linhagens precoces. Pela seleção simultânea de caracteres agronômicos desejáveis, destacaram-se as linhagens H81-32, H25-59, H25-56, H25-66, H25-57 e H81-34 em Tianguá; e H50/86-35, H25-64, H81-34, H25-66, H25-54, H25-60, H50/86-36, H25-58, H50/86-38 e H50/86-37 em Teresina. H81-34 e H25-66 foram promissoras nos dois ambientes. H25-56 destacou-se por apresentar coloração branca, padrão desejável pelo mercado consumidor.

PALAVRAS-CHAVE: *Phaseolus lunatus*, parâmetros genéticos, variabilidade genética.

INTRODUCTION

Phaseolus lunatus L., popularly known as fava or lima bean, has significant economic importance, particularly in northeastern Brazil, where it serves both as a source of income and food for family farming, being consumed as green and dry beans (Carvalho et al. 2022). Its cultivation is mainly conducted under rainfed conditions by small farmers, who predominantly use native varieties with indeterminate growth habit, often intercropped with other crops in traditional agriculture systems, primarily for self-consumption (Assunção Neto et al. 2022).

In 2023, Brazil produced approximately 10,372 tons, in an area equivalent to 33,153 ha, with the Ceará state being the largest producer, accounting

for 3,514 tons (IBGE 2024). Exploring the cultivation of this legume, which remains underutilized, can be a valuable approach to strengthen global food security by reducing dependence on other legumes such as soybean and common bean (Adebo 2023).

Lima bean is a legume with distinct characteristics that differentiate it from other types of beans and, although it is an autogamous species, it has a mixed reproduction system, with a high rate of cross-fertilization (Penha et al. 2016). This requires specific approaches and greater rigor in genetic breeding programs.

There are currently no developed lima bean cultivars in Brazil, only native varieties maintained and conserved by traditional farmers over generations. Thus, genetic breeding studies for this legume are crucial, since they will offer important agronomic information for the selection of superior genotypes.

Studies on the mean and variance components enable the estimation of genetic parameters such as the coefficient of genetic variation and heritability, the latter being a key parameter for breeders, since its estimated values guide selection (Santos et al. 2018). However, studies reporting estimates of genetic parameters and the use of selection indices in lima bean remain scarce in the literature. Therefore, this study aimed to identify early and productive lima bean lines with commercial-standard seeds, developed within the breeding program of the Universidade Federal do Piauí.

MATERIAL AND METHODS

The lima bean parents used in the biparental crosses originated from Argentina, Brazil and the United States. The crosses were advanced up to the F_6 generation, using the modified bulk method, when individual plants were selected to obtain lines, which were later evaluated in the $F_{6:8}$ generation in Tianguá (Ceará state) and Teresina (Piauí state), in Brazil.

In Tianguá, 34 lineages were evaluated from February to June 2023, at the experimental area of the Instituto Federal de Educação, Ciência e Tecnologia do Ceará (3°43'58.06''S, 41°0'44.00''W and 775 m of altitude). In Teresina (05°05'S, 42°05'W and 72.7 m of altitude), 40 lineages were evaluated from March to July 2023, at the experimental area of the Universidade Federal do Piauí.

The experiment followed a randomized block design, with three replications. The useful plot consisted of two rows of 5 m, with 10 plants each, with spacing of 0.5 m between plants and between rows. Two lima bean seeds were planted per hole, previously treated with fungicide. Fertilization with the formulation NPK (06-24-12) was conducted, according to the soil analysis and recommendations by Lopes et al. (2010).

Quantitative traits were evaluated according to the following descriptors for *P. lunatus* L. (IPGRI 2007): number of days to flowering - period between emergence and the time when 50 % of the plants showed flowers; number of days to maturation - period between emergence and the time when 50 % of the pods were mature; plant height - measured in cm from the cotyledon scar to the tip of the plant; number of pods per plant - amount of pods collected from each plant; pod length, width and thickness; number of grains per pod - measured from 10 randomly selected mature pods; seed length and width; seed thickness - 10 dry randomly selected seeds measured in mm; mass of 100 seeds - sampled randomly, expressed in grams; and grain yield - total mass of grains in the useful plot area, in grams.

The data referring to traits assessed in each environment were submitted to individual analysis of variance, adopting the following statistical model (Cruz et al. 2012): $Y_{ij} = \mu + G_i + B_j + e_{ij}$, where: Y_{ij} is the observation obtained in the plot with the i-th genotype in the j-th block; μ the overall mean; G_i the random effect of the i-th genotype (i = 1, 2, ..., g); B_j the random effect of the jth block (j = 1, 2, ..., r); and e_{ij} the experimental error.

Then, the homogeneity of the variances of the experimental errors was verified through the $F_{maximum}$, according to which the ratio between the largest and smallest residual mean square of the experiments must be < 7 to proceed with the joint analysis (Pimentel-Gomes 1990). The variance components were obtained using the moment method: a) estimates of variances and genetic parameters: genetic variance - $\sigma^2_g = (QMT - QMR)/r$; phenotypic variance - $\sigma^2_f = \sigma^2_g + (\sigma^2_e/r)$; environmental variance: $\sigma^2_e = QMR$; heritability - $h^2 = \sigma^2_g/(QMT/r)$; coefficient of genotypic variation - $CVg = (100\sqrt{\sigma^2_g})/m^\wedge$; genetic advance - $AG = ih^2\sigma_f$, where i is the intensity of selection; genetic advance as percentage of mean $AGM = [\sigma_f (GA/m^\wedge) \times 100$; b) selection index.

The classification of the genotypes was based on the classification sum index (Mulamba & Mock 1978), described by the following equation:

$$I_{MMi} = \sum_{j=1}^{m} n_{ij}$$

where I_{MMi} is the classification sum index and n_{ij} the classification number of the genotype i in relation to the trait j. The values of the genetic variation coefficients were used as economic weights. The analyses were conducted using the Genes software (Cruz 2016) and the R environment (R Core Team 2023).

RESULTS AND DISCUSSION

In the assessment conducted in Tianguá (Table 1), the lima bean lines differed in terms of number of days to flowering, number of days to maturation, plant height, number of pods per plant, pod length, pod width, pod thickness, seed thickness, mass of 100 seeds and grain yield. There were no significant differences among the evaluated lines for the number of grains per pod, seed length and width.

In the evaluation conducted in Teresina (Table 2), the lines differed from each other for most of the assessed traits, except for seed thickness. Such results are promising, regarding the selection of more productive lines with a shorter cycle.

The lima bean lines presented averages of 35 and 75 days for number of days to flowering and number of days to maturation, respectively, in Tianguá (Table 1). The averages for number of days to flowering and number of days to maturation were 46 and 91 days, respectively, in Teresina (Table 2).

The results indicated the possibility of selecting earlier lineages. In the study conducted by Gomes et al. (2010), there was a variation of 48-57 days for number of days to flowering, and 57-101

Table 1. Analysis of variance of the traits assessed in 34 lima bean lines from the $F_{6:8}$ generation (Tianguá, Ceará state, Brazil).

Sources of variation	DF	Mean square						
		NDF	NDM	PH	NPP	PL	PW	PT
Block	2	169.68	12.74	197.46	1,147,380.00	21.92	4.76	0.42
Genotype	33	195.85**	270.17**	207.91**	336,304.00**	85.56*	5.83*	1.84*
Residue	66	21.41	93.22	50.85	119,449.00	50.75	3.09	1.09
Mean		35.22	75.89	44.38	743.17	67.85	16.17	8.61
$CV_e\%$		13.13	12.72	16.06	46.50	10.49	10.74	12.17
Sources of variation	DF	Mean square						
		NGP	SL	SW	ST	HSM		GY
Block	2	0.11	3.14	1.69	0.23	14.68		1,268,585.00
Genotype	33	0.22[ns]	2.54[ns]	0.98[ns]	0.49*	85.80**		236,135.00**
Residue	66	0.14	1.60	0.86	0.27	24.72		93,808.00
Mean		3.02	11.34	8.03	5.08	35.14		618.38
$CV_e\%$		11.96	11.18	11.55	10.31	14.14		49.52

**, *, [ns]: significant at 0.1 and 5 % of probability and not significant, respectively. NDF: number of days to flowering; NDM: number of days to maturation; PH: plant height; NPP: number of pods per plot; PL: pod length; PW: pod width; PT: pod thickness; NGP: number of grains per pod; SL: seed length; SW: seed width; ST: seed thickness; HSM: 100-seed mass; GY: grain yield; $CV_e\%$: coefficients of variation; DF: degrees of freedom.

Table 2. Analysis of variance of the traits assessed in 40 lima bean lines in the $F_{6:8}$ generation (Teresina, Piauí state, Brazil).

Sources of variation	DF	Mean square						
		NDF	NDM	PH	NPP	PL	PW	PT
Block	2	74.85	579.26	64.93	152,868.00	120.95	1.50	3.19
Genotype	39	263.16***	534.69**	63.75***	86,924.00***	21.85*	1.86***	4.69[ns]
Residue	78	46.51	255.80	17.87	28,642.00	13.84	0.60	3.65
Mean		46.56	91.56	38.71	350.68	58.73	14.56	8.49
$CV_e\%$		14.64	17.46	10.92	48.26	6.33	5.36	22.49
Sources of variation	DF	Mean square						
		NGP	SL	SW	ST	HSW		GY
Block	2	0.17	1.82	1.81	0.95	209.62		36,428.00
Genotype	39	0.12**	0.89***	0.43***	0.35**	48.15***		19,696.00***
Residue	78	0.06	0.36	0.13	0.16	19.31		6,439.00
Mean		2.56	11.24	7.75	4.84	29.88		154.68
$CV_e\%$		9.56	5.38	4.68	8.29	14.70		51.87

***, **, *, [ns]: significant at 0.1, 1 and 5 % of probability and not significant, respectively. NDF: number of days to flowering; NDM: number of days to maturation; PH: plant height; NPP: number of pods per plot; PL: pod length; PW: pod width; PT: pod thickness; NGP: number of grains per pod; SL: seed length; SW: seed width; ST: seed thickness; HSW: 100-seed mass; GY: grain yield; CV_e: coefficients of variation; DF: degrees of freedom.

days for number of days to maturation with lima bean accessions with determined growth habit. These results differed from those observed in this study, where the lines presented a shorter cycle.

The average plant heights were 44.38 cm in Teresina and 38.71 cm in Tianguá, indicating a reduced stature and suggesting the possible presence of lines with determinate growth habit, which would facilitate mechanical harvesting.

The characters number of pods per plant, pod length, pod width, pod thickness, seed length, seed width and seed thickness presented averages of 743.17 pods, 67.85 mm, 16.17 mm, 8.61 mm, 11.34 mm, 8.03 mm and 5.08 mm, respectively, for the Tianguá environment. In the evaluation conducted in Teresina, the means for number of pods per plant, pod length, pod width, pod thickness, seed length, seed width and seed thickness were 350.68 pods, 58.73 mm, 14.56 mm, 8.49 mm, 11.24 mm, 4.84 mm and 4.84 mm, respectively.

In the study conducted by Carvalho et al. (2022), which included five populations of lima bean of indeterminate growth, means of 14.67, 54.28 and 29.41 mm were obtained for pod length, pod width and pod thickness, respectively; whereas the values for seed length, seed width and seed thickness were 13.99, 3.89 and 8.80 mm, respectively. These results differed from those observed in this study. In this context, seed size and technological quality of grains are important characteristics for the commercialization of lima bean.

Considering the number of pods per plant (743.17) and grain yield (618.38 kg ha⁻¹), the means obtained in Tianguá were higher than those in Teresina (350.68 pods and 154.68 kg ha⁻¹). This may be attributed to the climatic differences of the regions, geographic location and occurrence of diseases during the conduction of the experiments (Tables 1 and 2).

The obtained coefficients of variation ranged between 10.49 and 49.52 for the Tianguá environment, and from 4.68 to 51.87 for the Teresina environment. The quantitative traits, such as number of pods and yield, are controlled by multiple genes, and the expression of these traits is strongly influenced by environmental factors, as is the case for most agronomic traits of economic importance; thus, the environment influences their phenotypic manifestation (Cruz et al. 2012).

The estimated parameters (Tables 3 and 4) indicated that the environmental variance (σ^2_e) was higher than the genetic variance (σ^2_g) for most traits, except for the number of days to flowering and plant height, indicating a low genetic variability among the assessed lines. The variance components are important parameters, as they facilitate obtaining information about the genetic potential of the evaluated material and understanding the genetic potential of the populations to direct the breeder in the selection of superior genotypes (Baldissera et al. 2014).

For the lima bean lines evaluated in Tianguá, the heritability coefficient (h^2) was of medium magnitude (< 50 %) for most traits, except for the number of days to flowering, which indicated a high-magnitude heritability (73 %), and plant height (50 %) (Table 3). For the evaluation conducted in

Table 3. Genetic parameters for the traits assessed in 34 $F_{6:8}$ lima bean lines (Tianguá, Ceará state, Brazil).

Variables	σ^2_g	σ^2_e	σ^2_f	h^2	CVg	GA	GAM
NDF	58.14	21.41	79.56	0.73	21.64	13.42	38.12
NDM	58.98	93.21	152.20	0.38	10.11	9.84	12.97
PH	52.35	50.84	103.20	0.50	16.30	10.61	23.91
NPP	7,2284.88	119,449.38	191,734.26	0.37	36.17	340.06	45.75
PL	11.60	50.75	62.35	0.18	5.01	3.02	4.46
PW	0.93	3.01	3.95	0.25	5.98	0.97	6.00
PT	0.24	1.09	1.34	0.18	5.76	0.43	5.08
NGP	0.02	0.14	0.17	0.15	5.08	0.13	4.09
SL	0.31	1.60	1.91	0.16	4.92	0.46	4.07
SW	0.04	0.86	0.90	0.04	2.56	0.09	1.14
ST	0.07	0.27	0.34	0.20	5.26	0.25	4.92
HSW	20.35	24.72	45.08	0.45	13.83	6.24	17.77
GY	47,442.52	93,807.61	141,250.14	0.33	35.22	260.04	42.05

σ^2_g: genetic variance; σ^2_e: residual variance; σ^2_f: individual phenotypic variance; h^2: heritability; CVg: coefficient of genotypic variation; GA: genetic advancement; GAM: genetic advance as percentage of mean (%); NDF: number of days to flowering; NDM: number of days to maturation; PH: plant height; NPP: number of pods per plot; PL: pod length; PW: pod width; PT: pod thickness; NGP: number of grains per pod; SL: seed length; SW: seed width; ST: seed thickness; HSM: 100-seed mass; GY: grain yield.

Table 4. Genetic parameters for the traits in 40 $F_{6:8}$ lima bean lines (Teresina, Piauí state, Brazil).

Variables	σ^2_g	σ^2_e	σ^2_f	h^2	CVg	GA	GAM%
NDF	72.21	46.51	118.73	0.60	18.24	13.65	29.31
NDM	92.96	255.79	348.76	0.26	10.52	10.25	11.19
PH	15.26	17.87	33.16	0.46	10.10	5.46	14.12
NPP	19,427.18	28,642.29	48,069.47	0.40	39.74	182.53	52.05
PL	2.67	13.83	16.51	0.16	2.78	1.35	2.30
PW	0.41	0.60	6.96	0.40	4.44	0.85	5.85
PT	0.34	3.65	4.00	0.08	6.93	0.35	4.20
NGP	0.02	0.06	0.08	0.26	5.68	0.15	5.97
SL	0.17	0.36	0.54	0.32	3.74	3.74	6.56
SW	0.09	0.13	0.23	0.43	4.07	0.42	5.51
ST	0.06	0.16	0.22	0.28	5.29	0.28	5.86
HSW	9.61	19.31	28.92	0.33	10.37	3.68	12.32
GY	4,419.04	6,439.04	10,858.09	0.40	42.97	87.36	56.47

σ^2_g: genetic variance; σ^2_e: residual variance; σ^2_f: individual phenotypic variance; h^2: heritability; CVg: coefficient of genotypic variation; GA: genetic advancement; GAM: genetic advance as percentage of mean (%); NDF: number of days to flowering; NDM: number of days to maturation; PH: plant height; NPP: number of pods per plot; PL: pod length; PW: pod width; PT: pod thickness; NGP: number of grains per pod; SL: seed length; SW: seed width; ST: seed thickness; HSM: 100-seed mass; GY: grain yield.

Teresina (Table 4), the estimates were of low to medium magnitudes (h^2 < 70 %), ranging from 8 to 60 %, and the number of days to flowering presented the highest coefficient (60 %). These results indicate the possibility of selecting for the earliest lines, and with desirable height.

In studies using common bean, high-magnitude heritability coefficients were calculated for plant height (85.13 %) and number of grains per pod (75 %) by Santos et al. (2020), and medium-magnitude (67 %) for number of days to flowering by Rachman et al. (2018); allowing to infer that these would be parameters more easily selected for a breeding program.

A high genotypic coefficient of variation is a positive factor for breeding, and its relationship with the environmental coefficient of variation provides valuable information for selection (Cruz et al. 2012). When analyzed in combination with heritability estimates, these parameters enable comparisons of genetic variability between populations and help to predict the expected gains from selection (Santos et al. 2020).

In the study conducted in Tianguá, overall genetic advancement was observed for all the evaluated traits (Table 3), which was verified for number of days to flowering (38.12 %), number of days to maturation (12.97 %), plant height (23.91 %), mass of 100 seeds (17.77 %), number of pods per plant (45.75 %) and grain yield (42.05 %). This indicated that these traits are controlled by additive genes and that the selection will be efficient for their improvement.

In the evaluation conducted in Teresina (Table 4), there were greater gains for number of days to maturation (11.19 %), plant height (14.12 %) and mass of 100 seeds (12.32 %), as well as gains greater than 20 % for number of days to flowering (29.31 %), number of pods per plant (52.05 %) and grain yield (56.47 %). Carvalho et al. (2022) obtained lower gains for number of pods per plant and grain yield (8.57 and 24.44) than those observed in this study.

These outcomes are promising, because the high-magnitude gains obtained for the aforementioned traits were satisfactory. This enables the selection of lines with a shorter cycle, associated with production components, that is, they guarantee early production and less risk, due to drought and climate change, where lines have the potential to be assessed in value for cultivation and use trials.

Selection is an important strategy in breeding, as obtaining superior genotypes includes selecting and recombining families and individuals (Carias et al. 2017). The use of indices enables the combination of information and the selection from a set of parameters for the crop (Sousa et al. 2020).

Exploring the combination of different traits through selection indices may facilitate the identification of superior genotypes, allowing breeding programs to be more efficient in obtaining high-performance cultivars (Buzzello et al. 2015). However, studies addressing this for lima bean are limited.

In this study, the Mulamba & Mock (1978) non-parametric selection index was used to identify promising lines based on agronomic traits

Table 5. Genotypic coefficient of variation for the traits assessed in $F_{6:8}$ lima bean lines (Tianguá, Ceará state; Teresina, Piauí state).

Variables	Genotypic coefficient of variation (CVg)												
	NDF	NDM	PH	NPP	PL	PW	PT	NGP	SL	SW	ST	HSW	GY
Tianguá	21.64	10.11	16.30	36.17	5.01	5.98	5.76	5.08	4.92	2.56	5.26	13.83	35.22
Teresina	18.24	10.52	10.10	39.74	2.78	4.44	6.93	5.68	3.74	4.07	5.29	10.37	42.97

NDF: number of days to flowering; NDM: number of days to maturation; PH: plant height; NPP: number of pods per plot; PL: pod length; PW: pod width; PT: pod thickness; NGP: number of grains per pod; SL: seed length; SW: seed width; ST: seed thickness; HSM: 100-seed mass; GY: grain yield.

Table 6. Ranking of the 34 lima bean lines evaluated in Tianguá (Ceará state, Brazil), based on the Mulamba & Mock (1978) non-parametric selection index.

Lineage	% Gain	Lineage	% Gain
H81-32	111.20	H46-40	25.21
H25-59	82.83	H46-52	23.14
H25-56	72.53	H81-33	21.28
H25-66	66.10	H94-29	19.37
H25-57	59.50	H25-53	17.48
H81-34	53.44	H46-42	15.70
H50/86-38	49.13	H25-63	14.13
H25-58	45.83	H94-31	12.55
H50/86-36	42.81	H46-49	11.13
H25-62	40.48	H46-50	9.51
H94-30	38.34	H46-47	8.03
H25-64	36.36	H46-43	6.55
H50/86-35	34.50	H46-48	5.15
H50/86-37	32.84	H46-45	3.75
H25-54	31.25	H25-68	2.45
H25-55	29.37	H46-44	1.23
H46-46	27.29	H46-41	0.00

Table 7. Ranking of the 40 lima bean lines evaluated in Teresina (Piauí state, Brazil), based on the Mulamba & Mock (1978) non-parametric selection index.

Population	% Gain	Population	% Gain
H50/86-35	99.30	H25-55	27.85
H25-64	85.16	H46-52	25.82
H81-34	77.16	H46-41	23.93
H25-66	72.89	H46-45	22.21
H25-54	68.82	H25-65	20.66
H25-60	64.00	H25-59	19.01
H50/86-36	59.95	H46-40	17.40
H25-58	57.04	H46-39	15.82
H50/86-38	54.30	H46-42	14.26
H50/86-37	51.21	H81-32	12.81
H25-53	48.63	H46-51	11.49
H25-56	45.80	H94-31	10.25
H46-43	42.95	H46-49	9.08
H25-62	40.58	H46-47	7.91
H25-67	38.60	H46-44	6.81
H25-57	36.34	H94-29	5.68
H81-33	34.33	H94-30	4.35
H46-46	32.52	H25-63	3.06
H25-61	30.89	H46-50	1.49
H46-48	29.33	H25-68	0.00

simultaneously, where the values of the genetic variation coefficients were used as economic weights (Table 5).

The ranking of lines and the corresponding gains were determined for the traits evaluated in 34 lima bean lines in Tianguá (Table 6). The top six lines exhibited gains higher than 50 %, namely: H81-32 (111.20 %), H25-59 (82.83 %), H25-56 (72.53 %), H25-66 (66.10 %), H25-57 (59.50 %) and H81-34 (53.44 %).

In the evaluation of 40 lima bean lines in Teresina, H50/86-35 (99.30 %), H25-64 (85.16 %), H81-34 (77.16 %), H25-66 (72.89 %), H25-54 (68.82 %), H25-60 (64.00 %), H50/86-36 (59.95 %), H25-58 (57.04 %), H50/86-38 (54.30 %) and H50/86-37 (51.21 %) exhibited gains higher than 50 % (Table 7).

Selection based on a single or a limited number of traits is inefficient, as it may yield superior genotypes for the chosen traits, but with a less favorable performance for other important traits not considered (Cruz et al. 2012). However, the use of selection indices enables the integration of information from multiple variables, allowing the breeder to assign economic weights according to the selection criteria of interest.

CONCLUSIONS

1. The evaluated lima bean lines exhibited genetic variability for number of days to flowering onset, indicating the potential for selecting earlier-flowering genotypes;
2. In terms of simultaneous selection for desirable agronomic traits, H81-32, H25-59, H25-56, H25-66, H25-57 and H81-34 were noteworthy in Tianguá (Ceará state), and H50/86-35, H25-64, H81-34, H25-66, H25-54, H25-60, H50/86-36, H25-58, H50/86-38 and H50/86-37 in Teresina (Piauí state). Among them, H81-34 and H25-66 proved promising in both environments;

3. Additionally, H25-56 had white seeds, a desirable trait for the consumer market.

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