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Phenotypic Variability and Yield Component Analysis of Lima Bean (*Phaseolus lunatus* L.) Genotypes under Coastal Conditions of Peru

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ABSTRACT

Background: Lima bean (*Phaseolus lunatus* L.) is an important grain legume cultivated in tropical and subtropical regions and contributes significantly to food security and local agriculture, particularly in Peru. However, information on the agronomic variability of lima bean germplasm under coastal conditions of Peru remains limited. This study aimed to evaluate the phenotypic variability and yield-related traits of lima bean genotypes from the INIA Germplasm Bank.

Methods: Seven genotypes were evaluated under field conditions in Pisco, Ica (Peru), using a randomized complete block design with four replications. Twelve agronomic and morphological traits related to pod, seed and yield components were recorded. Data were analyzed using analysis of variance, Pearson correlation, principal component analysis and hierarchical clustering.

Result: Significant differences among genotypes were observed for most traits, indicating considerable phenotypic variability. Grain yield per plant showed positive correlations with the total number of pods per plant and the number of marketable pods. The first two principal components explained 51.14% of the total variation and separated genotypes mainly according to yield components and morphological traits. Cluster analysis grouped the genotypes into three clusters, identifying genotype Ac4 as the most promising material due to its favorable association with yield-related traits and lower incidence of pest-infested pods.

Key words: Coastal conditions, Genetic variability, Germplasm, Multivariate analysis, *Phaseolus lunatus* L.

INTRODUCTION

Lima bean (*Phaseolus lunatus* L.) is a legume widely cultivated in tropical and subtropical regions and is valued for its high genetic diversity and adaptability to diverse edaphoclimatic conditions, particularly warm and humid environments (Carvalho *et al*., 2022; de Assunção *et al*., 2022). The crop plays a key role in smallholder farming systems due to its nutritional value and productive potential. However, limited dissemination of its nutritional properties and suboptimal management practices have contributed to a decline in cultivated areas, with the crop persisting mainly in small plots managed by local farmers (López *et al*., 2023). The conservation and evaluation of genetic resources are therefore essential, as germplasm banks act as reservoirs of genetic variability, enabling the identification of valuable agronomic traits and the selection of superior genotypes for breeding programs (de Brito *et al*., 2020).

From an evolutionary perspective, *P. lunatus* originated from a broad region extending from Mexico to Peru, where two major genetic pools-the Mesoamerican and Andean-have been described (Bitocchi *et al*., 2017). The crop is used for both fresh and dry grain consumption and is appreciated for its seed size, creamy texture and distinctive flavor (López-Alcocer *et al*., 2016). Lima bean seeds are nutritionally rich, with protein contents ranging from approximately 14.2 to 24.9%, mainly composed of globulins, glutelins and albumins, along with low fat content, high carbohydrate levels and appreciable dietary fiber (Ibeabuchi *et al*., 2019; Palupi *et al*., 2022). These characteristics make lima bean an important source of plant-based protein. In addition, *P. lunatus* shows resilience to several biotic and abiotic stresses, highlighting its potential for cultivation under challenging environmental conditions (Soares *et al*., 2025).

In Peru, lima bean is a traditional crop, with a production of approximately 19,500 tons over about 10,651 ha, concentrated mainly in the Lambayeque (70.9%) and Ica

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(27.4%) regions, with a national average yield of approximately 1,800 kg ha^{-1} (MIDAGRI, 2026). Despite its agronomic importance, information on the genetic variability and performance of germplasm collections remains limited (Espinoza *et al*., 2021).

Phenotypic characterization of pods, seeds and yield components is a key tool for assessing variability and identifying genotypes with agronomic potential (Dadther-Huaman *et al*., 2024). Therefore, the present study aimed to evaluate the phenotypic and agronomic variability of lima bean genotypes from the National Institute of Agrarian Innovation (INIA) Germplasm Bank through pod and seed morphological traits and yield components under field conditions in Pisco, Ica, Peru. The findings provide valuable information for future breeding programs focused on improving lima bean productivity.

MATERIALS AND METHODS

The study was conducted at the San Juan de Cóndor Experimental Center of the Chincha Experimental Agricultural Station (EEA Chincha), belonging to INIA, located in the district of Independencia, Pisco Province, Ica, Peru, from May to December 2025. The experimental site is situated at 13°44′28.29″S and 75°57′59.06″W, at an altitude of 293 m above sea level. During the study period, the mean monthly maximum temperature was 28.84°C and the mean monthly minimum temperature was 12.45°C, with a mean monthly relative humidity of 88.68%. Precipitation was negligible during the experimental period, according to records from the National Meteorology and Hydrology Service of Peru (SENAMHI, 2026).

Seven lima bean genotypes (five promising accessions and two cultivars) from the INIA Germplasm Bank were evaluated in this study based on their agronomic potential and availability in the germplasm collection (Table 1).

The experimental field was prepared by plowing, harrowing and ridging. Sowing was carried out with a spacing of 2 m between rows and 2 m between plants, over a total area of 1000 m². Three seeds were planted per hill and subsequently thinned to leave only one plant per planting point. Fertilization was applied at a rate of 50 kg N ha^{-1}, 50 kg P_2O_5 ha^{-1} and 50 kg K_2O ha^{-1} at 20 days after sowing. Pest control targeted primarily *Prodiplosis longifila*, with the application of Imidacloprid (300 g L^{-1}) at a rate of 1 mL L^{-1}, applied every 15 days for a total of three applications. Irrigation was performed monthly by gravity, with a total of five applications. The experiment was established following a randomized complete block design (RCBD) with four blocks, where the experimental unit consisted of a 20 m long row. Two plants were randomly selected and evaluated per experimental unit. To minimize border effects, two plants at each end of the row were excluded from evaluation.

Soil analysis indicated a sandy loam texture, with an organic matter content of 0.5%, available phosphorus of 8.89 ppm, available potassium of 383.02 ppm, electrical conductivity of 45.7 mS m^{-1}, pH of 8.3 and a calcium carbonate equivalent of 4.41%. Regarding exchangeable bases, the soil contained 14.94 cmol kg^{-1} of calcium, 1 cmol kg^{-1} of magnesium, 2.21 cmol kg^{-1} of sodium and 0.76 cmol kg^{-1} of potassium.

Twelve yield and morphological traits were evaluated: total number of pods per plant (TPP), pest-infested pods (IP), marketable pods (MP), empty pods (EP), pod length (PL), pod width (PW), seed length (SL), seed width (SW), seed thickness (ST), number of seeds per pod (NSP), hundred-seed weight (HSW) and grain yield per plant (GYP).

Analysis of variance (ANOVA) was used to evaluate differences among genotypes. Prior to analysis, data were assessed for normality and homogeneity of variances. When significant genotype effects were detected, means were separated using Tukey's test at $p \leq 0.05$. The coefficient of variation (CV) was calculated to assess experimental precision, while the magnitude of genotype effects was estimated using partial eta squared ($\eta^2 p$) and the coefficient of determination (R^2). Pearson correlation analysis was performed, followed by multivariate approaches including principal component analysis (PCA) and hierarchical clustering based on standardized data using Euclidean distance and Ward's minimum variance method (Ward.D2). The cophenetic correlation coefficient was calculated to evaluate the consistency of the dendrogram. A significance level of $\alpha = 0.05$ was adopted for all tests. All statistical analyses were conducted using R version 4.5.1 (R Core Team, 2025) and RStudio version 2026.1.0.392 (Posit Team, 2026).

RESULTS AND DISCUSSION

Agronomic variability and genotype performance

The ANOVA revealed significant differences among genotypes for most traits evaluated (Table 2), confirming substantial phenotypic variability among the evaluated lima bean genotypes under coastal conditions of Peru. Such variability is essential in germplasm characterization studies because it allows the identification of genotypes with agronomic potential and supports their use in breeding programs (Dadther-Huaman *et al*., 2023; Srivastava *et al*., 2025).

However, certain traits, including EP, PL and SW, did not differ significantly among genotypes (p>0.05; Table 2). This pattern may indicate lower genetic variability for these

Table 1: Lima bean genotypes evaluated from the INIA Germplasm Bank.

National code	Bank code	Genotype
PER014581	phl003	Ac4 (accession)
PER014599	phl024	Ac12 (accession)
PER014582	phl004	Ac15 (accession)
PER014589	phl011	Ac27 (accession)
PER014613	phl 038	Ac30 (accession)
-	-	1548 (cultivar)
-	-	Serrucho (cultivar)

traits within the evaluated germplasm or a stronger influence of environmental factors on their expression. In legume germplasm studies, it is common for structural traits under strong hereditary control, such as certain seed and pod characteristics, to display limited variability among genotypes (Souza *et al*., 2024; Aybar-Peve *et al*., 2025a). Similarly, although ST was significant in the ANOVA, Tukey's test did not clearly differentiate genotypes (Table 2), which may occur when differences among means are small or when observed values overlap among treatments.

Genotype effects were quantified using partial eta squared (η^2p), a statistic that estimates the proportion of total variance explained by each factor in the ANOVA model. This metric is widely used in legume studies to assess the relative contributions of genetic and environmental factors to agronomic and yield trait expression (Sarakatsianos *et al*., 2024; Bredu and Zhang, 2025). In this study, the highest η^2p values were recorded for NSP (0.85) and HSW (0.78) (Table 2), indicating that these yield components were highly effective in differentiating genotypes. In grain legumes, traits directly related to seed formation and weight generally show strong genetic control and high agronomic relevance for yield determination (Ton and Anlarsal, 2017; Michalitsis *et al*., 2024). Conversely, PL (0.24) and EP (0.33) showed moderate genotype effects, suggesting either lower genetic variability or greater environmental influence on their expression.

Coefficients of variation (CV) ranged from 5.2% to 27.1% (Table 2), indicating generally adequate experimental precision under field conditions. The lowest CVs were observed for SL and ST (5.2%), reflecting high measurement stability, while the highest CV occurred for GYP (27.1%), which is consistent with previous studies evaluating lima bean germplasm (Dadther-Huaman *et al*., 2023). Yield components in legumes are often strongly affected by genotype × environment interactions, generating variation in trait expression under different conditions (Ligarreto-Moreno and Pimentel-Ladino, 2021; Gayosso *et al*., 2025). In coastal production systems such as those of the Ica region, variability in yield-related traits may be influenced by water availability, soil properties and microclimatic conditions that interact with the genetic potential of each genotype (Dadther-Huaman *et al*., 2023; Aybar-Peve *et al*., 2025a).

Overall, these results demonstrate considerable agronomic variability among the evaluated genotypes, highlighting the INIA germplasm bank as a valuable source of diversity for breeding programs. The presence of genotypes with contrasting agronomic performance suggests that some accessions possess traits suitable for selection in future productivity evaluations.

Relationships among traits

Pearson correlation analysis was conducted to assess the relationships among the 12 evaluated traits in the lima bean genotypes (Fig 1). Understanding associations between agronomic traits is essential for identifying

Table 2: Mean comparison, ANOVA and effect size for yield components and pod and seed traits of lima bean genotypes under field conditions.

Genotype	TPP	IP (%)	MP (%)	EP (%)	NSP	PL (mm)	PW (mm)	SL (mm)	SW (mm)	ST (mm)	HSW (g)	GYP (g plant^{-1})
Ac4	132.95 a	32.55 b	32.21 ab	34.97 a	1.67 b	94.94 a	17.39 a	26.20 a	11.60 a	6.66 a	202.61 ab	134.16 a
Serrucho	128.93 a	38.56 ab	32.66 a	29.86 a	1.72 b	87.79 a	16.91 a	23.75 abc	10.83 a	6.05 a	158.96 c	122.64 ab
Ac30	125.74 a	32.35 b	29.70 abc	40.30 a	1.65 b	85.79 a	14.22 ab	20.94 c	10.61 a	6.18 a	184.20 b	111.57 ab
Ac12	122.77 a	40.00 ab	27.17 abc	30.95 a	1.88 b	92.71 a	15.70 ab	23.90 ab	11.23 a	6.59 a	177.84 bc	125.45 ab
Ac15	111.55 ab	39.16 ab	21.92 bc	34.93 a	1.81 b	85.95 a	15.02 ab	23.26 bc	9.75 a	6.08 a	186.69 b	67.45 b
1548	92.59 ab	47.01 a	19.34 c	35.16 a	2.25 a	91.10 a	12.17 b	22.89 bc	7.32 a	6.02 a	182.45 bc	65.93 b
Ac27	67.92 b	40.49 ab	29.84 abc	37.30 a	2.30 a	92.27 a	12.95 ab	23.29 bc	8.42 a	6.09 a	212.86 a	84.87 ab
F-value	6.255	3.042	5.007	1.464	17.299	0.949	3.943	6.459	2.594	2.779	10.689	4.28
p-value	<0.01	<0.05	<0.01	0.246	<0.001	0.486	<0.05	<0.001	0.0545	<0.05	<0.001	<0.01
Signif.	**	*	**	ns	***	ns	*	***	ns	*	***	**
η^2_p	0.68	0.50	0.63	0.33	0.85	0.24	0.57	0.68	0.46	0.48	0.78	0.59
R^2 (model)	0.71	0.65	0.69	0.38	0.86	0.26	0.69	0.73	0.64	0.54	0.79	0.60
CV (%)	16.9	15.0	16.6	16.9	6.8	8.2	13.1	5.2	19.6	5.2	5.7	27.1

Means followed by the same letter within a column are not significantly different according to Tukey's HSD test ($p \leq 0.05$). η^2p: Partial eta squared for the genotype effect; R^2: Coefficient of determination of the model; CV: Experimental coefficient of variation calculated as the square root of the residual mean square divided by the overall mean × 100. ns: Not significant; * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$. TPP: Total number of pods per plant; IP: Pest-infested pods; MP: Marketable pods; EP: Empty pods; NSP: Number of seeds per pod; PL: Pod length; PW: Pod width; SL: Seed length; SW: Seed width; ST: Seed thickness; HSW: Hundred-seed weight; GY: Grain yield per plant.

potential indirect selection criteria in breeding programs, since correlated traits may influence yield performance simultaneously (Espinoza *et al*., 2021; López *et al*., 2023).

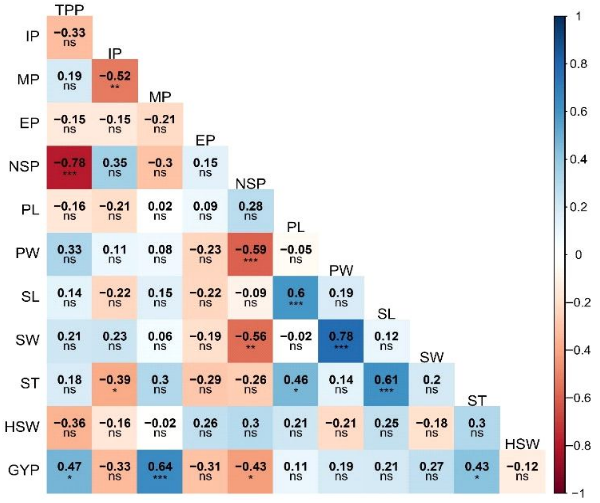
Significant positive correlations were observed between GYP and MP (r = 0.64***), as well as between GYP and TPP (r = 0.47*), indicating that an increase in the number of pods per plant can enhance the productive potential of genotypes by increasing the number of reproductive structures available for seed formation. Similar results were reported by Vásquez *et al*. (2024) in lima bean genotypes from the INIA germplasm bank, who found a positive association between TPP and GYP. In contrast, Brilhante *et al*. (2025) found no significant relationship between these traits in Mexican bean germplasm, suggesting that the contribution of TPP to grain yield may depend on genetic background and environmental conditions.

GYP also exhibited a positive correlation with ST (r = 0.43*), suggesting that seed size traits may contribute to the expression of grain yield per plant, consistent with Dadther-Huaman *et al*. (2023), who reported that seed size traits can influence yield expression in lima bean. This observation indicates that genotypes producing larger or thicker seeds may contribute to increased yield per plant. In contrast, GYP showed a negative correlation with NSP (r = -0.43*), while NSP was strongly negatively correlated with TPP (r = -0.78***). These relationships likely reflect a physiological trade-off during reproductive development, where plants allocate resources between the number of reproductive structures and the number of seeds produced per pod. Similar compensatory mechanisms have been reported across several legume species (Chauhan *et al*., 2023; Manson *et al*., 2025).

Principal component analysis (PCA)

The PCA biplot showed that the first principal component (PC1) explained 30.33% of the total variability, while the second principal component (PC2) accounted for 20.82% (Fig 2), together capturing 51.14% of the observed variation. This cumulative proportion indicates that a considerable fraction of the phenotypic diversity in the evaluated germplasm can be described using a reduced number of components. Previous studies in lima bean have reported that the first two principal components can explain between 59.5% and 84.5% of the total variability in agromorphological germplasm evaluations (Espinoza *et al*., 2021; Damas *et al*., 2023).

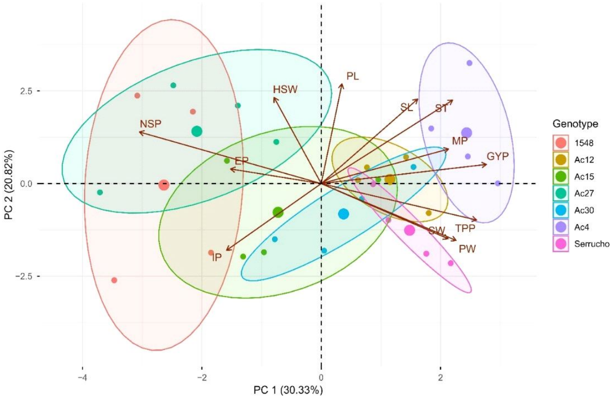
The PCA biplot revealed a clear separation among the evaluated accessions (Fig 2), highlighting the presence of agronomic variability within the studied collection. Notably, genotype Ac4 was strongly associated with yield-related traits, including GYP and MP. Furthermore, this genotype was positioned in the direction opposite to IP, suggesting a lower association with the incidence of pest-infested pods. In contrast, EP was oriented opposite to TPP in the biplot, indicating an inverse relationship between the number of empty pods and the total number of pods per plant. Similar patterns have been reported by Krisnawati *et al*. (2025), who observed a negative association between EP and yield components in grain legume genotypes. This pattern may reflect differences in reproductive efficiency among genotypes, where materials producing a higher



	TPP	IP	MP	EP	NSP	PL	PW	SL	SW	ST	HSW
IP	−0.33 ns										
MP	0.19 ns	−0.52 **									
EP	−0.15 ns	−0.15 ns	−0.21 ns								
NSP	−0.78 ***	0.35 ns	−0.3 ns	0.15 ns							
PL	−0.16 ns	−0.21 ns	0.02 ns	0.09 ns	0.28 ns						
PW	0.33 ns	0.11 ns	0.08 ns	−0.23 ns	−0.59 ***	−0.05 ns					
SL	0.14 ns	−0.22 ns	0.15 ns	−0.22 ns	−0.09 ns	0.6 ***	0.19 ns				
SW	0.21 ns	0.23 ns	0.06 ns	−0.19 ns	−0.56 **	−0.02 ns	0.78 ***	0.12 ns			
ST	0.18 ns	−0.39 *	0.3 ns	−0.29 ns	−0.26 ns	0.46 *	0.14 ns	0.61 ***	0.2 ns		
HSW	−0.36 ns	−0.16 ns	−0.02 ns	0.26 ns	0.3 ns	0.21 ns	−0.21 ns	0.25 ns	−0.18 ns	0.3 ns	
GYP	0.47 *	−0.33 ns	0.64 ***	−0.31 ns	−0.43 *	0.11 ns	0.19 ns	0.21 ns	0.27 ns	0.43 *	−0.12 ns

Significance levels are indicated as p≤0.001 (***), p≤0.01 (**), p≤0.05 (*) and not significant (ns). TPP: Total number of pods per plant; IP: Pest-infested pods; MP: Marketable pods; EP: Empty pods; NSP: Number of seeds per pod; PL: Pod length; PW: Pod width; SL: Seed length; SW: Seed width; ST: Seed thickness; HSW: Hundred-seed weight; GY: Grain yield per plant.

Fig 1: Heatmap of pearson correlation coefficients among agronomic traits evaluated in lima bean genotypes.

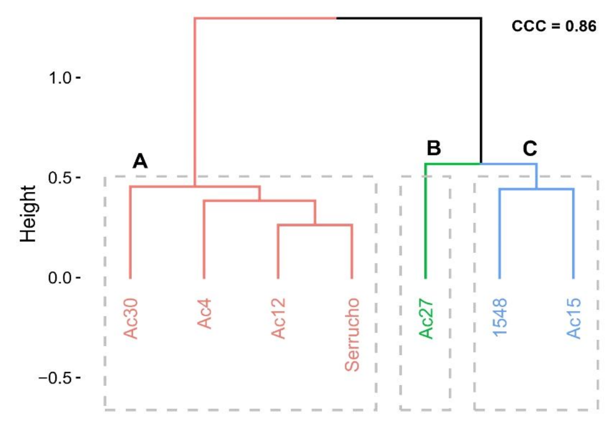


PC: Principal component; TPP: Total number of pods per plant; IP: Pest-infested pods; MP: Marketable pods; EP: Empty pods; NSP: Number of seeds per pod; PL: Pod length; PW: Pod width; SL: Seed length; SW: Seed width; ST: Seed thickness; HSW: Hundred-seed weight; GY: Grain yield per plant.

Fig 2: Principal component analysis (PCA) biplot showing the distribution of lima bean genotypes and agronomic traits in the first two principal component dimensions.

proportion of productive pods tend to exhibit a lower frequency of empty pods. In legumes, empty pods may result from pollination failure, early seed abortion or environmental stresses affecting seed filling (Morales-Elias *et al*., 2025).

PC1 was mainly associated with yield components, notably NSP (0.81), GYP (0.74) and TPP (0.70) (Table 3). PC2 was primarily influenced by pod and seed morphological traits, including PL (0.72), SL (0.61), ST (0.60) and HSW (0.62) (Table 3), capturing variability related mainly to seed and pod morphology. In agromorphological characterization studies of legume germplasm, it is common for yield-related traits to explain most of the variation in PC1, while morphological traits contribute more strongly to subsequent components (Dadther-Huaman *et al*., 2023; Aybar-Peve *et al*., 2025a).



CCC: Cophenetic coefficient correlation.

Fig 3: Hierarchical cluster dendrogram of lima bean genotypes based on euclidean distance using the ward.D2 method derived from 12 agronomic traits.

Cluster analysis and identification of promising genotypes

Hierarchical cluster analysis grouped the seven lima bean genotypes into three distinct clusters (Fig 3). The cophenetic correlation coefficient (CCC = 0.86) indicated a high level of agreement between the dendrogram and the original distance matrix, confirming that the clustering structure accurately reflects the similarity relationships among the evaluated genotypes. Previous studies in legume germplasm diversity have reported variable CCC values; for instance, Brilhante *et al*. (2025) reported a CCC of 0.54, whereas other studies obtained values similar to those observed here (0.86; de Paula *et al*., 2024).

Cluster A included four genotypes (Ac30, Ac4, Ac12 and Serrucho) and was characterized by the highest mean TPP (127.6) and GYP (123.46 g), coupled with a relatively lower incidence of pest-infested pods (IP = 35.86%; Table 4). Within this cluster, genotype Ac4 stood out based on the ANOVA results (Table 2). This performance aligns with the PCA results (Fig 2), where Ac4 was closely associated with yield-related traits and less related to pest incidence, indicating superior agronomic performance under the evaluated field conditions. Cluster B consisted of genotype Ac27, which exhibited the lowest TPP (67.92) and a moderate GYP (84.87 g), despite having the highest NSP (2.30) and HSW (212.86 g). This pattern suggests that yield in Ac27 may be constrained primarily by a reduced

Table 3: Eigenvalues, percentage of variance and cumulative variance of the first four principal components for yield components and pod and seed traits of lima bean genotypes.

Principal components	PC1	PC2	PC3	PC4
Eigen value	3.64	2.5	1.69	1.16
Explained variance (%)	30.33	20.82	14.06	9.63
Cumulative variance (%)	30.33	51.14	65.21	74.84
Individual characters PC score				
TPP	0.7	-0.26	-0.30	0.2
IP	-0.42	-0.48	0.59	-0.28
MP	0.57	0.25	-0.45	-0.28
EP	-0.41	0.11	-0.23	0.77
NSP	-0.81	0.37	0.15	-0.32
PL	0.09	0.72	0.37	0.06
PW	0.6	-0.41	0.49	0.22
SL	0.43	0.61	0.42	0.01
SW	0.57	-0.40	0.55	0.17
ST	0.59	0.6	0.22	-0.03
HSW	-0.21	0.62	0.13	0.31
GYP	0.74	0.14	-0.25	-0.28

PC: Principal component; TPP: Total number of pods per plant; IP: Pest-infested pods; MP: Marketable pods; EP: Empty pods; NSP: Number of seeds per pod; PL: Pod length; PW: Pod width; SL: Seed length; SW: Seed width; ST: Seed thickness; HSW: Hundred-seed weight; GY: Grain yield per plant.

Table 4: Cluster means of yield components and pod and seed traits in lima bean genotypes.

Traits	Cluster A (n = 4)	Cluster B (n = 1)	Cluster C (n = 2)
TPP	127.6	67.92	102.07
IP	35.86	40.49	43.08
MP	30.43	29.84	20.63
EP	34.02	37.3	35.04
NSP	1.73	2.3	2.03
PL	90.31	92.27	88.53
PW	16.05	12.95	13.59
SL	23.69	23.29	23.07
SW	11.07	8.42	8.54
ST	6.37	6.09	6.05
HSW	180.9	212.86	184.57
GYP	123.46	84.87	66.69

TPP: Total number of pods per plant; IP: Pest-infested pods; MP: Marketable pods; EP: Empty pods; NSP: Number of seeds per pod; PL: Pod length; PW: Pod width; SL: Seed length; SW: Seed width; ST: Seed thickness; HSW: Hundred-seed weight; GY: Grain yield per plant.

number of reproductive structures rather than seed size or seed weight. Similar observations have been reported in legumes, where the number of pods per plant is often a stronger determinant of yield than seed-associated traits (Dadther-Huaman *et al*., 2023; Dadther-Huaman *et al*., 2024; Aybar-Peve *et al*., 2025b). Cluster C grouped genotypes 1548 and Ac15, which displayed intermediate TPP but the lowest GYP (66.69 g) and the highest IP (43.08%). Damage caused by pod-boring insects represents an important constraint in grain legume production, potentially reducing yield by up to 72% in some cases (Wang *et al*., 2024). Evaluating genotypic responses to pest pressure is therefore crucial for identifying materials with improved tolerance or resistance (Indiati *et al*., 2021; El Fakhouri *et al*., 2022).

Overall, the clustering analysis highlights clear agronomic differentiation among the evaluated genotypes, supporting the identification of promising accessions for breeding. Cluster A, particularly genotype Ac4, demonstrated high yield potential combined with lower pest incidence, making it a valuable candidate for future selection and productivity improvement programs.

CONCLUSION

The present study revealed significant agronomic variability among the evaluated lima bean genotypes under coastal conditions of Peru, highlighting the INIA germplasm bank as a valuable source of genetic diversity for breeding programs. Correlation and multivariate analyses indicated that the total number of pods per plant and the number of marketable pods are strongly associated with grain yield per plant, suggesting that these traits can serve as reliable indirect selection criteria in lima bean improvement programs. Furthermore, principal component and cluster analyses identified genotypes with favorable agronomic performance, with genotype Ac4 standing out due to its association with higher yield components and lower incidence of pest-infested pods. These findings contribute to a better understanding of the phenotypic variability of lima bean germplasm and provide useful information for selecting promising materials for future breeding efforts aimed at improving productivity and resilience in smallholder farming systems.

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Disclaimers

Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this manuscript.

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