



Phenotypic Diversity Indices and Multivariate Analysis of Peruvian Common Bean (*Phaseolus vulgaris* L.) Germplasm

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ABSTRACT

Background: *Phaseolus vulgaris* L. is a globally important legume due to its nutritional value and its contribution to food security and agricultural sustainability. Although Peruvian germplasm exhibits high phenotypic variability, information regarding accessions from the INIA Germplasm Bank remains limited. This study characterized the phenotypic diversity of 66 accessions using diversity indices and multivariate analyses under coastal Peruvian conditions.

Methods: A total of 35 agro-morphological traits (18 qualitative and 17 quantitative) were evaluated using CIAT descriptors. Diversity was assessed using Shannon and Pielou evenness indices, as well as multivariate analyses including hierarchical clustering based on Gower distance, FAMD, PCA and MCA.

Result: High phenotypic variability was observed, resulting in four distinct clusters. FAMD showed that hundred-seed weight, leaf width and length and primary seed color were the main contributors to total variance. PCA revealed a positive correlation between seed weight and leaf traits, whereas the number of pods per plant and seeds per pod showed a negative association with these variables. MCA and diversity indices highlighted seed color, growth habit and standard petal pigmentation as key discriminating traits. Cluster II exhibited the highest dispersion and phenotypic diversity, whereas Cluster IV showed higher yield-related components, demonstrating the potential of these accessions for use in breeding programs and genetic resource conservation.

Key words: Cluster analysis, FAMD, Morphological traits, Phenotypic variation, Plant genetic resources.

INTRODUCTION

The common bean (*Phaseolus vulgaris* L.), is one of the most important food crops worldwide due to its widespread consumption and high nutritional value. Its grains contain approximately 50-60% carbohydrates and 15-25% proteins, in addition to significant amounts of vitamins and minerals (Cid-Gallegos *et al.*, 2023). These characteristics make common bean a key component of food security, particularly in developing countries, where it represents an accessible source of nutrients and a strategic crop for income generation among small- and medium-scale farmers (Lamz-Piedra *et al.*, 2023; Curay *et al.*, 2024). Furthermore, common bean contributes to the sustainability of agricultural systems through its ability to fix atmospheric nitrogen via symbiosis with soil bacteria, thereby reducing dependence on synthetic fertilizers (Karavidas *et al.*, 2022).

Genetic resources of *P. vulgaris* exhibit broad genetic diversity, mainly structured into the Mesoamerican and Andean gene pools, reflecting their evolutionary differentiation and high potential for breeding programs (Long *et al.*, 2020; Delfini *et al.*, 2021). In Peru, several studies have demonstrated that common bean germplasm possesses considerable phenotypic variability, representing an important basis for the selection of promising materials (Aybar-Peve *et al.*, 2025a). In this sense, the use of multivariate analyses has proven effective for identifying patterns of variation and relationships among traits in common bean, highlighting the contribution of vegetative

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growth and reproductive traits to diversity structuring (Long *et al.*, 2020). Complementarily, phenotypic diversity indices

allow quantification of the variability present within germplasm collections, facilitating the identification of accessions with high agronomic potential (Aydin and Baloch, 2019; Ventura-Neyra *et al.*, 2026). However, despite advances in the characterization of common bean in Peru, information regarding the phenotypic diversity of the accession collection maintained in the Germplasm Bank of the National Institute of Agrarian Innovation (INIA) remains limited, restricting the efficient utilization of these genetic resources in breeding programs. In this context, the present study aimed to characterize the phenotypic diversity of 66 common bean accessions from the INIA Germplasm Bank through the application of diversity indices and multivariate analyses, in order to identify materials with potential for breeding programs and contribute to the conservation and sustainable use of plant genetic resources.

MATERIALS AND METHODS

The study was conducted at plot 7 of the Cercado Grande field at the Chinchá Agricultural Experimental Station (EEA Chinchá) of INIA, located in the district of Alto Larán, Chinchá Province, Ica Department, Peru ($13^{\circ}27'29.58''\text{S}$, $76^{\circ}08'01.10''\text{W}$; 61 m a.s.l.), during the period from May to October 2024. During this period, the average monthly temperature was 17.3°C , with maximum and minimum values of 21.8°C in October and 12.7°C in September, respectively. The average monthly relative humidity was 86.9%, according to data obtained from the National Service of Meteorology and Hydrology of Peru (SENAMHI, 2026).

Prior to the conduct of the experiment, a physicochemical characterization of the soil was performed. The results showed a soil pH of 8.3 and an electrical conductivity of 16.2 mS m^{-1} . Equivalent calcium carbonate content was 3.09% and organic matter content was 1.10%. Available phosphorus reached $398.29 \text{ mg kg}^{-1}$, whereas total nitrogen content was 0.06%. Soil texture was classified as loam. Regarding exchangeable bases, concentrations of Ca^{2+} [$9.89 \text{ cmol}(+) \text{ kg}^{-1}$], Mg^{2+} [$2.42 \text{ cmol}(+) \text{ kg}^{-1}$], Na^{+} [$4.27 \text{ cmol}(+) \text{ kg}^{-1}$] and K^{+} [$0.57 \text{ cmol}(+) \text{ kg}^{-1}$] were determined.

A total of 66 common bean accessions, representing part of the genetic diversity in the INIA Germplasm Bank, were evaluated. The regeneration sites of each accession, as well as their respective identification codes within the germplasm bank, are presented in Table 1.

To evaluate phenotypic diversity, 35 agro-morphological traits (18 qualitative and 17 quantitative) (Table 2) were analyzed according to the descriptors established by the International Center for Tropical Agriculture (CIAT) (Muñoz *et al.*, 1993).

The accessions were arranged systematically in the experimental field, consisting of 66 subplots corresponding to experimental units, each representing a distinct accession. In each experimental unit, observations were recorded from five plants for each evaluated trait, except for

DE, DF, DPM, DH and HSW, whose values were recorded at the experimental unit level.

Each experimental unit covered an area of 17 m^2 and consisted of four rows of 5 m length, with 0.85 m spacing between rows and 0.30 m between plants, resulting in a total experimental area of $3,231 \text{ m}^2$ including border effects. Three seeds were sown per hill and one row was left as separation between accessions.

All experimental units received the same agronomic management, including phytosanitary control of pests such as *Bemisia tabaci*, *Crociosema aporema* and *Empoasca kraemeri* using imidacloprid (350 g L^{-1}), emamectin benzoate (50 g kg^{-1}) and alpha-cypermethrin (100 g L^{-1}) at doses of 0.6 mL L^{-1} , 0.5 g L^{-1} and 0.75 mL L^{-1} , respectively. Furrow irrigation was used, with a total of seven applications during the growing season. Soil fertilization consisted of 80 kg ha^{-1} of N, 100 kg ha^{-1} of P_2O_5 and 50 kg ha^{-1} of K_2O .

Hierarchical clustering analysis was performed using Gower distance as the dissimilarity measure and the Ward.D2 agglomerative method and the goodness of fit was evaluated through the cophenetic correlation coefficient. Quantitative traits were compared among the clusters obtained from hierarchical clustering through analysis of variance (ANOVA), followed by Tukey's honestly significant difference (HSD) test. Subsequently, factorial analysis of mixed data (FAMD) was applied to the dataset. Additionally, principal component analysis (PCA) and multiple correspondence analysis (MCA) were performed to support the interpretation of quantitative and qualitative trait contributions identified in the FAMD. For qualitative traits, chi-square (χ^2) tests were conducted and Shannon diversity (H') and Pielou evenness (J') indices were calculated. All analyses were performed using R version 4.5.1 (R Core Team, 2025) and R-Studio version 2026.1.0.392 (Posit Team, 2026), considering a significance level of $\alpha = 0.05$.

RESULTS AND DISCUSSION

Cluster analysis

Hierarchical clustering analysis based on Gower distance grouped the 66 accessions into four distinct clusters (Fig 1). The cophenetic correlation coefficient indicated a moderate fit ($\text{CCC} = 0.63$) between the original distance matrix and the generated dendrogram, suggesting an acceptable representation of the dissimilarity structure among the accessions. Higher values ($\text{CCC} = 0.86$) have been reported in previous studies that evaluated a lower number of quantitative and qualitative traits (de Paula *et al.*, 2024), as well as fewer accessions and variables (Camargo-Cobefías *et al.*, 2026). This variation may be associated with the larger number of evaluated traits, the size of the germplasm collection and the environmental variability considered in the present study.

Tukey's mean comparison analysis revealed significant differences among clusters for the evaluated

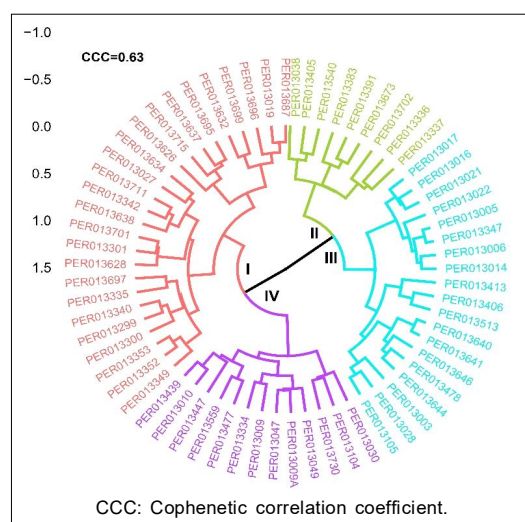


Fig 1: Hierarchical dendrogram of 66 common bean accessions based on Gower distance and the Ward.D2 method.

quantitative traits (Table 3), reflecting broad phenotypic variability among accessions. Cluster I exhibited significantly higher mean values for MSL (176.54), PLL (7.53), PLW (8.34), CLL (12.06), PW (1.19) and DH (132.80), indicating predominance of traits associated with vegetative growth, larger leaf size and late maturity. Traits related to plant architecture, vegetative growth and phenology have been identified as important sources of differentiation in common bean due to their association with adaptation processes and genetic divergence (Long *et al.*, 2020; González *et al.*, 2021).

Cluster IV showed superior performance for yield-related traits, particularly NPP (21.12) and NSP (5.57), whereas Cluster II presented the lowest mean values for these variables (NPP = 10.67; NSP = 4.42), indicating lower expression of reproductive traits. Previous studies have highlighted these traits as key yield components and important selection criteria in common bean breeding programs (Long *et al.*, 2020; Sundharaiya *et al.*, 2023).

Table 1: Identification codes and regeneration sites of common bean accessions.

Nº	Accession code	Bank code	Regeneration site	Nº	Accession code	Bank code	Regeneration site
1	PER013003	Ph.v. 0005	Cajamarca	34	PER013383	G19786	Amazonas
2	PER013005	Ph.v. 0002	Amazonas	35	PER013391	G19833	Amazonas
3	PER013006	Ph.v. 0003	Amazonas	36	PER013405	LI0017	Lima
4	PER013009	Ph.v. 0006-A	Ancash	37	PER013406	LI0018	Lima
5	PER013009A	Ph.v. 0006-3	Ancash	38	PER013413	LI0025	Lima
6	PER013010	Ph.v. 0007	Ancash	39	PER013439	LI0054	Lima
7	PER013014	Ph.v. 0011	Apurímac	40	PER013447	LI0062	Lima
8	PER013016	Ph.v. 0013	Ayacucho	41	PER013477	LI0095	Lima
9	PER013017	Ph.v. 0014	Ayacucho	42	PER013478	LI0096	Lima
10	PER013019	Ph.v. 0016	Ayacucho	43	PER013513	LI0134	Lima
11	PER013021	Ph.v. 0018	Cajamarca	44	PER013540	LI0169	Lima
12	PER013022	Ph.v. 0019	Cajamarca	45	PER013559	LI0190	Lima
13	PER013027	Ph.v. 0024	Cajamarca	46	PER013626	0008	Cajamarca
14	PER013028	Ph.v. 0025-A	Cajamarca	47	PER013628	0010	Cajamarca
15	PER013030	Ph.v. 0027	Cusco	48	PER013632	14B	Cajamarca
16	PER013038	Ph.v. 0035	Cusco	49	PER013634	0016	Cajamarca
17	PER013047	Ph.v. 0044	Cusco	50	PER013637	0019	Cajamarca
18	PER013049	Ph.v. 0046-B	Cusco	51	PER013638	0020	Cajamarca
19	PER013104	Ph.v. 0102	Loreto	52	PER013640	0022	Cajamarca
20	PER013105	Ph.v. 0103	Loreto	53	PER013641	0023	Cajamarca
21	PER013299	G19339	Cajamarca	54	PER013644	0026	Cajamarca
22	PER013300	G19339	Cajamarca	55	PER013646	0028	Cajamarca
23	PER013301	G19340	Cajamarca	56	PER013673	0055	Cajamarca
24	PER013334	G19447	Cajamarca	57	PER013687	0069	Cajamarca
25	PER013335	G19451	Cajamarca	58	PER013695	0002	Cajamarca
26	PER013336	G19457	Amazonas	59	PER013696	0003	Cajamarca
27	PER013337	G19469	Cajamarca	60	PER013697	0004	Cajamarca
28	PER013340	G19366	Cajamarca	61	PER013699	0006	Cajamarca
29	PER013342	G19376 (40)	Amazonas	62	PER013701	0008	Cajamarca
30	PER013347	G19388	Cajamarca	63	PER013702	0009	Cajamarca
31	PER013349	G19395	Cajamarca	64	PER013711	0019	Cajamarca
32	PER013352	G19600	Cajamarca	65	PER013715	0023	Cajamarca
33	PER013353	G19601	Cajamarca	66	PER013730	0038	Cajamarca

These findings suggest that accessions from Clusters I and IV may constitute valuable parental sources for breeding programs aimed at improving vegetative vigor and yield potential, respectively. In contrast, Cluster III displayed intermediate phenotypic performance for most evaluated traits, indicating moderate agronomic differentiation relative to the remaining groups.

Factorial analysis of mixed data (FAMD)

The simultaneous integration of quantitative and qualitative traits is essential for understanding phenotypic variation in common bean and its usefulness in breeding programs (Scarano *et al.*, 2014; Córdova-Sinarahua *et al.*, 2026). In this context, the FAMD explained 18.2% of the total variation in the first two dimensions (Fig 2), revealing

differentiation and grouping of the accessions into four clusters. Cluster III exhibited lower intragroup variability, whereas Cluster II showed greater dispersion despite being composed of fewer accessions. Recent studies in common bean reported 35.8% of explained variance in the first dimensions (Sinkovič *et al.*, 2025), which may be associated with differences in the number of evaluated accessions and traits among studies.

Dimension 1 was mainly associated with traits related to yield (HSW), vegetative growth (MSL), leaf morphology (PLW, PLL and CLL) and seed traits (PSC and SSC) (Table 4), suggesting a phenotypic gradient associated with plant growth, organ size and seed variability. Similar results were reported by Sinkovič *et al.* (2025), who identified a high contribution of traits associated with seed weight, size and

Table 2: Agro-morphological traits used to evaluate the phenotypic diversity of 66 common bean accessions from Peru.

Crop stage	Traits	Unit	Acronym	Trait type
Seedling	Days to emergence	#	DE	CNT
	Hypocotyl color	-	HC	CLT
	Vein color of the primary leaf	-	VCL	CLT
	Hypocotyl length	cm	HL	CNT
	Epicotyl length	cm	EL	CNT
	Primary leaf length	cm	PLL	CNT
	Primary leaf width	cm	PLW	CNT
Flowering	Days to flowering	#	DF	CNT
	Wing color	-	WC	CLT
	Standard petal blade color	-	SPC	CLT
	Standard petal color pattern	-	SPP	CLT
	Venation in standard petal lobe	-	SV	CLT
	Growth habit	-	GH	CLT
	Main stem length	cm	MSL	CNT
	Compound leaf length	cm	CLL	CNT
	Compound leaf width	cm	CLW	CNT
	Days to physiological maturity	#	DPM	CNT
Physiological maturity	Pod color at physiological maturity	-	PCM	CLT
Harvest	Days to harvest	#	DH	CNT
	Pod color at harvest	-	PCH	CLT
	Pod profile	-	FP	CLT
	Pod apex type	-	PAT	CLT
	Direction of apex curvature	-	DAC	CLT
	Primary seed color	-	PSC	CLT
	Secondary seed color	-	SSC	CLT
	Seed coat pattern	-	SCP	CLT
	Seed venation	-	SVS	CLT
	Seed hilum ring color	-	SHC	CLT
	Seed shape	-	SS	CLT
	Pod length	cm	PL	CNT
	Pod width	cm	PW	CNT
	Pod apex length	cm	PAL	CNT
	Number of pods per plant	#	NPP	CNT
	Number of seeds per pod	#	NSP	CNT
	100-seed weight	g	HSW	CNT

CNT: Quantitative; CLT: Qualitative; #: Number of days; -: Not applicable.

coloration in the differentiation of common bean accessions. Likewise, Nogueira *et al.* (2021) highlighted the importance of seed traits in breeding programs, whereas Ibrahim *et al.* (2020) indicated that seed color constitutes a relevant attribute for breeders, farmers and consumers. Dimension 2 showed predominance of variables related to yield (NPP and NSP), vegetative pigmentation (HC and VCL) and reproductive morphology (SPC, PSC, SS and PW), reflecting substantial variability in reproductive and pigmentation-related traits among accessions. Similar findings were reported by Ventura-Neyra *et al.* (2026) in lima bean accessions.

On the other hand, Dimension 3 was mainly determined by phenological variables (DF and DH), in addition to pod-related (PCM) and seed-related traits (PSC and SSC). Ventura-Neyra *et al.* (2026) and Machado *et al.* (2022) reported that traits associated with earliness contribute significantly to differentiation among accessions and represent important attributes for adaptation to different environments. Likewise, Sinkovič *et al.* (2025) reported that seed traits are determinant factors in the multivariate differentiation of common bean accessions.

Principal component analysis (PCA)

The variance explained by the first two principal components (48.7%; Fig 3) indicated an adequate representation of the phenotypic diversity among the evaluated accessions. Similar values have been reported in common bean and other legume species, where the first two dimensions explained between 24% and 70% of the total variability (Long *et al.*, 2020; Dadther-Huaman *et al.*, 2024).

PC1 showed predominance of variables related to yield and leaf morphology, particularly HSW, NPP, PLW, PLL and CLL, indicating an association between vegetative growth, organ size and productivity. Similar results were described by Aybar-Peve *et al.* (2025b) and Camargo-Cobenañas *et al.* (2026), who reported that yield-related traits constitute key factors in the phenotypic differentiation of legume accessions. PC2 was mainly determined by phenological variables such as DF, DPM and DH, coinciding with previous studies that identified phenology as one of the main components of variation in common bean (Meza-Vásquez *et al.*, 2015; Long *et al.*, 2020).

Positive correlations among HSW, PLW and CLL evidenced an association between vegetative growth and seed weight, whereas NPP and NSP showed an opposite pattern relative to leaf morphology and seed weight variables, suggesting possible physiological compensation mechanisms between the number of reproductive structures and individual seed size. Similar patterns have been reported in several legume species (Manson *et al.*, 2025; Camargo-Cobenañas *et al.*, 2026).

The distribution of accessions revealed differentiation among clusters. Cluster I was mainly associated with vegetative growth (MSL), seed weight (HSW) and leaf morphology traits (CLL and PLW), whereas Clusters III

Table 3: Mean comparison of 17 quantitative traits among clusters based on ANOVA and Tukey's honestly significant difference (HSD) test.

Cluster	DE	HL	EL	PLL	PLW	DF	MSL	CLL	CLW	DPM	DH	PL	PW	PAL	NPP	NSP	HSW
(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(cm)	(g)	(g)
I (n=25)	11.40a	4.05a	2.46a	7.53a	8.34a	61.24a	176.54a	12.06a	7.65a	104.36a	132.80a	11.09a	1.19a	0.96ab	12.10b	4.85b	58.13a
II (n=9)	11.22ab	3.93a	2.30a	7.27ab	7.92ab	56.78a	99.02b	11.05ab	7.84a	96.22a	122.67b	11.73a	1.14ab	1.16a	10.67b	4.42b	56.01a
III (n=19)	9.21b	3.59a	2.74a	6.57b	6.41c	59.11a	108.22b	10.40b	7.12a	97.89a	125.05b	9.78b	1.12ab	0.82b	15.74ab	4.97ab	37.27b
IV (n=13)	10.23ab	3.46a	2.30a	6.83ab	6.46bc	61.00a	86.63b	10.25b	7.71a	98.69a	121.54b	9.67b	0.98b	0.86b	21.12a	5.57a	25.70b
p-value	0.026	0.123	0.35	0.0106	<0.001	0.0844	<0.001	<0.001	0.259	0.0201	<0.001	<0.001	<0.01	<0.001	<0.001	<0.01	<0.001

Means followed by the same letter within a column are not significantly different ($p < 0.05$). n: Number of accessions per cluster.

and IV were mainly related to NPP and NSP. In contrast, Cluster II exhibited greater dispersion, reflecting high variability among its accessions and the absence of clearly defined associations with the evaluated variables. Similar results were reported by Aybar-Peve *et al.* (2025a), who indicated that genotypes with greater dispersion tend to exhibit higher phenotypic diversity. This variability may be influenced by differences in plant architecture, genotype $\times$ environment interaction and adaptation strategies (Maqueira-López *et al.*, 2021).

Multiple correspondence analysis (MCA)

The variation explained by the first two MCA dimensions (15.4%; Fig 4) indicated an adequate representation of the

phenotypic diversity of the 18 evaluated qualitative traits, a common pattern in multiple correspondence analyses due to the high number of categories and the discrete nature of morphological variables (Santa Cruz-Padilla *et al.*, 2025; Aybar-Peve *et al.*, 2025b).

Cluster III exhibited lower dispersion and greater phenotypic uniformity, whereas clusters I and IV showed

Table 4: Eigen values, explained variance, cumulative variance and contributions of agro-morphological traits to the first three dimensions of the FAMD.

Dim	Eigen value	Variance (%)	Cumulative variance (%)
1	8.37	10.73	10.73
2	5.81	7.45	18.19
3	4.44	5.69	23.88

Contribution (%)			
Trait	Dim 1	Dim 2	Dim 3
HL	2.38	0.69	2.37
EL	0.27	1.59	0.01
PLL	5.18	1.48	1.6
PLW	7.82	2.28	0.03
MSL	5	0.03	4.26
CLL	5.8	0.45	0.13
CLW	2.24	0.05	1.35
PL	4.45	0.58	0.77
PW	3.1	5.71	0.17
PAL	1.35	0	0.36
NPP	3.88	6.11	0.29
NSP	0.98	4.12	0.58
DE	1.83	0.27	1.77
DF	0.46	3.96	4.68
DPM	1.53	2.7	2.32
DH	2.68	0.68	7.13
HSW	7.81	3.66	0.5
HC	2.75	8.51	2.64
VCL	1.48	9.11	4.07
WC	4.35	5.22	4.16
SPC	5.59	8.58	7.19
SPP	1.12	0.01	0.21
SV	3.46	0.44	0.99
GH	3.56	3.21	5.38
PCM	1.59	3.24	9.35
PCH	0.14	1.76	1.38
PP	0.75	1.45	1.14
PAT	0.15	0.14	0.18
DAC	0.2	1.64	1.22
PSC	6.59	8.5	11.8
SSC	5.14	3.22	12.49
SCP	1.46	0.58	1.1
SVS	1.43	2.01	0.04
SHC	2.18	0.92	4.84
SS	1.31	7.1	3.52

Dim: Dimension.

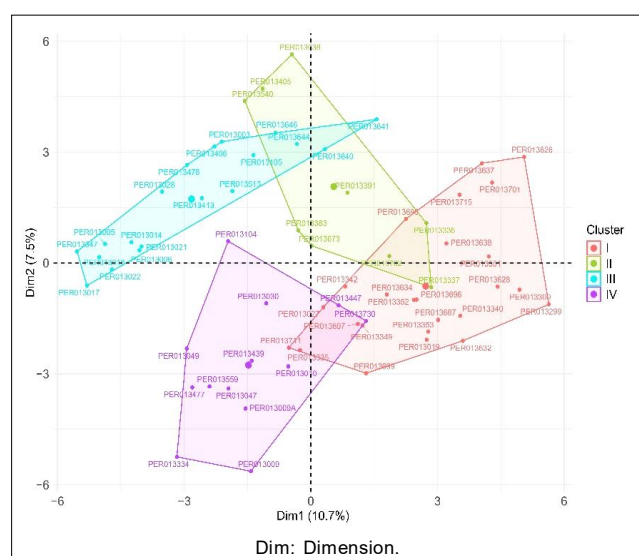


Fig 2: FAMD factorial plane showing the distribution of 66 common bean accessions according to the clusters identified in the hierarchical clustering analysis.

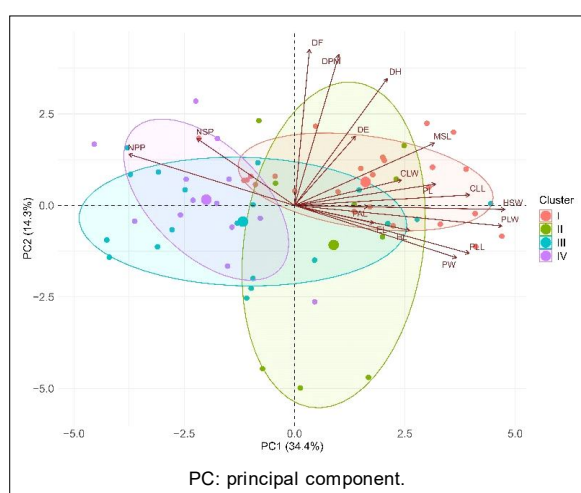


Fig 3: PCA biplot of 66 common bean accessions based on 17 quantitative traits and grouped according to the clusters identified by hierarchical clustering.

Table 5: Diversity indices and chi-square association estimated globally and by cluster for 18 qualitative traits in 66 common bean accessions.

Traits	S	χ^2	p-value	Overall		Cluster I		Cluster II		Cluster III		Cluster IV	
				H'	J'	H'	J'	H'	J'	H'	J'	H'	J'
PSC	9	80.816	<0.001	1.925	0.876	1.568	0.806	1.273	0.918	0.826	0.596	1.378	0.856
GH	8	31.429	0.0668	1.702	0.819	0.784	0.714	1.677	0.936	1.764	0.906	1.992	0.958
SSC	10	67.433	<0.001	1.546	0.671	1.585	0.885	1.889	0.971	0.206	0.297	0.687	0.625
PCM	7	46.719	<0.001	1.443	0.741	1.186	0.855	1.677	0.936	0.943	0.858	0.79	0.719
SPC	7	81.642	<0.001	1.407	0.723	0.653	0.943	1.311	0.946	0.409	0.373	0.937	0.676
SS	6	33.159	0.0045	1.39	0.776	1.32	0.82	1.369	0.987	1.188	0.857	0.271	0.391
VCL	4	49.253	<0.001	1.003	0.723	0.944	0.859	0	-	0	-	1.205	0.869
PCH	4	15.973	0.0674	0.994	0.717	0.873	0.795	1.149	0.829	0.436	0.629	1.266	0.913
SCP	3	10.263	0.114	0.975	0.887	0.659	0.6	1.099	1	0.993	0.904	1.012	0.921
HC	3	51.434	<0.001	0.965	0.879	0.839	0.763	0	-	0	-	0.898	0.818
FP	3	18.798	0.0045	0.806	0.734	0.708	0.644	0	-	0.681	0.982	0.859	0.782
WC	3	49.204	<0.001	0.735	0.669	0	-	0.687	0.991	0.206	0.297	0.687	0.625
SHC	2	24.953	<0.001	0.682	0.983	0.593	0.855	0.349	0.503	0.336	0.485	0.54	0.779
SPP	2	14.048	0.0028	0.677	0.976	0.673	0.971	0.637	0.918	0.336	0.485	0.617	0.89
SV	2	29.948	<0.001	0.647	0.933	0.593	0.855	0.687	0.991	0	-	0.271	0.391
SVS	2	19.049	<0.001	0.647	0.933	0.367	0.529	0.687	0.991	0.624	0.9	0.429	0.619
DAC	2	6.276	0.0989	0.451	0.65	0.593	0.855	0	-	0.206	0.297	0.54	0.779
PAT	2	2.512	0.4732	0.079	0.113	0	-	0	-	0.206	0.297	0	-

S: richness; χ^2 : chi-square statistic; H': Shannon diversity index; J': Pielou evenness index.

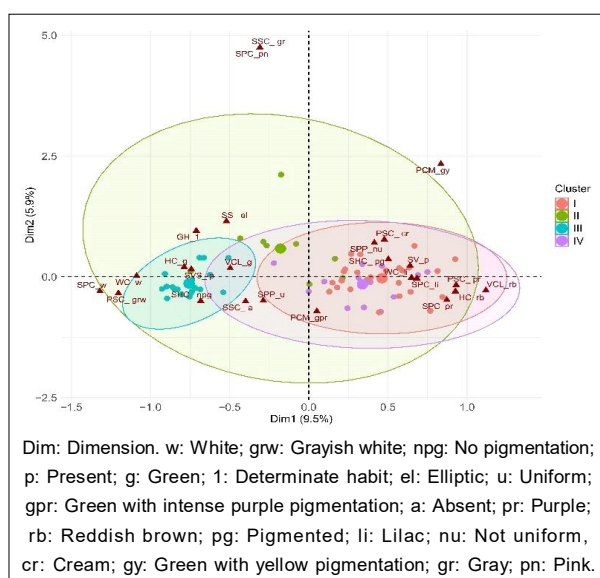


Fig 4: MCA biplot of 66 common bean accessions based on 18 qualitative traits and grouped according to the clusters identified by hierarchical clustering, showing the 25 categories with the highest contribution.

partial overlap due to similarities in lilac and purple floral pigmentation, as well as cream and purple seed coloration. In contrast, Cluster II presented greater dispersion within the factorial plane, reflecting high phenotypic diversity despite being composed of a smaller number of accessions.

The categories with the highest contribution were mainly associated with seed traits (SSC_gr and PSC_grw), flower traits (SPC_pn and SPC_w) and pod traits (PCM_gy). Similar results were reported by Aybar-Peve *et al.* (2025b), who identified a high contribution of categories associated with pod and seed coloration in Andean common bean accessions. Likewise, Carvalho *et al.* (2016) indicated that seed coloration constitutes a trait of commercial and cultural importance, whereas Zhu *et al.* (2017) reported that this variability depends on epistatic interactions related to flavonoid and anthocyanin biosynthesis.

Diversity indices

The high diversity observed for PSC ($H' = 1.925$), GH ($H' = 1.702$), SSC ($H' = 1.546$), PCM ($H' = 1.443$) and SPC ($H' = 1.407$) (Table 5) revealed substantial phenotypic variability within the evaluated collection. Likewise, PSC ($J' = 0.876$) and GH ($J' = 0.819$) exhibited high evenness values, reflecting a relatively homogeneous distribution of their categories. Similar results were reported by Long *et al.* (2020); Savić *et al.* (2020); Kouam *et al.* (2023) and Patel *et al.* (2025), who documented high phenotypic diversity in common bean and other legume accessions, mainly in seed- and flower-related traits.

The higher diversity values observed for PSC, SSC, PCM and SPC are consistent with the findings of Savić *et al.* (2020), who identified high diversity in seed and flower

traits, indicating that these descriptors constitute important sources of phenotypic differentiation in common bean. Likewise, Romero-Astudillo *et al.* (2024) reported that the high diversity recorded in *Phaseolus vulgaris* L. may be associated with its broad geographic distribution and historical selection processes.

Most variables showed significant association with the clustering structure, particularly PSC ($p < 0.001$), SPC ($p < 0.001$), SSC ($p < 0.001$), HC ($p < 0.001$), VCL ($p < 0.001$), WC ($p < 0.001$) and PCM ($p < 0.001$), indicating high discriminatory capacity among clusters. Similar to the findings reported by Ventura-Neyra *et al.* (2026), internal diversity measured through H' and J' does not necessarily guarantee high discriminatory power among groups, since some descriptors may exhibit high diversity but low statistical significance in the χ^2 test. In contrast, variables combining high diversity and significant association with the clustering structure constitute more efficient descriptors for phenotypic differentiation.

At the cluster level, Cluster II exhibited higher diversity values for traits mainly associated with seed, flower and pod characteristics, particularly SSC ($H' = 1.889$), PCM ($H' = 1.677$), SPC ($H' = 1.311$) and SS ($H' = 1.369$), in addition to high evenness values ($J' > 0.7$), indicating balanced category frequencies. These results are consistent with the greater dispersion previously observed in MCA and FAMD, reflecting high phenotypic heterogeneity among its accessions. In contrast, cluster IV exhibited higher diversity in variables related to vegetative growth and pigmentation, including GH ($H' = 1.992$), VCL ($H' = 1.205$), PCH ($H' = 1.266$), HC ($H' = 0.898$) and PP ($H' = 0.859$), indicating substantial morphological variability among its accessions. Conversely, Cluster III showed lower diversity levels and greater phenotypic uniformity, a pattern similar to that reported by Ventura-Neyra *et al.* (2026); Dadther-Huaman *et al.* (2024) and Espinoza de Arenas *et al.* (2022).

CONCLUSION

Diversity indices and multivariate analyses revealed high variability among the four clusters, confirming the wide phenotypic diversity present in the 66 Peruvian common bean germplasm accessions. The FAMD identified hundred-seed weight, primary leaf width and primary seed color as the main contributors to overall variability, whereas Cluster II exhibited the highest phenotypic dispersion and trait diversity. In contrast, Cluster IV showed greater agronomic potential, as it presented higher yield-related components.

MCA and PCA analyses showed a positive association between hundred-seed weight and leaf traits, whereas the number of pods per plant and seeds per pod were negatively associated with morphological variables and seed weight. Likewise, primary seed color and growth habit were the most discriminating qualitative traits, evidencing high diversity and evenness among accessions.

Overall, the results demonstrate a broad genetic base within the evaluated germplasm, identifying key traits for

the selection of genotypes with potential use in breeding programs and for the sustainable conservation of common bean genetic resources.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Conflict of interest

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

REFERENCES

- Aybar-Peve, L., Cervantes-Zamudio, R., Camargo-Cobefias, M., Chihuan-Palomino, E., Rojas-Meza, M. and Terán-Rojas, J. (2025b). Phenology, growth and yield of nine common bean (*Phaseolus vulgaris* L.) lines under agroclimatic conditions of Chinchá, Peru. *Bioagro*. **37(3)**: 277-288.
- Aybar-Peve, L., Medina-Portilla, N., Camargo-Cobefias, M., Chihuan-Palomino, E. and Terán-Rojas, J. (2025a). Agromorphological characterization and phenotypical diversity of common bean from Peru. *Tropical and Subtropical Agroecosystems*. **28**: 69.
- Aydin, M.F. and Baloch, F.S. (2019). Exploring the genetic diversity and population structure of Turkish common bean germplasm by the iPBS-retrotransposons markers. *Legume Research*. **42(1)**: 18-24. doi: 10.18805/LR-423.
- Camargo-Cobefias, M., Almidon-Ramirez, K., Rojas-Meza, M. and Terán-Rojas, J. (2026). Phenotypic variability and yield component analysis of lima bean (*Phaseolus lunatus* L.) genotypes under coastal conditions of Peru. *Legume Research*. 1-8. doi: 10.18805/LRF-946.
- Carvalho, M., Castro, I., Matos, M., Lino-Neto, T., Silva, V., Rosa, E. and Carnide, V. (2016). Agro-morphological characterization of cowpea (*Vigna unguiculata*) accessions: Basis to breeding. *Revista de Ciências Agrárias*. **39(4)**: 506-517.
- Cid-Gallegos, M. S., Gómez y Gómez, Y. de las M., Corzo-Ríos, L. J., Sanchez-Chino, X. M., Moguel-Concha, D., Borges-Martínez, E. and Jiménez-Martínez, C. (2023). Potencial nutricional y bioactivo de frijol (*Phaseolus vulgaris*) en la salud humana. *Investigación y Desarrollo en Ciencia y Tecnología de Alimentos*. **8(1)**: 309-318.
- Córdova-Sinarahua, D., Linares-Huapaya, S. and Manco-Céspedes, E.I. (2026). Phenotypic and agromorphological diversity reveals detailed information about accessions with productive potential for cotton (*Gossypium barbadense* L.) in northeastern Peru. *Plants*. **15**: 314.
- Curay, Q.S.E., Telenchana, A.C.E. and Artieda, R.J.R. (2024). Agricultural production and its impact on food security. *Revista Científica Arbitrada Multidisciplinaria Pentaciencias*. **6**: 228-235.
- Dadther-Huaman, H., Gambini-de la Cruz, T.A., Coaquira-Mendoza, B., Garay-Duran, D., Parco-Quinchori, J., Quispe-Castro, R., Aybar-Peve, L., Contreras-Liza, S. and Casa-Coila, V.H. (2024). Agromorphological characterization and phenotypical diversity of the pallar germplasm collection (*Phaseolus lunatus* L.) from INIA, Peru. *Tropical and Subtropical Agroecosystems*. **27**: 97.
- de Paula, E., Almeida, R.N. de, Santos, T. de O., Souza Neto, J.D. de, Riva-Souza, E.M., Posse, S.C.P., Souza, M.N., Madella de Oliveira, A.F., Santos Júnior, A.C., Santos, J.O., Pimenta, S., Bento, C.S. and Moulin, M.M. (2024). Genetic diversity of common bean (*Phaseolus vulgaris* L.) landraces based on morphological traits and molecular markers. *Plants*. **13**: 2584.
- Delfini, J., Moda-Cirino, V., Santos Neto, J. dos, Ruas, P. M., Sant'Ana, G.C., Gepts, P. and Gonçalves, L.S.A. (2021). Population structure, genetic diversity and genomic selection signatures among a Brazilian common bean germplasm. *Scientific Reports*. **11**: 2964.
- Espinoza de Arenas, M.L., Aquije, G.P.A., Surco, L.F.A., Espino, T.G. and Rojas, Y.Y. (2022). Morphoagronomic characterization and evaluation of the yield of twelve genotypes of lima bean (*Phaseolus lunatus* L.) of colored grains in the middle zone of the Ica Valley. *Ciencia Latina Revista Científica Multidisciplinaria*. **6(1)**: 927-946.
- González, A.M., Yuste-Lisbona, F.J., Weller, J., Vander Schoor, J.K., Lozano, R. and Santalla, M. (2021). Characterization of QTL and environmental interactions controlling flowering time in Andean common bean (*Phaseolus vulgaris* L.). *Frontiers in Plant Science*. **11**: 599462.
- Ibrahim, B.Y.A.R., Achigan-Dako, E.G., Aissata, M., Sekloka, E., Billot, C., Adje, C.O.A., Barnaud, A. and Bakasso, Y. (2020). Agromorphological characterization revealed three phenotypic groups in a region-wide germplasm of fonio (*Digitaria exilis* (Kippist) Stapf) from West Africa. *Agronomy*. **10(11)**: 1653.
- Karavidas, I., Ntatsi, G., Vougeleka, V., Karkanis, A., Ntanasi, T., Saitanis, C., Agathokleous, E., Ropokis, A., Sabatino, L. and Tran, F. (2022). Agronomic practices to increase the yield and quality of common bean (*Phaseolus vulgaris* L.): A systematic review. *Agronomy*. **12**: 271.
- Kouam, E.B., Kamga-Fotso, A.M.A. and Anoumaa, M. (2023). Exploring agro-morphological profiles of *Phaseolus vulgaris* germplasm shows manifest diversity and opportunities for genetic improvement. *Journal of Agriculture and Food Research*. **14**: 100772.
- Lamz-Piedra, A., Morales-Soto, A., Peteira Delgado-Oramas, B. and Florido-Bacallao, M. (2023). Caracterización de 11 líneas de frijol común (*Phaseolus vulgaris* L.) resistentes a zabrotes subfasciatus boheman en cuba. *Bioteología y Ciencias Agropecuarias*. **18**: 178-190.
- Long, J., Zhang, J., Zhang, X., Wu, J., Chen, H., Wang, P., Wang, Q. and Du, C. (2020). Genetic diversity of common bean (*Phaseolus vulgaris* L.) germplasm resources in chongqing, evidenced by morphological characterization. *Frontiers in Genetics*. **11**: 697.

- Machado, E.O., Ferraz, G.V., Almeida, R.C., Lopes, Â.C.A., Gomes, R.L.F. and Silva, V.B. (2022). Evaluation of lima bean accessions at high temperatures. *Revista Caatinga*. **35(4)**: 791-798.
- Manson, J.B., Denton, M.D., Lake, L., Brand, J. and Sadras, V.O. (2025). Linking pod-set and seed yield of faba bean across organ, phytomer, plant and population scales. *Journal of Experimental Botany*. **76(16)**: 4472-4489.
- Maqueira-López, L.A., Roján-Herrera, O., Solano-Flores, J. and Milagros-Santana, I. (2021). Germinación de semillas de frijol (*Phaseolus vulgaris* L.) a diferentes temperaturas. *Cultivos Tropicales*. **42(2)**: e03.
- Meza-Vázquez, K.E., Lépez-Ildefonso, R., López-Alcocer, J.J. and Morales-Rivera, M.M. (2015). Morphological and phenological characterization of wild bean (*Phaseolus*) species. *Revista Fitotecnia Mexicana*. **38(1)**: 17-28.
- Muñoz, A.G., Avila, G.G. and de Soto, J.F. (1993). Descriptores Varietales: Arroz, Frijol, Maíz, Sorgo. Centro Internacional de Agricultura Tropical (CIAT). Cali, Colombia.
- Nogueira, A.F., Moda-Cirino, V., Delfini, J., Brandão, L.A., Mian, S., Constantino, L.V., Zeffa, D.M., dos Santos Neto, J. and Gonçalves, L.S.A. (2021). Morpho-agronomic, biochemical and molecular analysis of genetic diversity in the mesoamerican common bean panel. *PLoS ONE*. **16(4)**: e0249858.
- Patel, T., Babbar, A., Behera, K., Kumar, J.A., Patel, M., Kujur, M.J. and Katara, V.K. (2025). Integrating diversity analysis and morphological characterization for strategic trait selection in advanced breeding lines of chickpea (*Cicer arietinum* L.). *Legume Research*. **48(12)**: 1969-1978. doi: 10.18805/LR-5468.
- Posit team (2026). RStudio: Integrated Development Environment for R (Version 2026.1.0.392) [Computer software]. Posit Software, PBC, Boston, MA. <http://www.posit.co/>.
- R Core Team (2025). R: A Language and Environment for Statistical Computing (Version 4.5.1) [Computer software]. R Foundation for Statistical Computing, Vienna, Austria. <https://www.R-project.org/>.
- Romero-Astudillo, M.J., Tapia, C., Giménez de Azcárate, J. and Montalvo, D. (2024). Diversity of common bean (*Phaseolus vulgaris* L.) and runner bean (*Phaseolus coccineus* L.) landraces in rural communities in the Andes highlands of cotacachi-ecuador. *Agronomy*. **14**: 1666.
- Santa Cruz-Padilla, A.E., Vasquez-Orrillo, J.L., Bardales-Lozano, R.M. and Murga-Orrillo, H. (2025). Assessment of phenotypic diversity of ñuña, a local common bean (*Phaseolus vulgaris* L.) from the northern Andes in Peru. *Genetic Resources*. **6(11)**: 1-13.
- Savić, A., Zorić, M., Brdar-Jokanović, M., Zdravković, M., Dimitrijević, M., Petrović, S., Živanov, D. and Vasić, M. (2020). Origin and diversity study of local common bean (*Phaseolus vulgaris* L.) germplasm from Serbia: Phaseolin and phenotyping approach. *Genetic Resources and Crop Evolution*. **67**: 2195-2212.
- Scarano, D., Rubio, F., Ruiz, J.J., Rao, R. and Corrado, G. (2014). Morphological and genetic diversity among and within common bean (*Phaseolus vulgaris* L.) landraces from the campania region (Southern Italy). *Scientia Horticulturae*. **180**: 72-78.
- Servicio Nacional de Meteorología e Hidrología del Perú (SENAMHI). (2026). Datos Hidrometeorológicos a Nivel Nacional. <https://www.senamhi.gob.pe/?p=estaciones>.
- Sinković, L., Tavakoli, H.H., Neji, M., Plestenjak, E., Dolničar, P., Meglič, V. and Pipan, B. (2025). Combining multi-criteria decision analysis with agro-morphological-biochemical-molecular traits of interest for use in breeding in promising common bean breeding lines (*Phaseolus vulgaris* L.). *Cogent Food and Agriculture*. **11(1)**: 2439551.
- Sundharaiya, K., Sathish, G., Palanikumar, M., Baskaran, R., Natarajan, K., Bharathikumar, K. and Gayathri, G. (2023). Genetic studies on yield and yield attributing traits in pole beans (*Phaseolus vulgaris* L.) under lower pulney hills of western ghats. *Legume Research*. **46(9)**: 1168-1173. doi: 10.18805/LR-5065.
- Ventura-Neyra, C.J., Dadther-Huaman, H., Gambini-de la Cruz, T.A., Zamata-Guzman, R.R., Meneses, L.A., Garay-Duran, D., Irigoien-Becerra, E., Saenz-Rodriguez, H., Parco-Quinchori, J.A., Espinoza-Ponte, Y.N. and Aybar-Peve, L. (2026). Agromorphological diversity and structuring of lima bean (*Phaseolus lunatus* L.) accessions from the national germplasm collection of INIA Peru. *Tropical and Subtropical Agroecosystems*. **29**: 26.
- Zhu, J., Wu, J., Wang, L. and Blair, M.W. (2017). Novel alleles for black and gray seed color genes in common bean. *Crop Science*. **57**: 1603-1610.