

Original Research Paper

Characterization of common bean (*Phaseolus vulgaris* L.) genotypes for morphological, maturity and yield traits

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ABSTRACT

A study was conducted to evaluate and characterize 100 bean germplasm for adaptability and yield potential in Kashmir, India. The highest phenotypic and genotypic coefficients of variation were recorded for pod yield per plant, 100 seed weight, seed yield per plant, and plant height. High heritability coupled with high genetic advance as per cent mean was observed for all traits except days to 50% flowering, days to pod initiation, days to mid pod filling, seed breadth, and seed thickness, indicating the predominance of additive gene action. Correlation analysis revealed that pod yield per plant was positively and significantly associated with pod weight, pod width, number of pods per plant, seed yield per plant, 100 seed weight, seed length, days to 50% flowering, and plant height. Principal component analysis identified five principal components with Eigen-values greater than 1, accounting for 76.26% of the total variability. Seed yield per plant, number of pods per plant, days to 50% flowering, and pod yield per plant contributed most to PC-1. Biplot analysis identified genotypes SK-B-36, SK-B-42, SK-B-54, SK-B-49, SK-B-27, and SK-B-10 as superior for pod yield and related traits.

Keywords: Augmented design, characterization, common bean, principal component analysis, variability

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is an important leguminous crop cultivated worldwide for its edible dry, fresh, and green beans (Hussein et al., 2020; Nadeem et al., 2021). It originated in South Mexico and Central America (Vavilov, 1951) and comprises dry, green, shelling, and popping bean types. The species consists of two major gene pools, Andean and Mesoamerican, which gave rise to two distinct cultivar groups based on morphological, biochemical, and molecular studies (Beebe et al., 2000). In India, beans are cultivated across diverse regions, including Jammu and Kashmir, covering about 15.5 mha with an annual production of 6.4 Mt (FAO, 2023). In Jammu and Kashmir, the crop occupies 4.26 thousand hectares with an annual production of 39.17 thousand metric tons (Anonymous, 2023).

It is a rich source of minerals, vitamins, carbohydrates, dietary fibre, and proteins in dried seeds (21.1%) and fresh pods (1.7%) (Sundharaiya et al., 2023). Its consumption has increased due to health benefits, including cholesterol reduction, diabetes management, and cardiovascular protection (Sundharaiya et al.,

2023). The crop also improves soil fertility through symbiotic nitrogen fixation (Assefa et al., 2019), making it economically, nutritionally, and socially important (Rana et al., 2015).

Despite its significance, bean productivity in Kashmir remains below the international average due to the lack of high-yielding, early-maturing, and stress-resistant varieties (Shama et al., 2022). Germplasm characterization and evaluation are therefore essential for identifying adaptable, high-yielding genotypes. Morphological characterization remains a key approach for assessing genetic diversity and relationships among genotypes (Choudhary et al., 2018). Knowledge of genetic variability, heritability, and genetic advance is vital for parent selection in breeding programmes (Rana et al., 2015; Sundharaiya et al., 2023). Identification of diverse genotypes further facilitates genetic improvement of crops (Gupta et al., 2021; Choudhary et al., 2022). Accordingly, the present study was carried out to evaluate the agronomic performance and morphological diversity of common bean genotypes collected from national and international gene banks, and different regions of Jammu and Kashmir.



Table 1 : Genotypes used in the study

Genotype Code	Collection site/Maintenance
SK-FB-1, SK-FB-2, SK-FB-6, SK-FB-7, SK-FB-10, SK-FB-11, SK-B-7, SK-B-10, SK-B-30	Punjab Agriculture University, Ludhiana, India
SK-FB-3, SK-FB-4, SK-FB-8, SK-FB-13, SK-B-2, Shalimar French Bean-1	Division of Vegetable Science, Faculty of Horticulture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, India
SK-FB-5, SK-FB-9, SK-FB-12, SK-FB-14, SK-FB-15, SK-FB-16, SK-FB-17, SK-FB-18, SK-FB-22, SK-FB-23, SK-FB-24, SK-FB-25, SK-FB-26, SK-FB-27, SK-FB-30, SK-B-1, SK-B-6, SK-B-8, SK-B-9, SK-B-11, SK-B-31, SK-B-33, SK-B-34, SK-B-35, SK-B-36, SK-B-37, SK-B-41, SK-B-42, SK-B-43, SK-S-1, SK-S-3, SK-S-4	Akdeniz University, Turkey
SK-FB-19, SK-FB-20, SK-FB-21, SK-FB-31, SK-FB-32, SK-FB-33, SK-FB-34, SK-FB-35, SK-B-12, SK-B-13, SK-B-14, SK-B-15, SK-B-16, SK-B-17, SK-B-18, SK-B-19, SK-B-20, SK-B-21, SK-B-22, SK-B-23, SK-B-25, SK-B-26, SK-B-27, SK-B-29, SK-B-40, SK-B-44, SK-B-45, SK-B-46, SK-B-47, SK-B-48, SK-B-49, SK-B-50, SK-B-51, SK-B-52, SK-B-53, SK-B-54, SK-B-55, SK-B-56, SK-S-2, Shalimar Rajmash-1	Division of Genetics and Plant Breeding, Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Wadura, India
SK-FB-28, SK-FB-29, SK-B-3, SK-B-4, SK-B-5, SK-B-32, SK-B-38, SK-B-39	Dryland Agriculture Research Station, Rangreth, Srinagar
SK-B-24, SK-B-28	ICAR- National Bureau of Plant Genetic Resources, New Delhi, India
Arka Komal, Arka Anoop, Arka Sharath	ICAR-Indian Institute of Horticultural Research, Bangalore, India

MATERIALS AND METHODS

A set of one hundred common bean lines sourced from national and international gene banks as well as different regions of Jammu and Kashmir, including five checks *viz.*, Shalimar French Bean-1, Shalimar Rajmash-1, Arka Komal, Arka Anoop and Arka Sharath (Table 1).

The 100 genotypes were evaluated in augmented block design at Experimental Field, Division of Vegetable Sciences, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar during *kharif* 2023. Experimental field was divided into five blocks. In each block 19 genotypes and 5 checks were sown at a spacing of 45 cm row to row and 20 cm plant to plant. The farm was located at 34°12 North latitude and 74°892 East longitude with the altitude of 1685 meters above mean sea level. Standard agronomic practices recommended for growing common bean were followed for healthy crop growth.

The data were recorded on various qualitative traits such as plant growth, leaf, flower, pod, and seed as well as quantitative traits *viz.*, days to 50% flowering (DFF), days to pod initiation (DPI), days to mid pod filling (DMF), pod length (PL), pod thickness (PT), pod width (PW), number of pods per plant (NPP), pod weight (PW), pod yield per plant (PYPP), number of seeds per pod (NSPP), 100 seed weight (100SW), seed yield per plant (SYPP), seed length (SL), seed breadth (SB), seed thickness (ST) and plant height (PH). Observations were recorded from randomly selected five plants from each genotype, as per the descriptors developed by International Centre for Tropical Agriculture (CIAT, Columbia), United States Department of Agriculture (USDA) and Protection of Plant Varieties and Farmer's Rights Authority (PPV & FRA) (Sofi, 2019).

Statistical analysis

Germplasm was evaluated in Augmented Block Design (Federer, 1956) with five standard check varieties *viz.*,

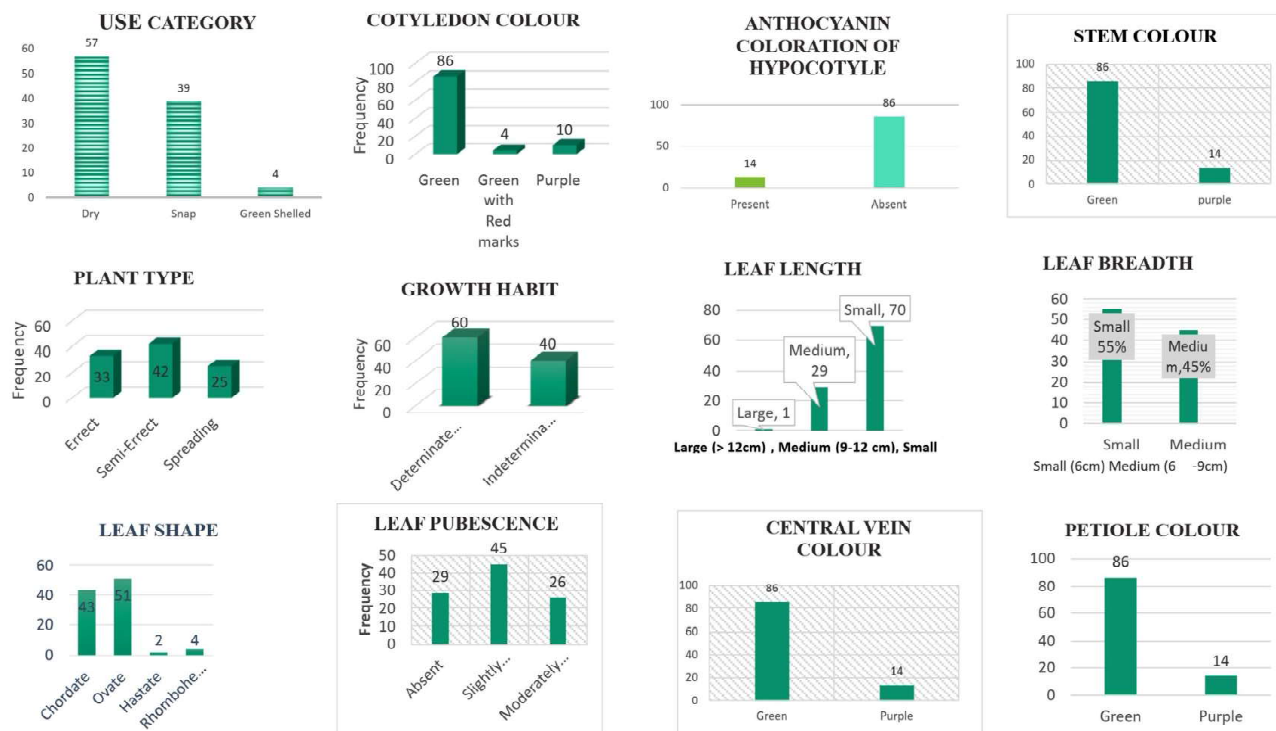


Fig. 1(a) : Frequency distributions of genotypes for qualitative traits

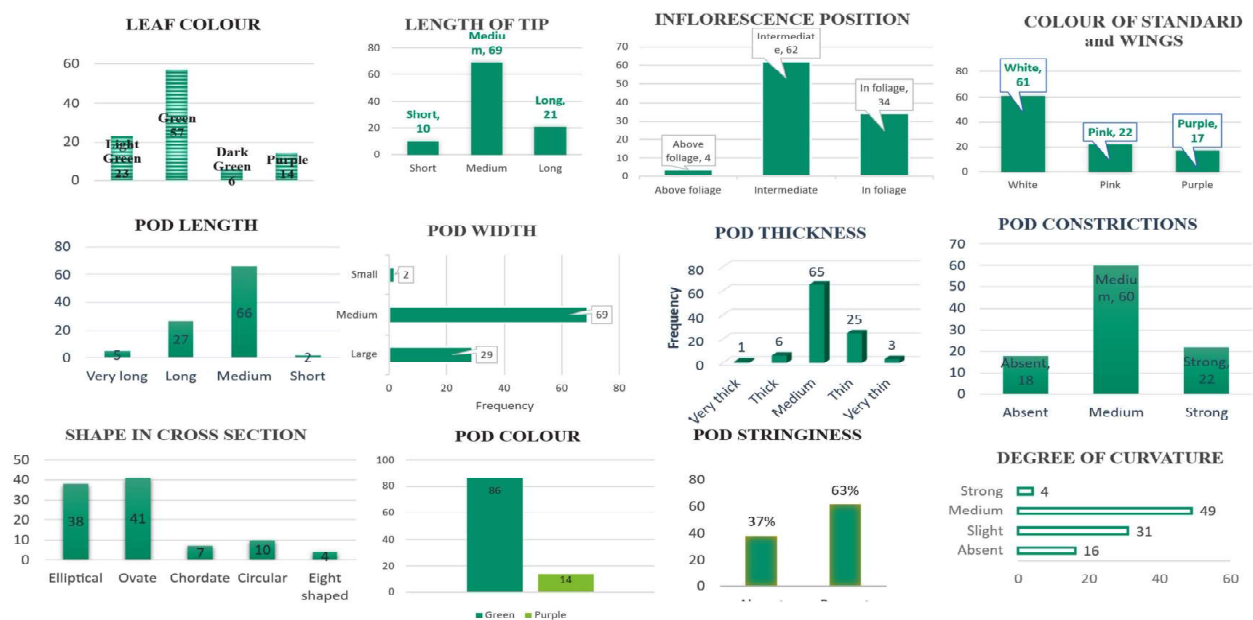


Fig.1(b) : Frequency distributions of genotypes for qualitative traits

Shalimar French Bean-1, Shalimar Rajmash-1, Arka Komal, Arka Sharath and Arka Anoop in 5 blocks. Frequency distribution graphs were obtained for all the qualitative traits. The analysis of variance, variability parameters, Pearson's correlation coefficients and principal component analysis were estimated using R-Studio software.

RESULTS AND DISCUSSION

Frequency distribution for qualitative traits

All qualitative traits exhibited considerable variability among the 100 common bean genotypes evaluated (Fig. 1). Pulse type genotypes predominated (57%), followed by snap (39%) and green-shelled types (4%).



Fig.1(c) : Frequency distributions of genotypes for qualitative traits

Green cotyledons (86%) and green hypocotyls (86%) were most common, while, anthocyanin pigmentation occurred in 14% of genotypes. Semi-erect (42%) and erect (33%) growth habits predominated, whereas 25% were spreading. Determinate growth habit was observed in 60% of genotypes and indeterminate climbing habit in 40%. Most locally collected lines were indeterminate climbers, while accessions from national and international gene banks were mainly determinate bush types. This reflects adaptation to local intercropping systems with maize and other crops in Jammu and Kashmir, whereas bush types are preferred in monocropping systems (Rana et al., 2015). Similar observations were reported by Sofi et al. (2011) and Jan et al. (2021). Determinate types are generally preferred because of their early maturity and ease of handling (Jan et al., 2021; Rana et al., 2015).

Most genotypes had small to medium leaves, with ovate (51%) and chordate (43%) leaf shapes predominating. Leaves were mainly green (57%), with varying degrees of pubescence. Green central veins and petioles were recorded in 86% of genotypes. The observed variation in leaf morphology may reflect differences in photosynthetic efficiency among genotypes (Jan et al., 2021). Intermediate inflorescence position was most frequent (62%), with regard to colour, white flowers predominated for both standard and wing colour (61%), followed by pink and purple.

Most genotypes exhibited medium pod length, width, thickness, constriction, and curvature. Ovate (41%) and elliptical (38%) pod cross-sections were

predominant, while green pod colour was observed in 86% of genotypes. Strings were present in 63% of pods, secondary colour was absent in 90%, and concave pod shape relative to the suture occurred in 76%. Pod texture was mainly rough (48%) or smooth (40%), and medium beak length and curvature were most common as also reported by Ganie & Wani (2022).

Kidney-shaped seeds predominated (46%), followed by cylindrical, circular, cuboidal, and oval types, corroborating earlier reports (Jan et al., 2021; Pramanik et al., 2022). Most genotypes possessed medium seed size, length, and width. Seed coat colour showed wide variation, with brown (32%), white (25%), and red (22%) being most common, reflecting the broad genetic base of common bean (Pramanik et al., 2022). Seed coat patterns were present in only 9% of genotypes, while 91% exhibited uniform seed colour.

Variability parameters for quantitative traits

Mean values for days to 50% flowering, days to pod initiation, and days to mid pod filling were 50.61, 61.29, and 74.07 days, respectively (Table 2). Genotypes SK-B-21 and SK-B-25 were late flowering, whereas SK-B-38, SK-FB-13, and SK-B-4 were the earliest. The highest values for days to pod initiation and mid pod filling were recorded in SK-B-21 and SK-B-10, respectively, while SK-FB-5 and SK-S-3 exhibited the lowest values for these traits.

Table 2 : Genetic variability parameters in common bean

Trait	Mean±SE	Range	PCV	GCV	H ²	GAM
DFF	50.61±0.34	43.35-58.67	6.62	6.55	97.83	13.37
DPI	61.29±0.34	55.80-69.12	5.48	5.26	92.34	10.43
DMF	74.07±0.36	66.25-83.77	4.89	4.03	67.92	6.86
PL	11.57±0.17	7.62-17.44	14.27	12.96	82.39	24.26
PT	10.50±0.11	6.45-13.66	10.54	10.11	92.11	20.02
PW (mm)	13.07±0.14	9.42-16.30	10.76	10.62	97.43	21.64
NPP	13.82±0.26	7.90-20.87	20.11	19.08	90.07	37.36
PW (g)	6.55±0.12	3.02-10.19	18.56	18	94.09	36.02
PYPP	89.95±2.22	38.18-154.91	25.92	24.88	92.13	49.27
NSPP	4.94±0.08	3.01-7.61	15.47	14.14	83.94	26.79
100SW	33.29±0.86	17.65-59.35	25.98	25.89	99.3	53.22
SYPP	22.65±0.73	8.12-43.72	32.87	32.49	97.73	66.27
SL	17.02±0.22	10.67-22.42	12.33	12	94.76	24.1
SB	11.66±0.10	9.45-15.43	8.03	7.14	78.94	13.08
ST	9.96±0.07	8.21-12.24	7.28	6.74	85.67	12.87
PH	88.57±5.36	37.14-174.83	61.32	61.3	99.96	126.44

DFF: days to 50% flowering; DPI: days to pod initiation; DMF: days to mid pod filling; PL: pod length; PT: pod thickness; PW: pod width; NPP: number of pods per plant; PW: pod weight; PYP: pod yield per plant; NSPP: number of seeds per pod; 100SW: hundred seed weight; SYPP: seed yield per plant; SL: seed length; SB: seed breadth; ST: seed thickness; PH: plant height

The mean values for pod length, pod thickness, pod width, number of pods per plant, and pod weight were 11.57 cm, 10.50 mm, 13.07 mm, 13.82, and 6.55 g, respectively. Pod length was highest in SK-FB-25, pod thickness in SK-FB-30, pod width in SK-B-48, number of pods per plant in SK-B-10, and pod weight in SK-B-27. Mean pod yield per plant, number of seeds per pod, 100 seed weight, and seed yield per plant were 89.95 g, 4.94, 33.29 g, and 22.65 g, respectively. Maximum pod yield was recorded in SK-B-10, whereas SK-FB-35 exhibited the highest number of seeds per pod. The highest 100 seed weight was observed in SK-B-36, while the highest seed yield per plant was recorded in SK-B-49. Mean seed length, breadth, and thickness were 17.02, 11.66, and 9.96 mm, respectively. Plant height averaged 88.57 cm and ranged from 37.14 to 174.83 cm, clearly distinguishing bush and pole growth types. The tallest plants were observed in SK-FB-3, SK-B-11, and SK-B-10. Similar wide variability for morphological, maturity, and yield traits has been reported by Pramanik et al. (2022) and Pedro et al. (2023).

Phenotypic coefficients of variation (PCV) were slightly higher than genotypic coefficients of variation

(GCV), indicating a minor environmental influence on trait expression. The highest PCV and GCV were recorded for plant height, seed yield per plant, 100 seed weight, and pod yield per plant, indicating substantial genetic variability.

Broad-sense heritability was high for all traits, suggesting a predominant genetic control and reliability of phenotypic selection. High heritability coupled with high genetic advance as per cent mean was observed for all traits except days to 50% flowering, days to pod initiation, days to mid pod filling, seed breadth, and seed thickness, indicating the predominance of additive gene action and the potential for effective selection and yield improvement. Jhanavi et al. (2018), and Murry et al. (2022) also reported similar results.

Correlation studies

Pod yield per plant exhibited significant positive correlations with days to 50% flowering, pod width, number of pods per plant, pod weight, seed yield per plant, 100 seed weight, seed length, and plant height, indicating that improvement in pod yield could be achieved through direct selection for these traits

Table 3 : Estimates of genotypic correlation coefficients among different characters in common bean

Trait	DFF	DPI	DMF	PL (cm)	PT (mm)	PW (mm)	NPP	PW (g)	PYPP (g)	NSPP	100 SW (g)	SYPP	SL (mm)	SB (mm)	ST (mm)	PH (cm)
DFF	1	0.96***	0.78**	-0.17	-0.16	0.06	0.36**	-0.05	0.22**	-0.01	0.04	0.24*	0.01	0.14	0.01	0.67***
DPI		1	0.82**	-0.12	-0.14	0.02	0.31**	-0.08	0.16	-0.01	0.01	0.20*	0	0.12	0	0.66***
DMF			1	-0.08	-0.1	0.02	0.14	0.09	0.02	0.04	0.02	0.13	-0.02	0.20*	0.02	0.54***
PL (cm)				1	0.83***	0.22*	-0.31**	0.19	-0.05	0.11	0.06	-0.19	0.03	-0.14	0	-0.21*
PT (mm)					1	0.43***	-0.13	0.22*	0.09	0.05	0.11	0	0.13	0.05	0.15	-0.22*
PW (mm)						1	0.22*	0.36***	0.40**	-0.13	0.38**	0.34***	0.12	0.04	0.15	-0.08
NPP							1	0	0.73***	-0.17	0.21*	0.67***	0.16	0.11	0.1	0.39***
PW (g)								1	0.64***	0.05	0.30**	0.21*	0.19	0.11	0.21*	-0.06
PYPP (g)									1	-0.12	0.34***	0.62***	0.24*	0.12	0.17	0.24*
NSPP										1	-0.27**	0.16	-0.26**	-0.16	-0.13	-0.02
100 SW (g)											1	0.69***	0.54***	0.50***	0.46***	-0.05
SYPP												1	0.32**	0.30**	0.31**	0.20*
SL (mm)													1	0.46***	0.35**	-0.14
SB (mm)														1	0.60**	0.04
ST (mm)															1	0.03
PH (cm)																1

ns $p \geq 0.05$, * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$. DFF: days to 50% flowering; DPI: days to pod initiation; DMF: days to mid pod filling; PL: pod length; PT: pod thickness; PW: pod width; NPP: number of pods per plant; PW: pod weight; PYP: pod yield per plant; NSPP: number of seeds per pod; 100SW: hundred seed weight; SYPP: seed yield per plant; SL: seed length; SB: seed breadth; ST: seed thickness; PH: plant height

(Table 3; Fig. 2). In contrast, pod length and number of seeds per pod showed negative but non-significant associations with pod yield, suggesting limited usefulness for indirect selection. Similar positive associations of pod yield with yield-contributing traits have been reported by Shah et al. (2021) for pod thickness, number of pods per plant, and pod weight, Murry et al. (2022) for number of pods per plant, pod length, average pod weight, and 100 seed weight and Fatema et al. (2023) for number of pods per plant, pod length, and number of seeds per pod.

Seed yield per plant showed significant positive associations with seed length, seed breadth, seed thickness, pod width, pod weight, plant height, days to 50% flowering, days to pod initiation, number of pods per plant, pod yield per plant, and 100 seed weight, whereas its association with pod length was negative and non-significant. These results suggest that selection based on these positively associated traits can effectively enhance seed yield.

Principal component analysis (PCA)

Sixteen correlated traits were grouped into five independent principal components with eigen values greater than one, collectively explaining 76.26% of the total variation (Table 4). PC1 accounted for 25.85% of the total variation and was mainly influenced by seed yield per plant, number of pods per plant, days to 50% flowering, and pod yield per plant, indicating

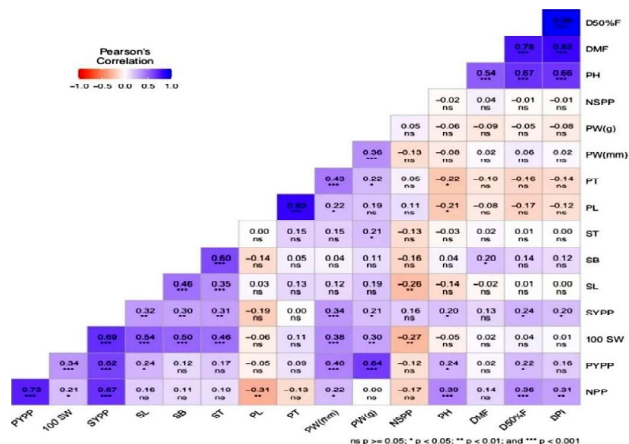


Fig. 2 : Pearson's correlation among different traits of common bean

their major contribution to genetic diversity. PC2 accounted for 20.64% of variation mainly contributed by days to pod initiation, days to 50% flowering, plant height, 100 seed weight, pod weight, and seed length. PC3 contributed 12.33% of the total variance and was mainly represented by pod length, pod thickness, and pod width. PC4 explained 10.57% of the variation, with major contributions from seed breadth, seed thickness, number of pods per plant, and pod yield per plant, whereas PC5 accounted for 6.87% of the variance and was largely influenced by number of seeds per pod and seed yield per plant (Table 5). Sofi et al. (2023), and Reddy et al. (2024) also reported similar results.

Table 4 : Eigen values and variation accounted by first five PCA for traits in common bean

Principal component	Eigen value	Variance (%)	Cumulative variance (%)
PC 1	4.13	25.85	25.85
PC 2	3.3	20.64	46.49
PC 3	1.97	12.33	58.82
PC 4	1.69	10.57	69.39
PC 5	1.09	6.87	76.26

Table 5 : Contribution of traits towards each PC's in common bean

Character	PC1	PC2	PC3	PC4	PC5
DFF	11.23	10.80	3.25	1.72	0.16
DPI	10.06	11.62	4.10	2.84	0.16
DMF	6.79	9.74	3.93	7.68	0.24
PL (cm)	1.48	3.98	30.22	3.40	0.20
PT (mm)	0.10	8.37	26.02	3.06	0.33
PW (mm)	2.87	6.42	8.97	1.64	4.54
NPP	11.85	0.03	0.83	14.35	2.03
PW (g)	1.80	7.63	4.41	3.46	1.56
PYPP (g)	11.21	3.12	0.92	17.31	0.44
NSPP	0.70	0.66	3.77	1.72	72.67
100SW (g)	8.14	9.43	2.42	1.89	0.04
SYPP (g)	13.59	2.38	0.50	4.54	10.20
SL (mm)	3.71	7.01	2.81	6.51	1.05
SB (mm)	5.49	2.51	4.82	18.71	2.70
ST (mm)	3.77	5.85	2.02	10.93	3.49
PH (cm)	7.16	10.40	0.95	0.18	0.15

The GT biplot based on PC1 and PC2 revealed trait associations and genotype profiles (Fig. 3). Pod yield per plant, seed yield per plant, number of pods per plant, 100 seed weight, seed dimensions, pod width, and pod weight were positively associated, whereas plant height, days to 50% flowering, days to pod initiation, and days to mid pod filling formed another positively associated group. Pod yield per plant was negatively associated with number of seeds per pod. Traits such as 100 seed weight, pod yield per plant, seed yield per plant, number of pods per plant, days to 50% flowering, days to pod initiation, plant height, and days to mid pod filling exhibited longer vectors, indicating the presence of substantial variation of these traits across hundred common bean genotypes, while traits located near the origin such as number of seeds per pod, pod length, pod thickness, pod width, seed thickness, seed breadth, seed length and pod weight

had little influence on the variation, which indicated that variation of these traits across genotypes is small, which is due to weak or lack of correlation with other traits. The results were supported by Shama et al. (2019) and Ummayah et al. (2022).

Genotypes positioned close to each other and overlapping on the biplot showed similar characteristics, whereas those far apart from each other and those found distantly far from the origin were genetically diverse. The genotype SK-B-48, SK-B-45, SK-FB-29 and SK-B-10 were realized to have diverged greatly from the other genotypes. The genotypic profiles in biplot revealed that genotype SK-B-36, SK-B-42, SK-B-54, SK-B-49, SK-B-27 and SK-B-10 were superior collectively for pod yield and its attributing traits among all the genotypes studied. These germplasm lines may be employed as a donor for associated traits.

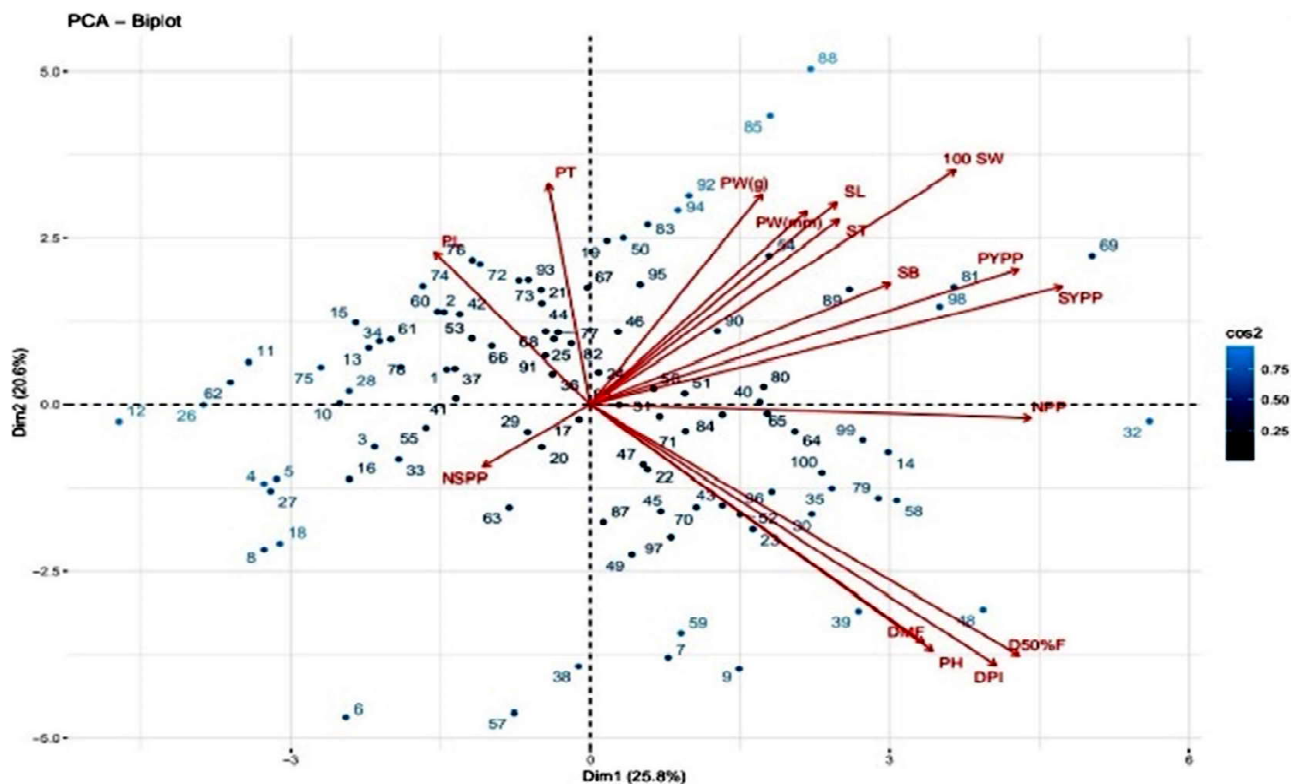


Fig. 3 : Biplot showing the distribution of genotypes and contribution of all the characters in first two PCs

CONCLUSION

The present study identified genetic variability among common bean genotypes, providing valuable opportunities for selection and genetic improvement. Based on correlation analysis, traits such as pod weight, pod width, number of pods per plant, 100 seed weight, seed length, plant height, and days to 50% flowering may be used as effective selection criteria for improving pod yield, while, seed dimensions, pod traits, plant height, number of pods per plant and 100 seed weight may be targeted for enhancing seed yield. Principal component analysis revealed that seed yield per plant, number of pods per plant, days to 50% flowering, and pod yield per plant contributed most to genetic divergence. Genotypes SK-B-36, SK-B-42, SK-B-54, SK-B-49, SK-B-27, and SK-B-10 are recommended as promising donor parents for yield owing to their superior performance for pod yield and related traits.

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