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Targeted genotype identification through D square and genetic modeling in Adzuki bean germplasm

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Abstract

In the present investigation twenty five genotypes of adzuki bean (*Vigna angularis var. angularis*) along with two check varieties (HPU-51 and TOTRU LOCAL) were assessed at the Genetics and Plant Breeding Research Block, College of Hill Agriculture, Chirbatiya campus Ranichauri, Tehri Garhwal, V.C.S.G. Uttarakhand University of Horticulture and Forestry, Bharsar in Augmented Block Design (ABD) during *Kharif*, 2024. Nine quantitative characters were studied to estimate the genetic variability, genetic components (variance, coefficient of variation, heritability, genetic advance and genetic advance as percent of mean), genetic divergence, extent of association and direct and indirect effects of the characters on yield and its component traits. The analysis of variance indicated the existence of sufficient amount of variability among genotypes for all the characters studied. The PCV was slightly higher than the GCV for all the traits studied indicating that they all interacted with the environment to some extent. Maximum GCV and PCV was observed in 100 seed weight followed by number of pods per plant, plant height and leaf width. High heritability coupled with high genetic advance was observed in plant height, indicating the character could be prominently governed by additive gene action. Mahalanobis D^2 analysis grouped genotypes into five clusters. Among the five clusters, Cluster I was the large and carried 7 genotypes, Whereas, maximum inter-cluster distance was observed between Clusters II and IV, indicating substantial diversity among the genotypes. Correlation studied seed yield per plant showed significant positive association with pod length, and leaf width indicating their major contribution to yield improvement. Principal component analysis (PCA) revealed that the first four principal components with eigenvalue greater than one, indicating that they are the most significant contributors to the total variability among the studied traits.

Keywords: Adzuki bean, Correlation, Genetic divergence, Genetic variability, Heritability, Mahalanobis D^2, Path coefficient

Introduction

Adzuki bean (*Vigna angularis var.angularis*) is an annual, diploid grain legume with diploid chromosome number 2n = 2x = 22 and belonging to the family Fabaceae (Leguminosae). It is predominantly self-pollinated and possesses a relatively small genome of approximately 538 Mb, making it an important genetic resource among Asian *Vigna* species [1]. Commonly referred to as azuki bean, red bean or lalchori, adzuki bean plays a vital role in food and nutritional security, particularly in East Asia. The crop is believed to have originated from wild relatives near the Himalayas, spreading naturally into East Asia where it was domesticated, likely in China or Japan around 12,000 years ago and subsequently spread to Korea, Taiwan, Nepal, Bhutan and parts of India [2]. Presently, major cultivation of adzuki bean is concentrated in northern and northeastern China and the middle and lower reaches of the Yellow and Yangtze River basins. Wild forms related to domesticated adzuki bean are distributed across parts of southern China, Bhutan, Nepal, and the Indian Himalayas. In India, the crop is cultivated in the northeastern hill region, including Arunachal Pradesh, where it is grown as a pulse crop [3].

Botanically, adzuki bean belongs to the tribe Phaseoleae, which includes economically important grain legumes such as soybean, mung bean, black gram and cowpea [4]. Within the genus *Vigna*, it is classified under the subgenus *Ceratotropis*, along with mung bean (*V. radiata*) and black gram (*V. mungo*), highlighting its close genetic affinity with other important Asian pulses [5, 6]. Owing to its ability to fix atmospheric nitrogen and its adaptability to diverse agro-ecological conditions, adzuki bean contributes to sustainable cropping systems, particularly in rainfed and hill agriculture.

In cultivation, adzuki bean performs well in well-drained loamy soils with a pH range of 5.5-7.5. The crop requires annual rainfall of 500-1750 mm and grows optimally at temperatures of 18-23 °C, while germination occurs at soil temperatures above 10-13 °C. Recommended agronomic practices include sowing depths of 2-4 cm, row spacing of 30-75 cm and seed rates ranging from 8-70 kg/ha [7]. Morphologically, the crop is an erect, bushy annual vine, generally attaining a height of 30-40 cm, with trifoliate leaves and determinate growth habit. Considerable phenotypic variation exists in seed coat colour, ranging from red and wine red to black, white, grey, mottled and speckled forms [8].

The seed coat of adzuki bean is relatively hard due to the presence of polyphenols and suberin in the palisade layer, which reduces water permeability and may adversely affect

germination in certain genotypes [9, 10, 11]. Nevertheless, the crop exhibits superior tolerance to moisture stress and performs well under rainfed conditions when compared to several other pulse crops [12]. These adaptive traits make adzuki bean a promising pulse for marginal environments.

From a nutritional standpoint, adzuki bean seeds contain 20-25% protein, approximately 59.5% carbohydrates, dietary fibre, essential amino acids, B-complex vitamins and important minerals such as iron, calcium, phosphorus and potassium [13, 14]. The crop is naturally gluten-free and is consumed both as whole seeds and sprouts. The presence of bioactive compounds such as polyphenols imparts antioxidant, antihypertensive and antidiabetic properties, thereby enhancing its functional food value [15]. Its balanced amino acid profile complements cereal-based diets, particularly in developing regions.

Globally, adzuki bean is cultivated for food, fodder and green manure. China, Japan and Russia countries are the principal producers, with China accounting for the largest share of global production. In 2019, world production of adzuki bean was estimated at approximately 1.25 million metric tons [16]. In India, adzuki bean is cultivated on a limited scale, mainly in mid-hill and northeastern regions such as Himachal Pradesh and Uttarakhand, where it forms part of traditional rainfed cropping systems [17, 18]. Its resilience to biotic and abiotic stresses further enhances its suitability for hill agriculture.

Domestication from its wild progenitor (*Vigna angularis* var. *nipponensis*) has resulted in substantial changes, including increased seed and pod size, non-twining growth habit, loss of seed dormancy and enhanced phenotypic diversity [9]. Genetic variability and diversity among adzuki bean germplasm are therefore critical for crop improvement programmes aimed at enhancing yield, adaptability and nutritional quality. Assessment of genetic variability, heritability, correlation and path coefficient analysis provides valuable information on the inheritance of yield and its component traits and assists in formulating effective selection strategies [19]. Hence, systematic evaluation of adzuki bean germplasm is essential for identifying superior genotypes and improving productivity under diverse agro-climatic conditions.

Given these perspectives, the present study was conducted to assess the extent of agro morphological variability, correlation and path relationships, and genetic divergence among the adzuki bean genotypes. The outcomes are expected to assist in identifying promising genotypes and trait associations for genetic enhancement of adzuki bean under mid- to high-altitude hill farming conditions.

Materials and Methods

The experiment was conducted during *kharif* season, 2024-25. Experimental field was situated at Genetics and Plant Breeding Research Block, College of Hill Agriculture, Chirbatiya Ranichauri, Tehri Garhwal, Uttarakhand, India. The altitude of the experimental field was about 2100 meter above from sea level. The site of experiment lay between 30º15 N latitude and 78º30 E longitude under mid hill zones of Uttarakhand. The climate of the experimental site is humid temperate characterized by chilled winters. The soil of Genetics and Plant Breeding Research Block was silty clay loam in texture, having acidic pH, EC with good fertility level. The data presenting the chemical properties of the soil of the experimental plot is mentioned in Table 1.The source of the experimental materials, 25 cultivated Adzuki bean (*Vigna angularis* L.) germplasm including two check varieties (TOTRU Local and HPU–51) seed materials were collected from NBPGR Shimla and laid out in Augmented Block Design (ABD) with the support of Indian Council of Agricultural Research (ICAR), All India Coordinated Research Network on Potential Crops. The details of the germplasm are presented in Table 2. At the time of harvest, growth and developmental parameters such as field emergence, days to 50% flowering, leaf length (cm), leaf width (cm), plant height (cm) were studied. Yield and yield attributing characters such as number of pods per plant, pod length (cm), number of seeds per pods, weight of 100 seeds (g) was taken into account. Standard methodology was applied and observations were recorded from 5 plants of each replication for each germplasm.

Data collection and analysis: The data collected were subjected to statistical analysis for genetic variability parameters including genotypic, phenotypic and environment variances calculated [20], coefficients of variation (GCV, PCV and ECV) [21], heritability (broad sense) [22], and genetic advance [23]. Correlation coefficients and path coefficient analysis were also conducted to determine the interrelationship among traits and their direct and indirect effects on seed yield. Further, Mahalanobis' D^2 statistics were applied for assessing genetic divergence among the germplasm and grouping them into clusters using Tocher's method [24, 25]. The experimental data obtained during the course of investigation was analyzed using AGRISTAT software, developed by Dr. N. Manivannan, TNAU, for the Augmented Block Design in field conditions (CD at 5% level of significance) and OPSTAT software, developed and maintained by Prof. O.P. Sheoran, Department of Mathematics and Statistics, CCS HAU, Hisar, for CRD-based laboratory data (CD at 1% level of significance).

Result and Discussion

Analysis of Variance (ANOVA)

Most of the plant breeders considered yield and other yield contributing characteristics as highly important crop improvement criteria [26]. In this study, yield and yield-contributing characters of 25 genotypes and 2 check varieties of Adzuki bean (Table 3) were studied to figure out how traits are inherited down over the generations and which genotypes are the best. The results based on mean sum of squares revealed that the block effects exhibited highly significant variation for all the traits under study. Similarly, the treatment effects also showed highly significant differences across all the genotypes for each character evaluated, indicating substantial genetic variability. The check entries displayed highly significant variation for all characters except for days to maturity, which showed a non-significant mean square value (2.49). The test entries demonstrated highly significant differences for all the traits, suggesting notable variability among the test genotypes.

Cluster composition based on D^2 Analysis

The analysis of genetic divergence in this study was performed by employing Mahalanobis D^2 statistics described by [25]. The 25 adzuki bean genotypes along with 2 check varieties were grouped into five distinct clusters based on Mahalanobis D^2 analysis (Table 4), indicating substantial genetic diversity. Cluster I was the largest, comprising seven genotypes followed by Clusters II (6 genotypes), IV and V (5 genotypes each), while Cluster III contained the fewest, that is only 4 genotypes. Both check varieties (HPU–51 and TOTRU LOCAL) were placed in Cluster I, suggesting similarity with respect to the traits studied. The observed clustering pattern reflects genetic divergence that can be exploited for selecting diverse parents in adzuki bean improvement programmes.

Similar clustering patterns have been reported earlier in adzuki bean and other legumes. [27], identified multiple accession groups based on phenological and yield traits, while [28] reported three to five major clusters reflecting genetic background, geographic origin and trait-specific variation. Comparable results using D^2 analysis have also been documented in french bean, mung bean and related legumes [29, 30, 31, 32, 33], mungbean [34] common bean [35], French bean [36], supporting the robustness of cluster analysis for assessing genetic diversity.

Inter and Intra cluster distances and Cluster means

The basic theme behind formation of clusters is to get the intra and inter cluster distances. These distances are used as index for parents with diverse origin. The intra and inter cluster values are means derived from D^2 values of cluster elements [37]. The highest

inter-cluster (Table 5) distance was observed between clusters II and IV (3.744), followed by clusters II-V (3.554), I-III (3.521) and III-IV (3.498), indicating substantial genetic divergence among these groups. The lowest inter-cluster distance was observed between clusters I and IV (2.635), suggesting a closer genetic relationship, while distances among clusters I-II (2.845) and I-V (3.084) were also comparatively low. Moderate divergence was recorded among the remaining cluster combinations. Among intra-cluster distances, cluster V exhibited the highest variability, followed by clusters IV and I, whereas cluster II (1.706) showed the lowest intra-cluster distance, indicating greater genetic uniformity. Overall, the D^2 analysis revealed considerable genetic variability among clusters, suggesting that hybridization between highly divergent clusters, particularly II with IV or V, may generate superior heterotic combinations. Similar wide ranges of inter-cluster distances have been reported in legumes using D^2 analysis, supporting its effectiveness for identifying genetically diverse parents in breeding programmes [30, 31, 38, 39].

The distances between two clusters are the measure of the degree of diversification. The greater the distances between two cluster the greater the divergences and lower the distances lower divergences. Large cluster distance specified that the genotypes present under these clusters have substantial genetic distance among them while lower intra-cluster distance indicates relative genetic closeness of genotypes [40].

Table 6 represents the comparison of cluster means for nine morphological traits. The results obtained from cluster means for different characters showed frequent variation present among clusters categorized according to D^2 analysis. Range of means made it conceivable to know the characters effecting divergence. The cluster mean for days to 50% flowering ranged from 58.00 days in cluster III to 67.00 days in cluster IV, indicating the relative earliness of cluster III. Mean maturity duration (DAS) varied from 105.83 days in cluster II to 113.60 days in cluster IV. The cluster mean for plant height was highest in cluster V (97.88 cm) and lowest in cluster I (67.03 cm). Mean leaf length was maximum in cluster III (10.27 cm) and minimum in cluster IV (5.84 cm). The mean number of pods per plant ranged from 13.00 in cluster I to 17.17 in cluster II. Mean pod length varied between 8.08 cm in cluster II and 9.98 cm in cluster III. The highest cluster mean for 100-seed weight was recorded in cluster V (14.15 g), while the lowest was observed in cluster II (8.14 g). The cluster mean for seed yield per plant, a key economic trait, was highest in cluster III (20.27 g) and lowest in cluster I (16.33 g), suggesting scope for yield improvement through recombination breeding.The observed results are consistent with the findings in Adzuki bean [28] and green gram [41].

Principal Component Analysis

The principal component analysis is the most frequently utilized re-justification approach for cluster analysis [26]. The objective of the principal component analysis is to determine the total variance in a collection of variables that account for the most variability in the data in a sequential manner. In general, traits are inter-correlated to various degrees, thus all of the principal components are not necessary to properly summarise the data [42]. The first vector (PC1) of any principal component analysis (PCA) explains the highest amount of the overall variation [43]. In this study, Principal component analysis (PCA) revealed that the first four principal components had eigenvalues greater than one, indicating that they are the most significant contributors to the total variability among the studied traits (Table 7). The first principal component (vector 1) accounted for 27.03% of the total variability and was mainly influenced by days to 50% flowering and days to maturity. Vector 2 contributed 19.41% to the total variance, with high positive loadings from days to 50% flowering, days to maturity, plant height, leaf length, 100-seed weight, pod length and yield per plant indicating their substantial contribution to this component. The cumulative proportion of variance explained by the first three principal components was higher than the contribution of the subsequent components, suggesting a reasonable dimensionality reduction and indicating that these components effectively summarize the variation among the traits. These findings are in agreement with the work in adzuki bean [28, 44], where the first few principal components explained a substantial proportion of the total variability and were largely influenced by phenological, yield and pod-related traits. Similar results in mungbean genotypes were found, where the first three PCs with eigenvalues greater than one explained approximately 78.80% of the total genetic variation [45]. Traits such as seed yield per plant, days to maturity, plant height and number of pods per plant contributed significantly to the initial PCs in explaining the maximum variance and paralleling in black gram [46]**.** PCA biplot (Figure 3) shows that certain accessions and characteristics could be less useful for crop development [26].

Genetic Component Analysis

Genetic variability is the base of all improvement programs. Selection can lead toimprovement incropplant only when sufficient genetic variability is present in the population. Larger variability ensures better chances of producing desired genotypes [47]. For the understanding the nature and extent of genetic variability, genotypic, phenotypic, environmental variance and genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV) and environmental coefficient of variance (ECV) were statistically computed. The results (Table 8) revealed that the estimates of phenotypic coefficient of

variation (PCV) were slightly higher than those of genotypic coefficient of variation (GCV) for all the traits studied. The extent of the environment influence on traits is explained by the magnitude of the difference between GCV and PCV. Large differences between GCV and PCV values reflect high environmental influence on the expression of traits [48, 49]. In this study,slight differences indicated minimum environmental influence and consequently greater role of genetic factors on the expression of the traits.High GCV and PCV values were observed for the traits 100 seed weight, number of pods per plant and plant height. Moderate values of GCV and PCV were observed for traits leaf width, days to 50% flowering, leaf length, pod length and yield per plant. Lowest value of GCV and PCV was observed for the trait days to maturity. The results in accordance with the findings in green gram [28, 49], adzuki bean [50] and mungbean [51].

Heritability, Genetic Advance and Genetic Advance as percent of mean

Estimation of the heritability helps in selection of desired genotypes from diverse genetic population and high heritability promotes the effective selection of a trait of interest. Heritability and the anticipated genetic advance as a percentage of the mean are directly linked to the extent of additive gene effects [23]. Heritability estimates can be divided into three categories which low heritability (5-10%), medium heritability (10-30%) and high heritability (30-60%) [52]. In this study, all the traits manifested high heritability estimates (Table 8) according to dabholkar classification, as it ranged from 69.42% recorded in the trait yield per plant to 99.06% in the trait days to 50% flowering**.** These results are in accordance to the findings of high heritability for all traits except plant height in adzuki bean [53] and documented high heritability estimates for phenological traits, seed weight, and yield-related characters in adzuki bean germplasm [28].

Genetic advance (GA) and genetic advance as percent of mean (GA%) provide additional insight into the genetic potential for improvement through selection and it is also a valuable indicator of the progress that could be achieved as a result of selecting the relevant population [54]. Genetic advance estimates can be divided into three classes such as high (>20%), moderate (10-20%) and low (<10%) [55]. In this study, moderate genetic advance as percent of mean was recorded in the trait 100 seed weight**,** plant height, no. of pods per plant, leaf width**,** days to 50% flowering and pod length. Moderate GAM indicates moderate action of both additive and non-additive genes on the control of those characteristics. While the lowest value of GAM was observed in the traits, yield per plant and days to maturity, suggesting limited progress through selection for this trait**.** The genetic advance for flowering and seed traits attributing them to additive gene action observed in adzuki bean [28]. High

heritability and genetic advance for quantitative traits including seed yield and related characters reported in cowpea [56]**.**

High heritability alone does not always imply effective selection, especially when estimated in the broad sense, as it includes both additive (fixable) and non-additive (non-fixable) genetic variances [23, 57]. Among all the characters studied, only plant height exhibited both high heritability and high genetic advance as a percentage of mean, indicating that this trait is primarily governed by additive gene action. Therefore, plant height can be considered a reliable selection criterion for genetic improvement in adzuki bean. Such interpretations are consistent with broader findings in legume breeding, where coupling high heritability (>70%) with substantial genetic advance (>30% of the mean) confirms additive gene control and predictive selection gains [23, 58].

Correlation Coefficient and Path coefficient Analysis

Grain yield, being a complex trait governed by multiple component characters, is often influenced by their cumulative effects. Therefore, correlation analysis has been used to determine the type and magnitude of association between a pair of characters. These associations provide a better understanding of the contribution of one trait in building up the genetic makeup of the other traits of a crop which in turn is helpful in deciding the parameters for selection, so that improvement in the associated characters can be done [59]. In this study, correlation analysis among quantitative traits (Table 9) revealed that seed yield per plant had a highly significant positive association with pod length (0.648**) and a significantly positive association with leaf width (0.379*). Leaf length showed highly significant positive correlation with leaf width (0.733*) and pod length was also significantly and positively correlated with 100-seed weight (0.345*). Plant height (0.137) and days to 50% flowering (0.154) exhibited positive but non-significant correlations with seed yield per plant. Whereas days to maturity (–0.047) showed a non-significant negative association with yield and leaf width was significantly and positively correlated with the number of pods per plant (0.459*). Overall, pod length, leaf length and leaf width emerged as key yield-associated traits and may serve as effective selection criteria for adzuki bean improvement programs. Therefore, path coefficient is quite helpful in determining the relative importance of direct and indirect influence of each component trait [60, 61, 62]. In this study, among the traits studied, pod length exhibited the highest positive direct effect (0.765) on grain yield (Table 10)**,** followed by days to 50% flowering (0.258)**,** number of pods per plant (0.255)**,** plant height (0.160) and leaf width (0.136)**,** indicating their major contribution to yield improvement. In contrast, days to maturity (-0.038), leaf length (-0.052) and 100-seed weight (-0.250) showed negative direct

effects on grain yield, suggesting a limited direct role of these traits in yield enhancement. The residual effect (0.336) indicated that most of the variability in grain yield was adequately explained by the characters included in the path analysis [63]. Among the traits, trait leaf width showed positive and significant (0.379*) and pod length showed positive and highly significant (0.648**) genotypic correlations with yield per plant. All other traits showed non-significant genotypic correlations yet their indirect effects through key yield-determining characters were substantial. Days to flowering contributed to yield mainly through indirect effects *via* leaf length (0.0038) and days to maturity contributed indirectly *via* days to 50% flowering (0.0061), leaf length (0.0076) and pod length (0.1154), while plant height and leaf length influenced yield indirectly primarily through days to maturity (0.0032 and 0.0055, respectively), leaf width (0.0319 and 0.0996,respectively), pod length (0.0348 and 0.2095, respectively) and number of pods per plant (0.0058 and 0.0375, respectively). Leaf width showed a significant positive association (0.379*) with yield and exerted favourable indirect effects through pod length (0.1068), pods per plant (0.1172), days to maturity (0.0091), 100 seed weight (0.0276) and plant height (0.0376), reflecting its role in assimilate production and partitioning. Pod length also exhibited a highly significant positive correlation with yield per plant (0.648**), supported by additional indirect contributions *via* plant height (0.0073) and leaf width (0.0190), confirming its central role in yield determination while the trait no. of pods per plant exhibited indirect effects on yield *via* days to maturity (0.0048), plant height (0.0036), leaf width (0.0624) and 100 seed weight (0.0456). Although 100-seed weight showed a negative and non-significant direct association with yield (-0.002), its positive indirect effects *via* pod length (0.2644), plant height (0.0434) and days to 50% flowering (0.195) suggest its supportive role in yield expression when combined with other traits. Similar results were noted in adzuki bean [62, 64, 65]. The positive correlation of seed yield with days to flowering, plant height and pods per plant was also observed in adzuki bean [64]. The characters 100 seed weight, pod length and pods per plant were showed significant correlation with yield in adzuki bean [65]. Also in adzuki bean the trait pods per plant exhibited positive direct effects on yield per plant [62]. Similar associations were observed rice bean [63, 66] and in mung bean it was noted significantly positive correlations of seed yield with pods per plant, plant height, days to 50% flowering and 100 seed weight [67]. Additionally, in urd bean significant positive correlations of seed yield with key component characters, reinforcing the importance of correlated trait selection across grain legumes [68]. In case of chickpea, grain yield has been reported to be positively associated with several yield-contributing traits observed significant positive correlations of seed yield with

biological yield, pods per plant, seeds per pod and 100-seed weight [69]. Similarly, it was reported that the significant positive associations of seed yield with biomass and pods per plant in desi chickpea, highlighting the importance of these traits in selection programmes [70].

Conclusion

The present study demonstrated substantial genetic variability among the evaluated adzuki bean germplasm, confirming the availability of exploitable genetic resources for crop improvement. High heritability coupled with comparatively higher genetic advance for plant height indicated the predominance of additive gene action, suggesting that this trait can be effectively improved through phenotypic selection. Mahalanobis D^2 analysis revealed considerable genetic divergence among the five clusters, with the greatest inter-cluster distance observed between Clusters II and IV, indicating that hybridization between these genetically distinct groups could broaden the genetic base and enhance the probability of recovering superior recombinants. Correlation and path coefficient analyses identified pod length as the most important trait associated with seed yield, owing to its strong positive correlation and highest direct effect, while leaf width also contributed positively to yield improvement. Principal component analysis further confirmed that a limited number of principal components explained most of the observed phenotypic variation, highlighting the importance of phenological and yield-related traits in discriminating among the germplasm. Collectively, these findings provide a useful framework for parent selection and trait-based breeding strategies aimed at developing high-yielding adzuki bean cultivars adapted to the temperate mid-hill environments of the north-western Himalayas. Future multi-environment evaluations will be valuable for validating the stability and wider applicability of the identified superior genotypes.

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Author contributions

Ritu Kumari Vashishtha wrote the manuscript and Dr. Pankaj Kumar contributed in writing, editing, supervision, and approved the final version of the manuscript.

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Data availability

The data that support the finding of the research study are available on reasonable request from the corresponding author. The data are not publicly available due to privacy or ethical restriction

Declarations

Competing interests

I declare that the authors have no competing interests as defined by Discover, or other interests that might be perceived to influence the results and/or discussion reported in this paper.

Ethics approval and consent to participate

All the genotypes of adzuki beans were collected and used in the research work with the permission of Principal Investigator and Co-Principal Investigator of the project of All India Coordinated Research Network on potential crops for the experiment.

Consent for publication

Not applicable.

Conflict of interest

The authors declare no competing interests.

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Table 1: Chemical properties of the soil of experimental plot

S. No.	Parameters	Value	Method Employed
1.	pH	6.38	Blackman Glass Electrode pH meter (Jackson, 1967)
2.	Organic Carbon	1.24%	Walkley and Black's method, 1934
3.	Available Nitrogen	423.36 kg/ha	Alkaline $KMnO_4$ method (Subbiah and Asija, 1956)
4.	Available Phosphorus	76.91 kg/ha	Olsen's extraction method (Olsen *et al*., 1954)
5.	Available Potassium	470.40 kg/ha	Neutral normal NH_4OAc Flame photometry method (Stanford and English, 1949)

Table 2: List of Adzuki bean Germplasm used in the investigation

Entry	Name of Germplasm	Entry	Name of germplasm
1.	IC 000293	15.	EC 340254
2.	IC 24105	15A.	HPU- 51 (C)
3.	IC 24522	15B.	TOTRU LOCAL (C)
4.	IC 108854	16.	EC 340263
5.	IC 360527	17.	EC 340265
5A.	HPU- 51 (C)	18.	EC 340267
5B.	TOTRU LOCAL (C)	19.	EC 340271
6.	IC 360533	20.	EC 340272
7.	IC 360534	20A.	TOTRU LOCAL (C)
8.	IC 618507	20B.	HPU- 51 (C)
9.	IC 000254	21.	EC 340273
10.	EC 59489	22.	EC 340275
10A.	TOTRU LOCAL (C)	23.	EC 340276
10B.	HPU- 51 (C)	24.	EC 340278
11.	EC 000249	25.	EC 340281
12.	EC 340240	25A.	TOTRU LOCAL (C)
13.	EC 000251	25B.	HPU- 51 (C)
14.	EC 340253		

Table 3: Analysis of variance for yield and yield contributing characters of 25 Adzuki bean germplasm and 2 check varieties

Source of variation	df	Days to 50% Flowering	Days to Maturity	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	No. of pods per plant	Pod length (cm)	100 seed weight (g)	Yield per plant (g)
Block	4	40.46**	16.67**	609.65**	3.72**	1.37**	6.42**	0.31**	14.33**	4.02**
Treatment	26	60.93**	24.34**	131.09**	1.07**	0.79**	5.67**	1.01**	3.62**	4.09**
Checks	1	22.50**	2.49	883.60**	0.40*	0.90**	10.02**	0.23**	3.19**	7.06**
Test Entry	24	68.53**	23.11**	205.19**	1.69**	1.03**	6.56**	1.00**	6.03**	3.91**
Check x Test	1	-82.83**	75.68**	-2399.80**	-13.11**	-5.01**	-19.93**	2.05**	-53.72**	5.41**
Error	4	0.14	1.45	0.83	0.06	0.001	0.29	0.002	0.13	0.41
Total	34	51.37	22.83	172.07	1.26	0.77	5.13	0.81	4.47	3.65

*, ** significant at 5% and 1% level, respectively

Table 4: Distribution of Adzuki bean germplasm for different cluster on Mahalanobis D^2 analysis

Clusters	No. of genotypes	Genotypes
I	7	EC000249, EC000251, EC340263, EC340267, EC340271, HPU – 51, TOTRU LOCAL
II	6	IC000293, IC24105, IC24522, IC360533, IC360534, EC59489
III	4	IC000254, EC340265, EC340272, EC340281
IV	5	IC108854, IC360527, IC618507, EC340240, EC340253
V	5	EC340254, EC340273, EC340275, EC340276, EC340278

Table 5: Average inter and intra cluster distance D^2 values for 27 Adzuki bean germplasm

Clusters	I	II	III	IV	V
I	**2.116**				
II	2.845	**1.706**			
III	3.521	3.466	**1.901**		
IV	2.635	3.744	3.498	**2.136**	
V	3.084	3.554	3.169	3.446	**2.583**

Table 6: Cluster mean for yield and its contributing characters of 27 Adzuki bean germplasm

Clusters		Days to 50% Flowering	Days to Maturity	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	No. of pods per plant	Pod length (cm)	100 seed weight (g)	Yield per plant (g)
I	Mean	61.00	111.29	67.03	8.97	6.33	13.00	8.36	11.05	16.33
	SE±	6.61	4.23	9.61	1.27	0.70	2.16	0.49	1.35	1.26
II	Mean	60.83	105.83	75.27	8.30	7.17	17.17	8.08	8.14	18.30
	SE±	6.68	3.71	7.27	0.55	0.42	0.98	0.66	1.24	1.58
III	Mean	58.00	112.50	70.05	10.27	7.90	16.25	9.98	11.35	20.27
	SE±	8.16	3.42	13.22	0.78	0.62	1.71	0.62	0.99	1.41
IV	Mean	67.00	113.60	69.80	7.52	5.84	13.60	9.86	12.13	19.02
	SE±	9.85	1.95	6.83	1.03	0.98	2.07	0.83	1.18	1.30
V	Mean	62.60	108.40	97.88	9.64	7.11	14.40	9.00	14.15	18.15
	SE±	5.81	8.42	0.67	0.96	2.70	0.70	1.93	2.28	9.79

Table 7: Principal Component Analysis (PCA) for Morphological and Yield-Related Traits in Adzuki Bean Germplasm

Characters	Vector1	Vector2	Vector3	Vector4	Vector5	Vector6	Vector7	Vector8	Vector9
Eigenvalues	2.433	1.747	1.235	1.031	0.878	0.810	0.589	0.161	0.116
Proportion	0.273	0.194	0.137	0.115	0.098	0.090	0.065	0.018	0.013
Cumulative Proportion	0.273	0.464	0.602	0.716	0.814	0.904	0.969	0.987	1.000
Variability (%)	27.03	19.41	13.68	11.51	9.73	9.03	6.51	1.79	1.29
Cumulative Variability (%)	27.03	46.44	60.12	71.63	81.37	90.40	96.91	98.70	100.00
Daysto50% Flowering	0.045	0.165	0.320	0.811	0.290	-0.275	0.012	-0.204	-0.096
DaystoMaturity	0.138	0.411	0.101	-0.411	0.243	-0.611	-0.447	0.029	0.002
Plantheight (cm)	-0.253	0.096	-0.533	0.103	0.518	0.371	-0.442	-0.147	-0.098
Leaflength(cm)	-0.488	0.005	-0.300	0.136	-0.389	-0.374	-0.030	0.183	-0.572
Leafwidth(cm)	-0.538	-0.277	-0.074	0.048	-0.038	-0.331	-0.059	-0.199	0.687
No. of pods per plant	-0.240	-0.413	0.224	-0.320	0.563	-0.137	0.374	-0.141	-0.351
Pod length (cm)	-0.347	0.475	0.293	-0.196	-0.236	0.248	0.068	-0.630	-0.106
100seedweight(g)	-0.092	0.545	-0.344	-0.007	0.222	-0.084	0.654	0.224	0.204

Table 8: Estimate of the Genetic components for yield and its contributing characters

S.No.	Characters	Mean	Variance		Coefficient of Variation (%)		Heritability (%)	Genetic Advance (GA)	GA as % of mean
			Vg	Vp	GCV (%)	PCV (%)			
1.	Days of 50% Flowering	61.93	15.20	15.34	6.30	6.33	99.06	7.99	12.91
2.	Days to Maturity	110.15	5.72	7.17	2.17	2.43	79.78	4.40	4.00
3.	Plant height (cm)	75.53	32.56	33.40	7.55	7.65	97.51	11.61	15.37
4.	Leaf length (cm)	8.87	0.25	0.31	5.66	6.31	80.48	0.93	10.47
5.	Leaf width (cm)	6.80	0.20	0.21	6.52	6.74	95.23	0.90	13.23
6.	No. of pods per plant	14.78	1.34	1.64	7.85	8.66	82.19	2.17	14.66
7.	Pod length (cm)	8.93	0.25	0.26	5.62	5.71	96.15	1.01	11.31
8.	100 seed weight (g)	11.22	0.87	1.00	8.32	8.93	86.84	1.79	15.97
9.	Yield per plant (g)	18.19	0.92	1.33	5.28	6.34	69.42	1.65	9.06

Table 9: Correlation coefficient among yield and its contributing characters in 25 germplasm and 2 check varieties

Characters	Days to 50% Flowering	Days to Maturity	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	No. of pods per plant	Pod length (cm)	100 seed weight (g)	Yield per plant (g)
Days to 50% Flowering	1.000	0.024	-0.072	-0.073	-0.065	-0.140	-0.042	0.076	0.154
Days to Maturity		1.000	-0.084	-0.145	-0.238	-0.125	0.151	0.239	-0.047
Plant height (cm)			1.000	0.234	0.235	0.023	0.045	0.271	0.137
Leaf length (cm)				1.000	0.733**	0.015	0.274	0.172	0.242
Leaf width (cm)					1.000	0.459*	0.139	-0.110	0.379*
No. of pods per plant						1.000	-0.105	-0.182	0.255
Pod length (cm)							1.000	0.345*	0.648**
100 seed weight (g)								1.000	-0.002
Yield per plant (g)									1.000

*, ** significant at 5% and 1% level, respectively

Table 10: Path coefficient analysis showing direct (diagonal) and indirect effect of different characters on seed yield of Adzuki bean

Characters	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Leaf Length (cm)	Leaf Width (cm)	No. of Pods per Plant	Pod length (cm)	100 Seed Weight (g)	Yield per Plant (g)
Days to 50% Flowering	**0.2580**	-0.0009	-0.0116	0.0038	-0.0088	-0.0358	-0.0322	-0.0189	0.154
Days to Maturity	0.0061	**-0.0383**	-0.0134	0.0076	-0.0323	-0.0319	0.1154	-0.0597	-0.047
Plant height (cm)	-0.0186	0.0032	**0.1600**	-0.0123	0.0319	0.0058	0.0348	-0.0679	0.137
Leaf length (cm)	-0.0187	0.0055	0.0375	**-0.0524**	0.0996	0.0038	0.2095	-0.0430	0.242
Leaf width (cm)	-0.0167	0.0091	0.0376	-0.0384	**0.1360**	0.1172	0.1068	0.0276	0.379*
No. of pods per plant	-0.0362	0.0048	0.0036	-0.0008	0.0624	**0.2553**	-0.0801	0.0456	0.255
Pod length (cm)	-0.0109	-0.0058	0.0073	-0.0144	0.0190	-0.0267	**0.7654**	-0.0864	0.648**
100 seed weight (g)	0.0195	-0.0091	0.0434	-0.0090	-0.0150	-0.0466	0.2644	**-0.2501**	-0.002

Residual effect = 0.336

*, ** significant at 5% and 1% level, respectively.

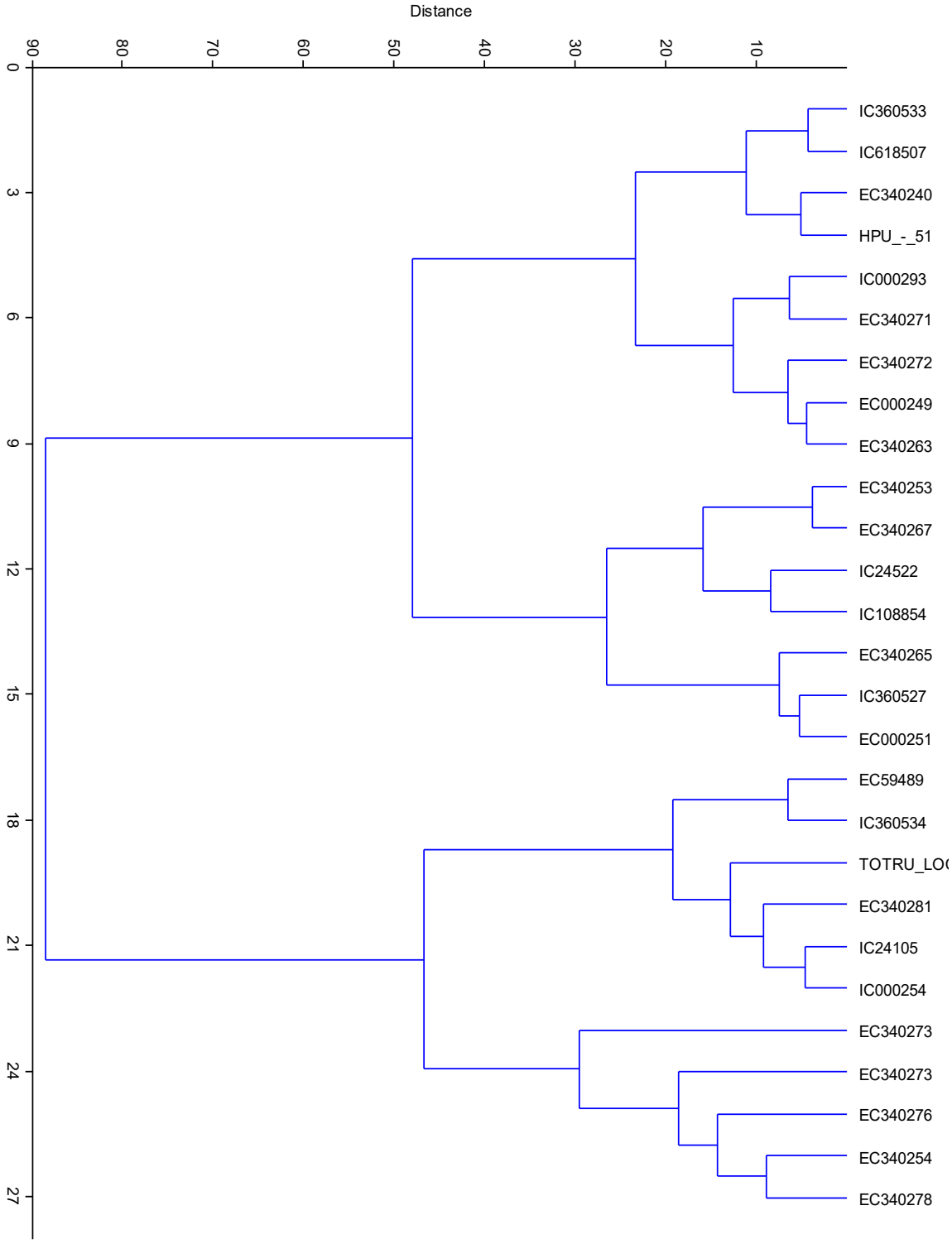


Figure 1: Dendrogram depicting cluster wise distribution of 25 Adzuki bean genotypes and 2 check varieties

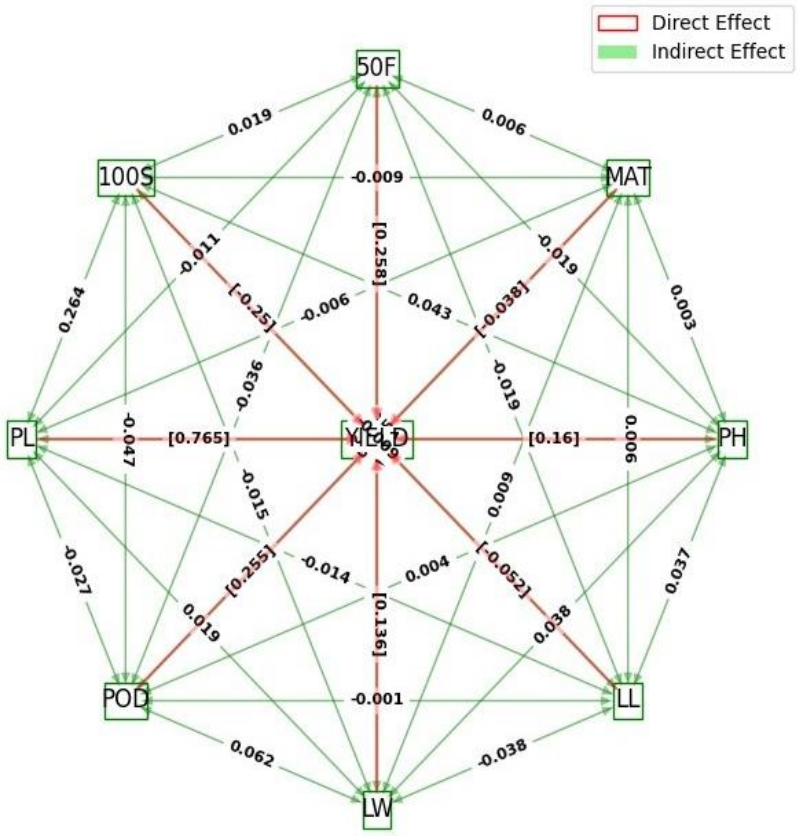


Figure 2: Path Diagram Showing Direct and Indirect Effects of Morphological and Yield-Related Traits on Seed Yield per Plant in Adzuki Bean Germplasm

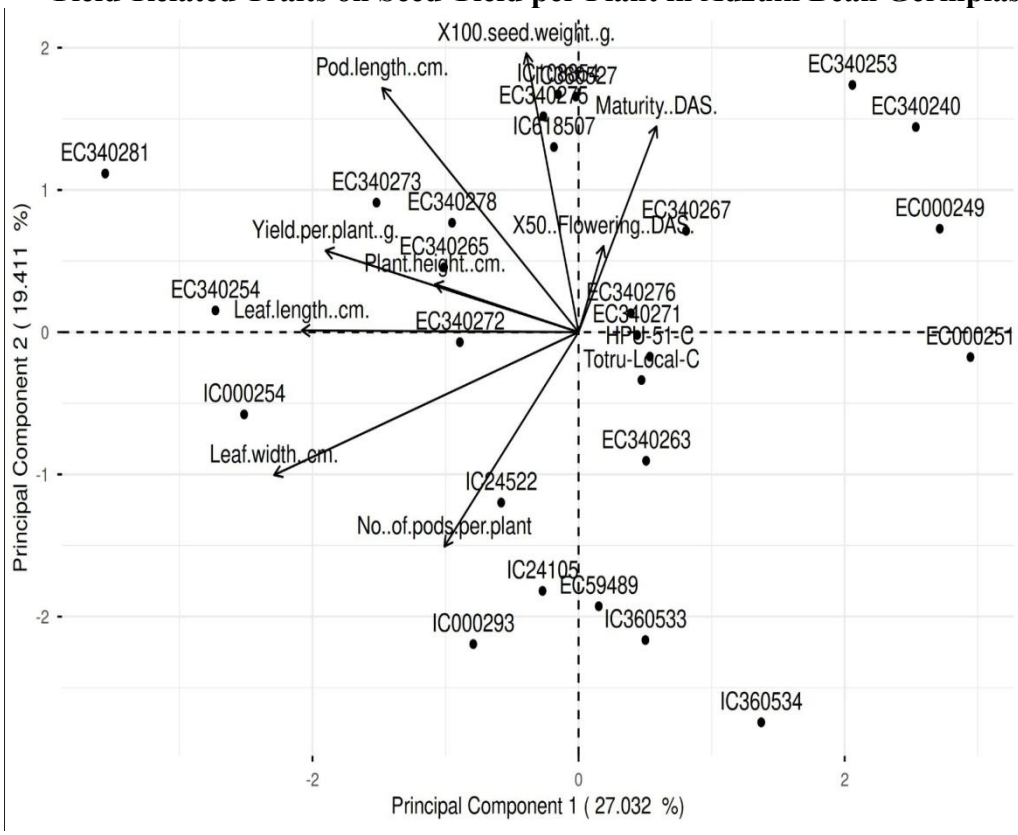


Figure 3: Principal Component Analysis (PCA) Biplot Representing the Distribution of Adzuki Bean Germplasm Based on Morphometric and Yield-Related Traits