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EXPLORING CORRELATIONS, DIVERSITY AND PRINCIPAL COMPONENT ANALYSIS OF AGRO-MORPHOLOGICAL AND SEED QUALITY TRAITS IN RAJMASH (*PHASEOLUS VULGARIS* L.)

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ABSTRACT

The study conducted during the year 2022-2023 at Dry Land Agriculture Research Station (DARS), Rangreth, Srinagar, Jammu and Kashmir, India aimed to study correlations, diversity and principal component analysis of Agro-Morphological and Seed Quality Traits in Rajmash (*Phaseolus vulgaris* L.). In this present investigation 40 genotypes including (5) checks were evaluated in Augmented block design to study variability of rajmash genotypes based on morphological traits. The analysis of variance for morphological and qualitative attributes found significant differences, providing adequate chance to select the genotypes with desired qualities. The cluster analysis for morphological, maturity, yield and quality characteristics arranged the rajmash genotypes into 3 clusters, with cluster II having the maximum number of genotypes (30), followed by III with 13 genotypes and cluster I with 2 genotypes. The inter-cluster distances were greater than the intra-cluster distances, indicating a high degree of variability among the genotypes of different cluster. The principal components formed were equal to number of characters (19). The Eigen values for different principal components were obtained through PCA and only 5 principal components were having Eigen values greater than one (>1) contributing 77.62 per cent of total cumulative percentage with component-1 having the maximum percentage of 38.52 per cent. In the present study, the viability of different genotypes were alive and can be used as planting materials for next generation. Standard germination also showed positive significant association with Tetrazolium test. Seed weight was positively correlated with all the field and seed quality parameters except for the seed breadth and germination. Vigour indices were positively correlated with standard germination, seedling length, seedling breadth, seed thickness and seedling dry weight and negatively correlated with electrical conductivity test. Dehydrogenase test showed positive correlation with all the parameters except for the seed length, breadth and thickness and seedling length.

Key words : Diversity analysis, Viability, PCA, Cluster, Electrical conductivity, Dehydrogenase.

Introduction

Common bean (*Phaseolus vulgaris* L.) a member of the *Leguminaceae* family is the most significant legume crop for direct human consumption and has a high yielding capacity as compared to gram and pea (Gulzar *et al.*, 2024). It is a short duration legume crop,

self-pollinated and diploid in nature having chromosome no. (2n=22). This is also termed as “King of Nutrition” due to its nutritional and health benefits (Vijayarani and Sabarimathi, 2021). It is an important source of protein and provides 15% of proteins and fulfills 30% of the caloric requirements of the world’s population and accounts for 50% of all the grain legumes consumed

globally (McConnel, 2010). It is a staple food crop and an essential source of protein and nutrients for millions of people worldwide (Los *et al.*, 2018). Common beans, often referred to as “Poor Man’s Meat” (Jackson *et al.*, 2020) are indeed unique from a nutraceutical perspective (Sheoran *et al.*, 2020). They provide a cost-effective source of high-quality protein, typically containing 21-25% protein content (Singh *et al.*, 2022).

Common bean is only grown as a specialty crop in Himachal Pradesh, Uttar Pradesh, Jammu & Kashmir and the North Eastern states of India. Common beans are a significant crop in Jammu and Kashmir, especially in the rainfed highlands where they are intercropped with maize on an area of about 30 thousand hectares, yielding about 17 thousand tonnes and having a productivity of about 0.56 tons ha⁻¹ (Anonymous, 2020). With an output of about 1.6 thousand tonnes and a yield of about 0.8 tons ha⁻¹, common bean is produced over an area of about 2 thousand hectares in Kashmir Valley (Saba *et al.*, 2016). According to Muthabi (2020) the average national yield in the United States is 1.98 tons ha⁻¹, which is significantly higher than that in other nations. Bean yields are affected by various biotic and abiotic factors. The common bean has been found to be extremely vulnerable to drought, especially during the flowering and grain-filling stages. According to Poleania *et al.* (2016), one abiotic factor that could result in yields dropping by 10% to 100% is drought. Bean cultivars with drought stress resistance have been produced through breeding to handle the growing challenges of climate change and to ensure food security in remote areas.

The Mahalanobis D² statistic has been widely recognized as a powerful tool for plant breeders to select suitable parental genotypes with a broader range of variability for various traits (Sinha *et al.*, 2020). The utilization of multivariate analysis tools like principal component analysis (PCA) has been found to be effective in assessing phenotypic diversity, identifying genetically distant Clusters of genotypes, and selecting key traits that contribute to overall variation in genotypes. PCA enables the natural grouping of genotypes and provides a reliable indicator of differences among them. Consequently, the primary objective of any plant breeding program is to develop improved genotypes that surpass the existing ones in terms of economic yield. Standard statistical procedures were applied to the recorded data. Genetic divergence analysis was conducted using the D² statistics introduced by Mahalanobis and described by Rao (1952) along with Principal Component Analysis (PCA).

Genetic diversity arises either due to geographical separation or due to genetic barriers to cross ability. Genetic diversity plays an important role in plant breeding because hybrids between lines of different origin generally display a greater heterosis than those between closely related strains. Genetic divergence serves as an important parameter for successful selection of parents for hybridization programme (Chandra *et al.*, 2009). The D² statistic proposed by Mahalanobis in 1936 measures the degree of diversification and determines the relative proportion of each component character to the total divergence. It measures divergence at two levels, namely, intra-cluster and inter-cluster levels, and thus helps in the selection of genetically divergent parents for exploitation in hybridization programmes. It gives a result based on magnitude of divergence and is independent of sample size. The D² technique has been used for assessing variability in various crops.

Materials and Methods

Experimental site : The current experiment was carried out during the year 2022-2023 at the Dry Land Agriculture Research Station (DARS), Rangreth for the field experiment under natural rain-fed conditions and the laboratory experiment was carried out in the laboratory of Seed Science & Technology at SKUAST-K (FOA) Wadura, Sopore, J & K, India

Materials used : In the current study, Forty rajmash genotypes were evaluated along with the five checks as follows: PPR-1, PPR-2, PPR-3, PPR-4, PPR-5, PPR-6, PPR-7, PPR-8, PPR-9, PPR-10, PPR-11, PPR-12, PPR-13, PPR-14, PPR-15, ALR-3, ALR-9, ALR-12, ALR-13, ALR-20, ALR-28, ALR-55, ALR-57, ALR-62, ALR-64, ALR-67, ALR-73, ALR-74, ALR-79, ALR-89, ALR-90, ALR-103, KDR-4, KDR-40, KDR-65, KDR-77, KDR-80, KDR-96, KDR-98, KDR-105, Shalimar Rajmash-1, Shalimar Rajmash-2, Jawala, Kailash, Baspa.

Traits under study : 10 morphological and 11 seed quality parameters studies under investigation given below:

Morphological : **DE-** Days to emergence, **DF-** Days to flowering, **DM-** Days to maturity, **PH-** Plant height, **PPP-** Pods per plant, **PW-** Pod weight, **PL-** Pod length, **SPP-** Seeds per pod, **SW-** Weight of 100 seeds, **SY-** Seed yield per plant.

Seed Quality : **SL-** Seed length, **SB-** Seed breadth, **ST-** Seed thickness, **G-** Germination percentage, **SLL-** Seedling length, **SDW-** Seedling dry weight, **VI₁-** Vigour index 1, **VI₂-** Vigour index 2, **SD-** Seed density, **EC-** Electrical conductivity, **DHY-** Dehydrogenase.

According to the procedures recommended by Baki and Anderson (1973), seedling vigour indices were estimated. Tetrazolium test was performed as per Moore (1985). According to Kittock and Law (1968), a DHA test (Dehydrogenase activity ($\text{OD g}^{-1}\text{ml}^{-1}$)) was conducted.

$$\text{Germination percentage} = \frac{\text{Number of seeds germinated}}{\text{Total number of seeds}} \times 100$$

$$\text{Vigour index 1} = \text{Standard Germination (\%)} \times \text{Seedling length (cm)}$$

$$\text{Vigour index 2} = \text{Standard Germination (\%)} \times \text{Seedling dry weight (mg)}$$

$$\text{Seed density} = \frac{\text{Weight of 100 seeds (g)}}{\text{Volume of water displaced by seed (cm}^3\text{)}}$$

Statistical analysis : Eigen values of principal components served as the basis for the selection criteria used to choose which principal components would be included in the subsequent study (Kovacic, 1994). According to Mohammadi and Prassanna (2003), it was assumed that Eigen values greater than unity suggested that the evaluated principal component weight is trustworthy. According to Rao, genotypes were grouped into various clusters based on different techniques. The procedure used in clustering of genotypes is that, any two genotypes. To test the significance of phenotypic and environmental correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1938) at $n-2$ df at two levels of probability, viz., 5% and 1%. One of the best methods for calculating the genetic distance between genotypes based on allelic frequencies at a sample of loci is the Mahalanobis (1928) D^2 statistic. For formation of clusters, the general criteria of grouping as suggested by Tocher were followed in the present study (Rao, 1952). Furthermore, genetic divergence among genotypes was explored through Non-hierarchical Euclidean cluster analysis, following the methods of Beale (1969) and Spark (1973).

Results and Discussion

Analysis of Augmented Block Design

In this present investigation 40 genotypes including (5) checks were evaluated in Augmented block design to study variability of rajmash (*Phaseolus vulgaris* L.) genotypes based on morphological traits. The descriptive statistics of morphological parameters studied for diversity analysis is presented in Table 1.

The analysis of variance (Tables 2 and Table 4) revealed that mean sum of squares for blocks showed significant results while ignoring treatments for all the

Table 1 : Descriptive statistics of morphological parameters.

Trait	Mean	Range	C.V. (%)
Days to emergence	13	9-17	8.52
Days to 50% Flowering	60.68	37-71	1.82
Days to maturity	103.98	90-119	1.00
Plant height(cm)	60.64	16-118	0.39
No. of pods per plant	25.42	10-40	5.46
Pod weight per plant	93.41	80-111	0.26
Pod length (cm)	12.11	5-16	4.91
No. of seeds per pod	5.77	3-7	11.72
100 seed weight(g)	36.75	18-57	2.26
Seed yield per plant(g)	63.48	16-157	10.79

characters except for the seeds per pod and seed thickness which showed non-significant results, whereas blocks showed non-significant results for all the traits while eliminating treatments except for the characters plant height, pod weight and germination percentage which showed the significant results. For every trait, variations resulting from different genotypes were highly significant. To enhance the performance of genotypes, variation resulting from genetic and non-genetic sources must be taken into account throughout the selection process (Comstock and Moll, 1963). Sofi *et al.* (2014a) and (2014b) reported findings that were similar for yield and yield attributing traits among 75 germplasm lines likewise found significant heterogeneity and also similar findings was recorded by Sajad *et al.* (2014) and Saba *et al.* (2017).

Similarly, treatments when ignoring blocks in Table 3 showed significant results, whereas treatments eliminating blocks were also significant for all the characters. For check, the mean sum of squares showed significant results for all the characters. The mean sum of squares for checks vs entries showed significance for all the characters. The standard error of difference was also computed and is presented in Table 5 to compare adjusted means for difference between two check varieties (Sc), difference between adjusted means of two test entries in the same block (Sb), difference between adjusted means of two test entries in different blocks (Sv) and difference between adjust test entry and check mean (Svc). Our findings were in close confirmity with the studies of Saba *et al.* (2017).

Diversity analysis on rajmash based on morphological characters

The diversity analysis was done on 22 morphological traits viz. days to emergence, days to 50% flowering, days to maturity, plant height(cm), number of pods per plant, pod weight per plant, pod length(cm), number of

Table 2 : Analysis of variance for Agro-morphological traits in common bean (*Phaseolus vulgaris*).

Source	Df	DE	DF	DM	PH	PPP	PW	PL	SPP	SW	SY
Blocks (ignoring genotypes)	3	18.19**	4.0*	122.95**	305.43**	75.98**	92.96**	5.66**	0.68	196.22**	2284.61**
Blocks (eliminating genotypes)	3	2.00	3.4	3.38	0.91**	1.38	0.42**	0.36	0.85	1.03	7.42
Genotypes (ignoring blocks)	44	9.26**	103.12**	80.2**	246.91**	81.01**	80.84**	5.2**	1.15*	149.56**	2411.77**
Genotypes (eliminating blocks)	44	8.15**	103.08**	72.1**	226.15**	75.92**	74.53**	4.84**	1.16*	136.23**	2256.51**
Genotypes	39	7.69**	16.74**	62.92**	179.91**	59.64**	56.78**	3.75**	1-.05*	116.63**	2068.74**
Checks	4	6.43**	649.3**	182.55**	470.08**	110.68**	123.49**	8.89**	0.7	70.57**	552.43**
Genotypes vs Checks	1	81.68**	1287.08**	346.8**	1967.09**	795.68**	848.65**	46.8**	6.53**	1749.79**	23227.48**
Error	12	1.13	1.13	1.05	0.05	1.68	0.06	0.33	0.43	0.6	34.18

DE- Days to emergence, **DF-** Days to flowering, **DM-** Days to maturity, **PH-** Plant height, **PPP-** Pods per plant, **PW-** Pod weight, **PL-** Pod length, **SPP-** Seeds per pod, **SW-** Weight of 100 seeds, **SY-** Seed yield per plant.

Table 3 : Standard error of means for Agro-morphological traits in common bean (*Phaseolus vulgaris*).

Source	Formula	DE	DF	DM	PH	PPP	PW	PL	SPP	SW	SY
Difference between two check varieties (Sc)	$\sqrt{2\text{MSE/R}}$	1.3	1.3	2.73	0.28	1.59	0.3	0.7	0.81	0.95	7.16
Difference between adjusted means of two test entries in the same block (Sb)	$\sqrt{2\text{MSE/R}}$	1.5	1.51	1.45	0.32	1.83	0.34	0.81	0.93	1.09	8.27
Difference between adjusted means of two test entries in different blocks (Sv)	$\sqrt{2(C+1)\text{MSE/C}}$	1.64	1.65	1.59	0.35	2	0.37	0.89	1.02	1.2	9.06
Difference between adjust test entry and check mean (Svc)	$\sqrt{\{(R+1)(C+1)\text{MSE}\}/R.C}$	0.75	0.75	1.58	0.16	0.92	0.17	0.41	0.47	0.55	4.13

DE- Days to emergence, **DF-** Days to flowering, **DM-** Days to maturity, **PH-** Plant height, **PPP-** Pods per plant, **PW-** Pod weight, **PL-** Pod length, **SPP-** Seeds per pod, **SW-** Weight of 100 seeds, **SY-** Seed yield per plant.

seeds per pod, 100 seed weight(g), seed yield per plant(g), seed length(mm), seed breadth(mm), seed thickness (mm), shape index, Standard germination (%), seedling length (cm), seedling dry weight (mg), viability test (Tz test), vigour index I, vigour index II, seed density, electrical conductivity (mS/cm/seed) and dehydrogenase activity ($\text{ODg}^{-1}\text{ml}^{-1}$).

The correlation matrix for all the traits revealed that days to emergence, days to flowering, days to maturity, plant height, pods per plant, pod weight, pod length, seeds per pod, seed weight and seed yield all are showing positive correlation for all traits. Seed length, seed breadth and germination percentage showed negative correlation for

all traits except pods per plant, seed weight, seed length, days to maturity and seed thickness where it showed positive correlation. Tutlani *et al.* (2023), Kumar *et al.* (2023) found similar results. Seed thickness, seedling length, seedling dry weight, seed density, electrical conductivity and dehydrogenase activity showed positive correlation for all traits except for days to flowering, days to maturity, pod length, seed length, seed breadth, seed thickness, germination and seedling length respectively. Similar results were found by Sofi *et al.* (2011), Rana *et al.* (2015) and Pravalika *et al.* (2024).

The principal components formed were equal to number of characters (19) in Table 6. The Eigen values

Table 4 : Analysis of variance of seed quality parameters in common bean (*Phaseolus vulgaris* L.).

Source of variation	df	SL	SB	ST	SI	G	SLL	SDW	VI ₁	VI ₂	SD	EC	DHY
Genotypes	44	1329.04**	317.68**	55.78**	26.91**	1229.23**	1035.06**	0.31**	8371089.07**	2446.43**	7321.29**	3924331.78**	1.93**
Error	90	6.99	5.91	6.15	2.21	6.98	7.42	0.00	56674.29	9.35	6.44	70.10	0.00
Total	134	1336.02	323.59	61.93	29.11	-	1042.48	0.31	8427763.37	2455.77	7327.73	3924401.88	1.93

SL- Seed length, SB- Seed breadth, ST- Seed thickness, G- Germination percentage, SLL- Seedling length, SDW- Seedling dry weight, VI₁- Vigour index 1, VI₂- Vigour index 2, SD- Seed density, EC- Electrical conductivity, DHY- Dehydrogenase.

Table 5 : Descriptive statistics of seed quality parameters.

Trait	Mean	Range	S.E	C.D.
Seed length (mm)	11.26	6.23-18.49	0.14	0.453
Seed breadth (mm)	4.86	2.46-8.39	0.13	0.416
Seed thickness (mm)	5.35	3.54-6.39	0.14	0.425
Shape index (si)	2.37	1.70-3.11	0.07	0.255
Germination percentage (%)	88.03	84.10-94.26	0.14	0.453
Seedling length (cm)	9.76	6.29-15.30	0.15	0.466
Seedling dry weight (g)	0.09	0.01-0.16	0.001	0.006
Vigour index I	860.43	468.23-1239.36	12.90	40.774
Vigour index II	8.24	1.70-15.53	15.35	0.524
Seed density (g/cc)	33.36	20.26-48.70	0.15	0.435
Electrical conductivity (mS/cm/seed)	569.71	317.53-1232.26	0.0003	1.434
Dehydrogenase activity (OD g ⁻¹ ml ⁻¹)	0.13	0.03-0.27	0.001	0.004

for different principal components were obtained through PCA (Kovacic, 1994) and only 5 principal components were having Eigen values greater than one (>1) contributing 77.62 per cent of total cumulative percentage with component-1 having the maximum percentage of 38.52 per cent (Mohammadi and Prassanna, 2003). For principal component-1, the trait pod weight contributed highest percentage of 12.968 per cent. For component-2 highest percentage was contributed by trait seed length (20.58%), while as in principal component-3, component-4 and component-5 the traits seed density, seedling length and electrical conductivity contributed highest with percentage of (35.06), (29.89) and (9.796), respectively. The important traits in these components were number of pods per plant, pod weight, seed length and 100-seed weight. Salehi *et al.* (2008), Bartlett (1947) in common bean using multivariate analysis, have identified similar results.

The cluster analysis for morphological, maturity, yield and quality characteristics arranged the rajmash genotypes into 3 clusters, with cluster II having the maximum number of genotypes (30), followed by III with 13 genotypes and cluster I with 2 genotypes. The inter-cluster distances were greater than the intra-cluster distances, indicating a high degree of variability among the genotypes of different cluster. Cluster means displayed a wide range of variance for all the attributes examined (Table 7). According to the analysis of the contributions of various traits to divergence, Cluster III had the greatest cluster

Table 6 : Eigen values of principal components.

S. no.	Traits	Eigen value	Percentage	Cumulative percentage
1	DE	7.319	38.521	38.521
2	DF	3.322	17.486	56.008
3	DM	1.558	8.200	64.208
4	PH	1.367	7.195	71.403
5	PPP	1.181	6.221	77.624
6	PW	1.070	5.632	83.257
7	PL	0.818	4.306	87.563
8	SPP	0.719	3.788	91.352
9	SW	0.456	2.400	93.752
10	SY	0.404	2.130	95.883
11	SL	0.315	1.660	97.543
12	SB	0.139	0.735	98.279
13	ST	0.112	0.591	98.871
14	G	0.094	0.498	99.369
15	SLL	0.065	0.343	99.713
16	SDW	0.026	0.141	99.854
17	SD	0.012	0.065	99.920
18	EC	0.008	0.043	99.964
19	DHY	0.006	0.035	100.00

DE- Days to emergence, **DF-** Days to flowering, **DM-** Days to maturity, **PH-** Plant height, **PPP-** Pods per plant, **PW-** Pod weight, **PL-** Pod length, **SPP-** Seeds per pod, **SW-** Weight of 100 seeds, **SY-** Seed yield per plant, **SL-** Seed length, **SB-** Seed breadth, **ST-** Seed thickness, **G-** Germination percentage, **SLL-** Seedling length, **SDW-** Seedling dry weight, **SD-** Seed density, **EC-** Electrical conductivity, **DHY-** Dehydrogenase activity.

Table 7 : Cluster means for different traits.

Clusters	DE	DF	DM	PH	P	PW	PL	SP	SW	SY
Cluster I	10.50	37.50	92.00	42.92	15.00	82.48	9.00	4.50	23.50	16.24
Cluster II	12.40	61.06	102.40	54.91	22.30	90.22	11.31	5.43	32.45	44.97
Cluster III	14.69	63.30	109.38	76.42	34.23	102.32	14.27	6.61	48.54	113.41

Clusters	SL	SB	ST	G	SLL	SDW	SD	EC	DHY
Cluster I	17.74	7.90	5.88	92.18	5.85	0.04	38.78	382.00	0.07
Cluster II	11.31	4.88	5.36	87.82	9.52	0.09	31.58	525.23	0.10
Cluster III	10.42	4.40	5.35	88.40	10.75	0.10	36.64	701.44	0.20

DE- Days to emergence, **DF-** Days to flowering, **DM-** Days to maturity, **PH-** Plant height, **PPP-** Pods per plant, **PW-** Pod weight, **PL-** Pod length, **SPP-** Seeds per pod, **SW-** Weight of 100 seeds, **SY-** Seed yield per plant, **SL-** Seed length, **SB-** Seed breadth, **ST-** Seed thickness, **G-** Germination percentage, **SLL-** Seedling length, **SDW-** Seedling dry weight, **SD-** Seed density, **EC-** Electrical conductivity, **DHY-** Dehydrogenase activity.

mean for days to emergence, days to 50% flowering, days to maturity, plant height, pods per plant, pod weight, pod length, seeds per pod, seed weight and Cluster I had

the highest cluster mean for seed length, seed breadth, seed thickness, germination percentage and seed density. Better genotypes for specific attributes can be chosen based on the cluster's mean performance. The cluster means for several morphological, yield-attributing traits and quality parameters showed that there was a significant diversity for each of these traits. Genotypes belonging to these clusters would be selected directly on the basis of these traits and can be used in breeding program. The findings in this study are similar to those reported by Boros *et al.* (2014), Javadin *et al.* (2014), Verma *et al.* (2014) and Panchbhaya *et al.* (2017) in french beans.

The diversity analysis of the rajmash (*Phaseolus vulgaris* L.) genotypes was carried out on the basis of 22 morphological traits *viz.* days to emergence, days to 50% flowering, days to maturity, plant height(cm), number of pods per plant, pod weight per plant, pod length(cm), number of seeds per pod, 100 seed weight (g), seed yield per plant (g), seed length (mm), seed breadth(mm), seed thickness (mm), shape index, Standard germination (%), seedling length (cm), seedling dry weight(g), viability test (Tz test), vigour index I, vigour index II, seed density, electrical conductivity (mS/cm/seed) and dehydrogenase activity (ODg⁻¹ml⁻¹).

The genotypes were analyzed by PCA (Principal Component Analysis) for diversity analysis. The analysis of variance revealed that mean sum of squares for blocks showed significant results while ignoring treatments for all the characters except for the seeds per pod and seed thickness which showed non-significant results, whereas blocks showed non-significant results for all the traits

while eliminating treatments except for the characters plant height, pod weight and germination percentage which showed the significant results. Similarly, treatments when

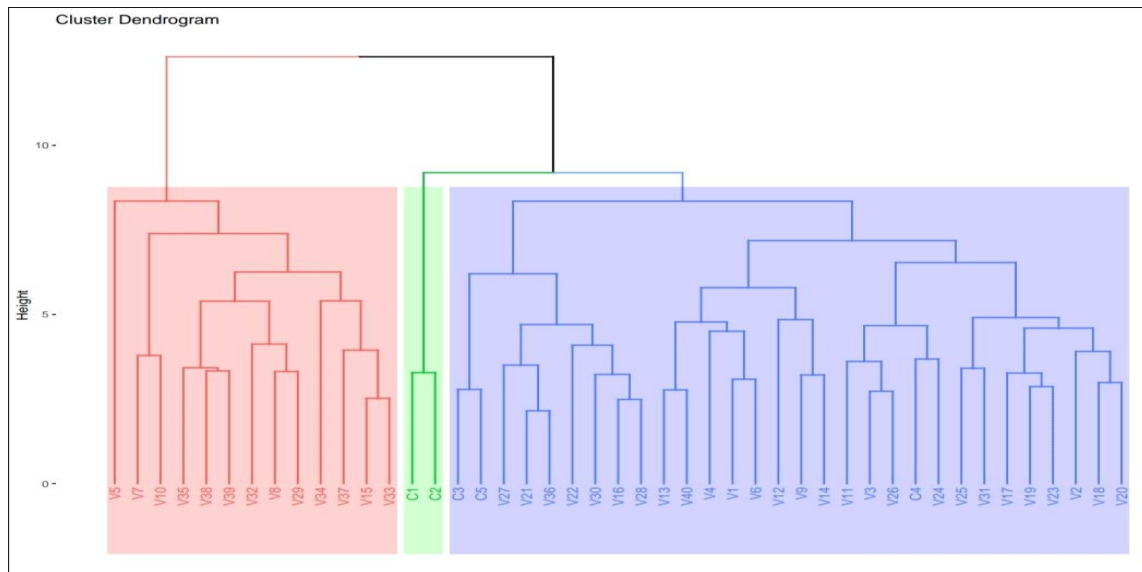


Fig. 1 : Clustering of genotypes under different cluster.

Table 8 : Contribution of various morphological and seed characters in different principal components.

S. no.	Traits	PC1	PC2	PC3	PC4	PC5
1	DE	1.243	0.917	28.461	0.256	1.117
2	DF	2.722	3.576	0.743	2.202	3.683
3	DM	1.396	12.630	1.146	2.196	5.468
4	PH	12.552	0.834	0.572	0.075	1.622
5	PPP	12.736	1.377	0.233	0.176	9.754
6	PW	12.968	0.851	0.247	0.066	2.520
7	PL	12.491	0.980	0.062	0.119	7.829
8	SPP	10.736	0.924	2.159	0.233	2.699
9	SW	12.291	1.708	0.033	0.028	1.565
10	SY	12.411	1.085	1.002	0.199	4.414
11	SL	0.270	20.582	1.384	1.345	2.372
12	SB	0.767	17.809	1.648	1.597	1.805
13	ST	0.028	5.270	0.349	4.484	1.508
14	GP	0.610	2.755	12.745	5.433	2.789
15	SLL	1.927	8.582	0.083	29.894	3.557
16	SDW	0.832	8.849	1.131	29.339	1.521
17	SD	0.340	1.351	35.061	0.688	7.825
18	EC	3.147	8.004	0.567	8.810	9.796
19	DHY	0.524	1.887	12.057	12.850	1.552

DE- Days to emergence, DF- Days to flowering, DM- Days to maturity, PH- Plant height, PPP- Pods per plant, PW- Pod weight, PL- Pod length, SPP- Seeds per pod, SW- Weight of 100 seeds, SY- Seed yield per plant, SL- Seed length, SB- Seed breadth, ST- Seed thickness, G- Germination percentage, SLL- Seedling length, SDW- Seedling dry weight, SD- Seed density, EC- Electrical conductivity, DHY- Dehydrogenase activity.

ignoring blocks showed significant results, whereas treatments eliminating blocks were also significant for all the characters. For check the mean sum of squares

Table 9 : Average intra and inter cluster distances.

Clusters	Cluster I	Cluster II	Cluster III
Cluster 1	3.27	7.18	9.97
Cluster II		5.05	6.59
Cluster III			5.21

showed significant results for all the characters. The mean sum of squares for checks vs entries showed significance for all the characters.

The principal components formed were equal to number of characters (19) in Table 8. The Eigen values for different principal components were obtained through PCA and only 5 principal components were having Eigen values greater than one (>1) contributing 77.62 per cent of total cumulative percentage with component-1 having the maximum percentage of 38.52 per cent. For principal component-1, the trait pod weight contributed highest percentage of 12.968 per cent. For component-2 highest percentage was contributed by trait seed length (20.58%), while as in principal component-3, component-4 and component-5 the traits seed density, seedling length and electrical conductivity contributed highest with percentage of (35.06), (29.89) and (9.796), respectively.

The cluster analysis revealed that all the genotypes were grouped into three clusters with maximum genotypes in cluster-2 followed by cluster-3 and cluster-1. The cluster analysis for morphological, maturity, yield and quality characteristics arranged the rajmash genotypes into 3 clusters, with cluster II having the maximum number of genotypes (30), followed by III with 13 genotypes and cluster I with 2 genotypes as per Fig. 1.

The average D² values between clusters *i.e.*, inter-

Table 10 : Correlation matrix for various morphological and seed quality traits in Rajmash (*Phaseolus vulgaris*).

Traits	DE	DF	DM	PH	PPP	PW	PL	SPP	SW	SY	SL	SB	ST	G	SLL	SDW	SD	EC	DHY
DE	1																		
DF	0.4	1																	
DM	0.25	0.48	1																
PH	0.19	0.35	0.17	1															
PPP	0.19	0.34	0.14	0.97*	1														
PW	0.21	0.37	0.17	0.97*	0.98*	1													
PL	0.2	0.34	0.1	0.94*	0.97*	0.97*	1												
SPP	0.06	0.22	0.03	0.85	0.88	0.87	0.89	1											
SW	0.21	0.34	0.14	0.94*	0.96*	0.96*	0.93*	0.87	1										
SY	0.16	0.29	0.18	0.95*	0.96*	0.96*	0.91*	0.91*	0.97*	1									
SL	-0.12	-0.22	-0.51	-0.01	0.02	-0.06	-0.01	-0.03	0.03	-0.01	1								
SB	-0.1	-0.29	-0.37	-0.14	-0.09	-0.12	-0.14	-0.15	-0.06	-0.11	0.81	1							
ST	0.04	-0.15	-0.24	0.02	0.01	0.02	-0.05	0.01	0.04	0.01	0.23	0.35	1						
G	-0.2	-0.14	0.25	-0.12	-0.2	-0.18	-0.25	-0.15	-0.21	-0.12	-0.17	-0.11	0.04	1					
SLL	0.12	0.32	0.45	0.29	0.25	0.29	0.27	0.31	0.25	0.28	-0.33	-0.3	-0.08	-0.01	1				
SDW	0.2	0.2	0.22	0.14	0.12	0.16	0.17	0.21	0.08	0.11	-0.34	-0.35	-0.08	-0.05	0.79	1			
SD	0.24	-0.13	0.02	0.1	0.1	0.08	0.08	0.06	0.11	0.12	0.25	0.16	0.09	-0.24	0.01	0.05	1		
EC	0.19	0.21	0.55	0.35	0.32	0.36	0.31	0.24	0.29	0.35	-0.47	-0.49	-0.23	0.16	0.36	0.24	0.08	1	
DHY	0.21	0.01	0.16	0.07	0.13	0.13	0.19	0.11	0.05	0.06	-0.19	-0.22	-0.17	0.05	-0.01	0.21	0.23	0.26	1

DE- Days to emergence, DF- Days to flowering, DM- Days to maturity, PH- Plant height, PPP- Pods per plant, PW- Pod weight, PL- Pod length, SPP- Seeds per pod, SW- Weight of 100 seeds, SY- Seed yield per plant, SL- Seed length, SB- Seed breadth, ST- Seed thickness, G- Germination percentage, SLL- Seedling length, SDW- Seedling dry weight, SD- Seed density, EC- Electrical conductivity, DHY- Dehydrogenase activity (*p-value at 0.01 and 0.05)

cluster (above diagonal) and within clusters i.e., intra-cluster (diagonal). Table 9 showed that the inter-cluster distances were greater than the intra-cluster distances, indicating a high degree of variability among the genotypes of different cluster. Cluster means displayed a wide range of variance for all the attributes examined. According to the analysis of the contributions of various traits to divergence, Cluster III had the greatest cluster mean for days to emergence, days to 50% flowering, days to maturity, plant height, pods per plant, pod weight, pod length, seeds per pod, seed weight and Cluster I had the highest cluster mean for seed length, seed breadth, seed thickness, germination percentage and seed density.

Viability test was performed before germination test by using tetrazolium solution and it was observed that all genotypes are viable. Germination test of rajmash (*Phaseolus vulgaris* L.) genotypes as per ISTA recommendations and then seedling length of each genotype were recorded. The highest germination percentage was recorded in SR-1(94.27%) and lowest germination percentage was recorded in ALR-3 (82.30%) whereas the maximum seedling length was measured in PPR-12(15.20cm) and lowest in SR-2(5.15cm).

Seedling dry weight was measured ranging from 0.016-0.168 mg. Among all genotypes highest seedling dry weight was recorded in PPR-10(0.168mg), whereas lowest was recorded in Kailash (0.016mg). Highest seedling vigour index I was seen in PPR-13(1380) and lowest was recorded in SR-2(461). Vigour index II were measured ranging from 2.1958-15.6072. In vigour index II, highest vigour index was recorded in PPR-10 (15.6072) and lowest in SR-2(2.1958). Electrical conductivity

recorded as per the (AOSA, 1983) protocol ranged from 317.8-1232.2 (mS/cm/seed). Highest electrical conductivity was measured in PPR-10 (1232.2mS/cm/seed), whereas lowest was measured in Baspa (317.8mS/cm/seed). Dehydrogenase activity recorded as per the Kittock and Law (1968) protocol ranged from 0.012-0.278 (OD g⁻¹ml⁻¹). Highest dehydrogenase activity was recorded in KDR-98 (0.278 OD g⁻¹ml⁻¹) and lowest was recorded in KDR-105 (0.012 OD g⁻¹ml⁻¹).

Conclusion

The diversity analysis revealed that the genotypes were grouped into three clusters, indicating a considerable difference in the attributes across the various genotypes. The yield contributing features were indirectly selected for because of the substantial and positive association between morphological traits. Widespread genetic variability is revealed by PCA analysis. The assessment of seed quality parameters provides valuable insights into the overall health and performance of common bean seeds. These parameters provided the comprehensive understanding of seed vigour, metabolic activity and potential for successful germination and growth. Other than checks PPR-7, PPR-10, PPR-15, KDR-40 and KDR-80 performed better for various morphological characters. PPR-5, PPR-12, KDR-65 and KDR-98 performed better for various seed quality parameters.

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