



Multivariate Analysis in Blackgram (*Vigna mungo* L. Hepper) Genotypes in India

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present study was contained black gram, 40 genotypes and experiment will be carried out in Randomized block design with 3 replications. The higher GCV & PCV found in biological yield, harvest index, number of cluster per plant, number of primary branches per plant. The traits were biological yield, harvest index, number of cluster per plant, number of primary branches per plant, seed yield per plant, seed index exposed higher heritability and higher genetic advance as percentage of mean. Regarding on D^2 values 40 black gram genotypes grouped in to 5 clusters. The intra cluster distance ranged from 0 to 30.38. The highest intra cluster distance found in cluster II (30.38). The highest inter cluster distance found between clusters III to cluster IV (168.86). The first principal component was more positively related to seed yield and its contributing traits such as days to maturity (0.305), biological yield (0.203), days to 50% flowering (0.180), seed index (0.018). The positive and negative loading shows the presence of positive and negative correlation trends between the components and the variables.

Keywords: *Black gram; genetic variability; heritability; genetic advance; diversity; PCA.*

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1. INTRODUCTION

Black gram [*Vigna mungo* (L.) Hepper] is a self-pollinated, annual, short duration dicotyledonous legume crop with chromosome number $2n=22$, and belongs to family fabaceae sub-family papilionaceae. Black gram cultivation on marginal lands under rain-fed conditions with low inputs has been an age-old practice in Asian countries. India is the primary center of origin of black gram [1]. Genetic improvement and development of high yielding varieties are dependent upon genetic variability [2] as it provides the base for selection. "Germplasm collection and judgment of genetic variability is the very first step in a crop breeding programme. Surveys of genetic variability with the help of suitable parameters such as GCV, heritability estimates and genetic advance are very necessary to start an efficient breeding programme" [3]. Heritability determines that portion of the total variation which is heritable. Genetic advance, expressed as per cent of the population mean, connotes the reaction of different characters towards selection under several selection intensities [4]. Heritability coupled with genetic gain is more reliable and efficient in forecasting gain under selection as compared to sole heritability estimates. Thereby, these two parameters should be given due consideration in conjointment for enriching genetic potential of the crop [5]. Genetic diversity is one of the criteria for parent's determination in the hybridization programmes. The accessibility of transgressive segregant in any breeding project depends upon the diversity between the parents associated. "The evaluation of genetic diversity through biometrical methodology, for example, Mahalanobis D^2 -statistic has made conceivable to pick genetically diverse parents" [6]. "The ordination techniques like, principal components analysis (PCA) followed by cluster analysis has been found to be useful tool for getting multi correlated variables into another set of uncorrelated variables, which can be utilized for classification of genotypes into homogenous groups" [7].

2. MATERIALS AND METHODS

The present experiment was carried out at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj (UP), during Rabi-2020-2021. The experimental materials comprising of 40 genotypes with one

check variety was grown under Randomized Block Design (RBD) with three replications. The morphological traits were recorded and subjected for statistical analysis. The software INDOSTAT were used for the statistical analysis.

3. RESULTS AND DISCUSSION

Analysis of variance showed the genotypes were significant for all the characters studied at both level of significance 1% and 5%, suggesting the existence of high genetic variability among the genotypes for all the traits.

Genotypic coefficient of variation was varied from 1.68% (Days to maturity) to 26.87% (Biological yield) Table1. The traits were biological yield (26.87%), harvest index (24.34%), number of cluster per plant (22.21%) showed higher genotypic coefficient of variation Similar results were reported by Arulbalachandran et al. [8], Sathees et al. [9]. The traits were seed index (18.66%), seed yield per plant (17.54%) showed moderate genotypic coefficient of variation. Phenotypic coefficient of variation varied from 3.45% (Days to maturity) to 27.91% (Biological yield). Similar results were reported by Aftab et al. [10], Shoba et al. [11]. The traits were biological yield (27.91%), harvest index (25.49%), number of cluster per plant (23.44%), number of primary branches per plant (22.49%), seed index (20.18%) showed higher phenotypic coefficient of variation Similar results were reported by Bishnoi et al. [12], Vinoth et al. [13]. The traits were seed yield per plant (18.89%), plant height (11.32%), number of pods per cluster (10.5%) showed moderate phenotypic coefficient of variation. Similar results were reported by Chauhan et al. [14], Sowmini et al. [15]. Heritability varied from 17.11% (Pod length) to 92.71% (Biological yield). The traits were biological yield (92.71%), harvest index (91.18%), number of cluster per plant (89.8%), number of primary branches per plant (88.65%), seed yield per plant (86.26%), seed index (85.49%), plant height (61.26%) showed higher heritability. Similar results were reported by Jeberson et al. [16], Baisakh et al. [17]. The traits number of pods per cluster (49.82%), number of seeds per pod (48.65%), days to 50% pod setting (43.07%) showed moderate heritability. Genetic advance varied from pod length (0.12%) to harvest index (17.8%). The traits wee harvest index (17.8%), biological yield (11.5%) showed moderate genetic advance. Genetic advance as percent mean was varied from 1.69% (Days to maturity) to 53.3% (Biological yield). The traits were biological yield

(53.3%), harvest index (47.88%), number of cluster per plant (43.36%), number of primary branches per plant (41.08%), seed index (35.54%), seed yield per plant (33.56%) showed higher genetic advance as percent mean. The

traits were plant height (14.28%), number of pods per cluster (10.77%) showed moderate genetic advance as percent mean. Similar results were reported by Patel et al. [18], Blessy et al. [19].

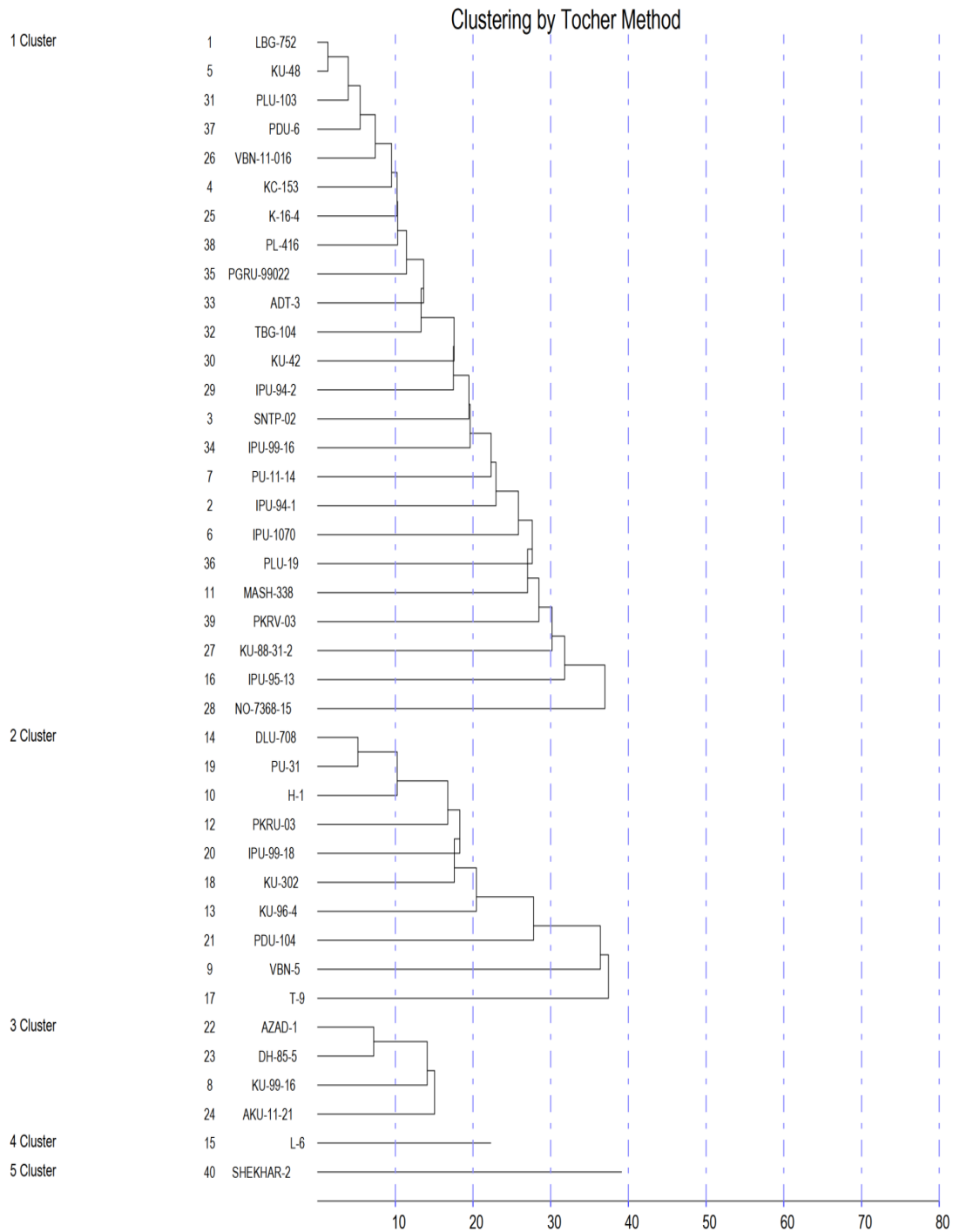


Fig. 1. Dendrogram D² clusters for black gram genotypes

Table 1. Genetic parameters for 13 quantitative characters in 40 black gram genotypes

Traits	GCV	PCV	h ² (Broad Sense)	G.A 5%	G.A as % of Mean 5%
Days to fifty percent flowering	2.33	4.67	24.85	1.36	2.39
Days to fifty percent pod setting	2.38	3.63	43.07	2.05	3.22
Plant height (cm)	8.86	11.32	61.26	6.26	14.28
Number of primary branches per plant	21.18	22.49	88.65	1.53	41.08
Days to maturity	1.68	3.45	23.7	1.64	1.69
Number of clusters per plant	22.21	23.44	89.8	2.87	43.36
Number of pods per cluster	7.41	10.5	49.82	0.51	10.77
Pod length (cm)	2.92	7.06	17.11	0.12	2.49
Number of seeds per pod	6.56	9.4	48.65	0.5	9.42
Biological yield (g)	26.87	27.91	92.71	11.5	53.3
Seed Index (g)	18.66	20.18	85.49	1.28	35.54
Harvest index (%)	24.34	25.49	91.18	17.8	47.88
Seed yield per plant (g)	17.54	18.89	86.26	2.55	33.56

Table 2. Cluster pattern of blackgram [*Vigna mungo* (L.) Hepper] 40 genotypes based on D² (Diversity)

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	24	LBG-752, KU-48, PLU-103, PDU-6, VBN-11-016, KC-153, K-16-4, PL-416, PGRU-99022, ADT-3, TBG-104, KU-42, IPU-94-2, SNTP-02, IPU-99-16, PU-11-14, IPU-94-1, IPU-1070, PLU-19, MASH-338, PKRV-03, KU-88-31-2, IPU-95-13 & NO-7368-15
2 Cluster	10	DLU-708, PU-31, H-1, PKRU-03, IPU-99-18, KU-302, KU-96-4, PDU-104, VBN-5 & T-9
3 Cluster	4	AZAD-1, DH-85-5, KU-99-16 & AKU-11-21
4 Cluster	1	L-6
5 Cluster	1	SHEKHAR-2

Table 3. Mean intra and inter-cluster distances among five (5) clusters in blackgram [*Vigna mungo* (L.) Hepper] by Tocher's method

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	24.76	52.38	52.8	97.45	66.86
Cluster 2	52.38	30.38	95.77	73.8	56.33
Cluster 3	52.8	95.77	18.3	168.86	130.67
Cluster 4	97.45	73.8	168.86	0	97.03
Cluster 5	66.86	56.33	130.67	97.03	0

Table 4. Cluster means for different characters in blackgram [*Vigna mungo* (L.) Hepper] by Tocher's method

Clusters	Days to fifty percent flowering	Days to fifty percent pod setting	Plant height (cm)	Number of primary branches per plant	Days to maturity	Number of clusters per plant	Number of pods per cluster	Pod length (cm)	Number of seeds per pod	Biological yield (g)	Seed Index (g)	Harvest index (%)	Seed yield per plant (g)
Cluster 1	57.26	65.94	42.31	3.51	97.57	6.47	4.76	4.68	5.19	24.31	3.71	34.64	8.19
Cluster 2	57.17	65.6	46.1	4.5	97.13	7.12	4.81	4.81	5.68	14.64	3.47	48.19	7.06
Cluster 3	57.58	63.17	44.32	2.44	97.25	4.71	4.25	4.43	4.8	23.85	3.47	23.26	5.47
Cluster 4	57	66.33	49.4	4.85	99.67	12.12	5.3	4.57	5.09	16.18	2.6	45.59	7.38
Cluster 5	49.33	67.33	49.75	5.32	87.33	7.1	6.39	5.48	6.05	21.71	4.16	34.74	7.54

Table 5. Eigen values, percent variability, cumulative percent variability and characters loading of six principle components for different genotypes of black gram

		Canonical Roots Analysis (P. C. A.)					
Sl. No.		1 Vector	2 Vector	3 Vector	4 Vector	5 Vector	6 Vector
	Eigen Value (Root)	4.85	1.93	1.55	1.36	1.15	0.67
	% Var. Exp.	37.33	14.83	11.92	10.50	8.83	5.13
	Cum. Var. Exp.	37.33	52.15	64.08	74.57	83.40	88.53
1	Days to fifty percent flowering	0.18	0.05	0.51	0.32	0.02	0.26
2	Days to fifty percent pod	-0.09	-0.29	-0.01	0.23	-0.65	0.53
3	Plant height (cm)	-0.17	0.29	-0.11	-0.40	-0.47	-0.11
4	Number of primary branch	-0.43	-0.01	0.11	-0.06	0.03	-0.09
5	Days to maturity	0.30	0.02	0.33	-0.07	-0.35	-0.36
6	Number of clusters per plant	-0.25	-0.25	0.43	-0.33	-0.10	-0.13
7	Number of pods per cluster	-0.35	-0.21	-0.17	-0.16	-0.15	0.14
8	Pod length (cm)	-0.41	0.09	-0.13	-0.02	0.10	-0.15
9	Number of seeds per pod	-0.36	0.07	-0.12	0.36	0.19	0.19
10	Biological yield (g)	0.20	-0.53	-0.28	-0.16	0.16	0.01
11	Seed Index (g)	0.02	-0.13	-0.33	0.54	-0.32	-0.57
12	Harvest index (%)	-0.34	0.09	0.37	0.30	0.02	-0.20
13	Seed yield per plant (g)	-0.11	-0.64	0.20	0.01	0.13	-0.20

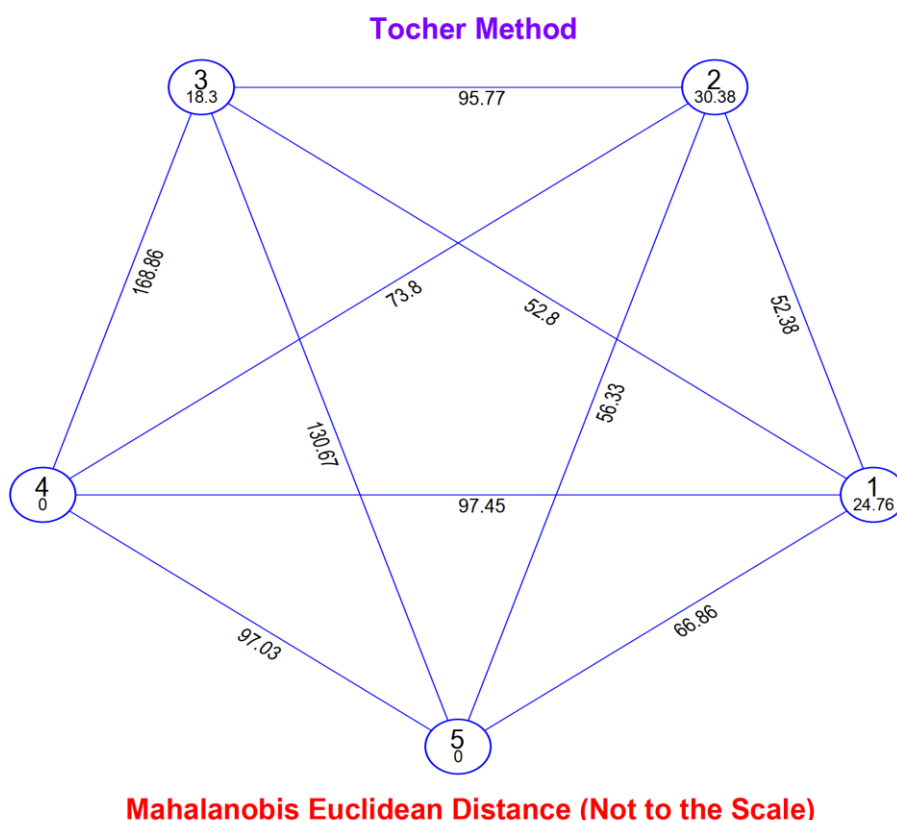


Fig. 2. Clustering by Tocher Method

Based on D2 values 40 black gram genotypes grouped in to 5 clusters (Table 2, Fig. 1). Similar results were reported by Elangaimannan et al. [20]. Among these cluster I contained highest number of genotypes (24) and cluster II (10), cluster III (4), cluster IV and V had each one genotypes. The intra cluster distance ranged from 0 to 30.38 (Table 3, Fig. 2). The highest intra cluster distance found in cluster II (30.38). Similar results were reported by Ghafoor et al. [21]. The highest inter cluster distance found between cluster III to cluster IV (168.86). The cluster mean of seed yield per plant varied from 7.06 (cluster II) to 8.19 cluster (I). Similar results were reported by Jayamani et al. [22]. The higher cluster mean of seed yield per plant found in cluster I (8.19) (Table 4). The higher diversity contribution percentage found in seed yield per plant (16.03%). Similar results were reported by Priya et al. [23].

Principal component analysis (PCA) explains the divergence of black gram genotypes. In present study, PCA was performed for thirteen quantitative traits of black gram. Out of 6 principal components (PCs), only 5 PCs exhibited more than 1.00 Eigen value viz., PC1

(4.85), PC2 (1.93), PC 3 (1.55), PC 4 (1.36), PC5 (1.15) showed about 83.40% (Table 5). Similar results were reported by Jeberson et al. [16]. Variability among the traits studied for each genotype. Hence, these 5 principal components were given due importance for the further explanation. The PC1 had 37.33%, PC2 showed 14.83%, PC3 11.92% exhibited, PC4 showed 10.50%, PC5 (8.83%). Similar results were reported by Mohanlal et al. [24].

The first principal component was more positively related to seed yield and its contributing traits such as days to maturity (0.305), biological yield (0.203), days to 50% flowering (0.180), seed index (0.018). Similar results were reported by Prakash et al. [25]. The second principal component was more positively related to seed yield and its contributing traits such as plant height (0.289), pod length (0.094), harvest index (0.085), number of seeds per pod (0.072), days to 50% flowering (0.046), days to maturity (0.023). Similar results were reported by Thirumalai et al. [26]. The third principal component was more positively related to seed yield and its contributing traits such as days to 50% flowering (0.507), number of cluster per

plant (0.0431), harvest index (0.373), days to maturity (0.332), seed yield per plant (0.199), number of primary branches (0.114). Similar results were reported by Ayesha et al. [27]. The fourth principal component was more positively related to seed yield and its contributing traits such as seed index (0.541), number of seeds per pod (0.364), days to 50% flowering (0.322), harvest index (0.298), days to 50% pod setting (0.234), seed yield per plant (0.015). Similar results were reported by Reddy et al. [28]. The fifth principal component was more positively related to seed yield and its contributing traits such as number of seeds per pod (0.194), biological yield (0.155), seed yield per plant (0.134), pod length (0.103), number of primary branches (0.026), harvest index (0.018). Similar results were reported by Jyothi et al. [29].

4. CONCLUSION

The analysis of variance revealed that the existence for all the traits. Hence, the data on all the 13 traits which showed significant difference among the entries were subjected to further statistical analysis [30].

The genotypes were NO-7368-15 (10.23g), VBN-11-016(9.99g), KU-88-31-2 (9.57g) PDU-104 (9.28g) exhibited highest seed yield per plant. The higher GCV & PCV found in biological yield, harvest index, number of cluster per plant, number of primary branches per plant. The traits were biological yield, harvest index, number of cluster per plant, number of primary branches per plant, seed yield per plant, seed index exposed higher heritability (Broad sense) and higher genetic advance as percentage of mean.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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