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Genetic components and traits relationship in a panel of Black gram [*Vigna mungo* (L.) Hepper] diverse genotypes

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ABSTRACT

Sixty black gram [*Vigna mungo* (L.) Hepper] genotypes consisting of germplasm lines, advanced breeding lines and released varieties were evaluated to devise the extent of genetic diversity. Trait association revealed that plot seed yield had positive significant relationship with most of the studied traits. The cluster analysis distributed the genotypes into seven clusters. Cluster I was largest with maximum 21 genotypes, followed by Cluster II and III comprising 12 and 9 genotypes, respectively. The first two principal components accounted 69.94% of the total variability among genotypes. The biplot and scatter plot matrix results were in accordance with correlation estimation, suggesting that indirect selection based on component traits would help in improving the seed yield in black gram. The genotypes under investigation demonstrated a wide range of diversity for considered traits. Furthermore, the presence of advanced breeding lines and released varieties in same cluster witnessed that only a small portion of the genetic diversity has been exploited in black gram genetic improvement program in India. It is recommended that diverse parents should be used to broaden the genetic base of cultivated black gram as well as to produce desirable recombinants for developing new improved black gram varieties.

Key words: Black gram, Cluster analysis, Genetic components, Traits association

Black gram or Urdbean is one of the important *kharif* and spring/summer pulse crop of many South Asian countries like of India, Pakistan, Nepal, Bangladesh, Thailand, Korea, (Ghafoor and Arshad, 2008). It is cultivated under a wide range of agro-ecological zones as subsistence monocrop or intercrop during *kharif, rabi* and summer season. It is grown in 4.50 million hectare area with 2.83 million tonnes production and 628 kg/ha productivity in India (Anonymous 2018). Blackgram is the least researched crop among all pulses group and has no any international centre of improvement on its mandate (Anon 1976). Although, it has been recognized as a potential crop in many countries, but due to dearth of information about available genetic variability led to least developed crop compared to other pulse crop (Ghafoor *et al*. 2003).

Understanding of existing genetic variability is a quintessential step for realizing true response to selection in breeding program. In addition, extensive utilization of the limited number of parents in varietal development has narrowed down the genetic base of the available breeding pool in urdbean (Gupta and Parihar, 2015). Since genetically diverse parents must be used for hybridization and crop improvement programme *via* getting desirable segregants to broaden the genetic base. To classify and measure the pattern of genetic diversity in germplasm of black gram principal component and cluster analysis have been utilized (Shanmugam and rangaswamy 1982, Dasgupta and Das 1984; 1985, Ghafoor *et al*. 2001, Elangaimannan *et al*, 2008, Chauhan *et al*, 2008, Katiyar and Dixit 2010, Jayamani and Sathya 2013, Hadimani *et al.* 2016,). In order to develop high yielding cultivars under changing climatic scenario to sustain its production, exploitation of the gene pool has paramount importance. The present study was undertaken to explore the extent of genetic diversity in black gram germplasm based on agronomic traits using multivariate analysis. Therefore, present investigation was attempted to decipher the genetic variation and to find out the relationship among the various quantitative traits in an experimental panel of black gram genotypes.

MATERIAL AND METHODS

Sixty genotypes of black gram were procured from All India Coordinated Research Project (AICRP) on MULLaRP. The experiment was executed at experimental field of Rajasthan Agricultural Research Institute, Durgapura, Jaipur, Rajasthan, India in a randomized block design with three replication during *kharif* seasons (July to October, 2015) with assured irrigated facilities to examine the genetic variation for quantitative characters. The crop was raised with recommended package and practices with 10 cm and 30cm plant to plant and inter-row distance, respectively. The data were recorded for following characters *viz.,* plant height (cm), branches/plant, pods/plant, pod length (cm), seeds/pod and plot yield (g) on five randomly selected plants from each replication. The descriptive statistics, *i.e.*, means, standard deviation and range was done in Microsoft Excel 2007. The hierarchal clustering, constellation plot, scatter plot matrix, principal components analysis and trait association were performed through SAS version 9.3.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA) for six quantitative traits of 60 black gram genotypes depicted significant differences ($p<0.05$) for mean sum of squares due to treatment among the genotypes for all the considered traits (Table 1). The presence of highly significant variation among these genotypes for different quantitative traits could be exploited in future breeding programmes through selection for the traits studied. Substantial genetic variation among urdbean genotypes for different yield contributing traits has been reported earlier by Elangaimannan *et al*, 2008, Chauhan *et al*, 2008, Katiyar and Dixit 2010, Jayamani and Sathya 2013, Hadimani *et al.* 2016.

Table 1. Analysis of Variance for 6 characters of black gram genotypes

Source of variation	Mean square	F value	p-value
Plant height	240.001	16.831	0.00000*
Branch/plant	3.327	22.533	0.00000*
Pods/plant	34.026	7.549	0.00000*
Seeds/pod	0.821	0.653	0.96488
Pod length	0.490	1.275	0.13305
Plot yield	25,804.846	55.728	0.00000*

* Showing Significant p-value < 0.05 significant

The principal component analysis was performed using variance-covariance matrix through transformation of all the quantitative attributes into a single index of similarity. It produced six eigen value for six eigen vectors and of them, only first three Eigen vectors were taken into consideration since these are accounted more than 80 % variation of total variation (Table 2). Eigen vectors of individual component are the decisive factors for their association with the original variables. The first three principle components (PC_1, PC_2 and PC_3) had eigenvalues 3.18, 1.01 and 0.70 respectively. Characters with maximum share to PC_1 were plant height, branches/plant and seeds/pod which contributed 53.08% of variation. Likewise, component second and third were associated with pods/plant and seeds/pods and contributed 16.86% and 11.71% of variation, respectively (Table 2). Similarly, if considered contribution of individual variables toward individual traits then it was also confirmed that Principal Component 2 explains more than 80% variance of character pods/plant. Correspondingly, Principal component 3 accounted more than 40% variance of plot yield. It has been depicted from figure 1 that principal component 2 has negligible contribution to the characters like plant height, seeds/pod, and plot yield (Fig 1). The pattern of the variation explained by different PCs for different traits is in agreement with the previous available reports in fieldpea and lathyrus (Parihar *et al*, 2013; 2014, Katiyar *et al.* 2016).

Table 2. Eigen values, proportional and cumulative per cent variation and principal component for 6 yield contributing traits in black gram

Number	Eigenvalue	Percent	Cum Percent	ChiSquare
1	3.18	53.08	53.08	142.17
2	1.01	16.86	69.94	43.69
3	0.70	11.70	81.65	26.27
4	0.49	8.21	89.86	16.35
5	0.43	7.30	97.16	11.74
6	0.17	2.83	100.00	.

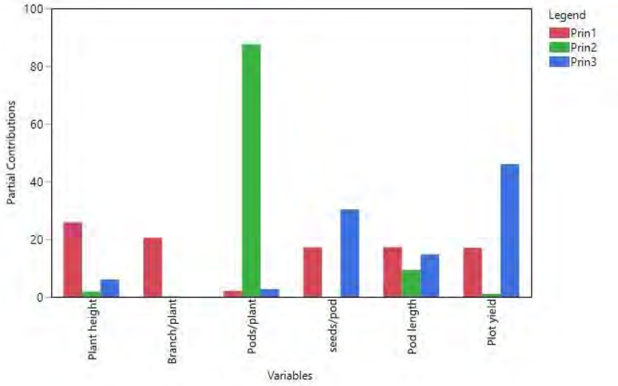

Fig. 1. partial contribution of variables via principal component in black gram genotypes

The trait association analysis demonstrated positive significant correlation of branches/plant with pods/plant, pod length and plot yield (Table 3). Significant positive correlation was found between plot yield and pod length. Similar kind of results for significant positive association of seed yield with other yield attribute has been reported earlier in black gram (Uma and Meenakshi 2005; Chauhan *et al.* 2007; Shivade *et al.* 2011; Sohel *et al.* 2016). The given values of correlations suggested the possibilities of simultaneous improvement of associated characters. Therefore, emphasis must be given on aforementioned traits for improving the productivity *via* selection.

Genotypes distributed into seven distinct clusters using cluster analysis which was performed on the sixty genotypes of black gram using six quantitative characters. Cluster I was the largest cluster consisting of 21 genotypes (35%), followed by Cluster II (20%) comprising of 12 genotypes and Cluster III (15%) harboured 9 genotypes respectively (Table 4). Genotype in cluster VI had the highest plot yield than any other clusters. Cluster V congregated 8 genotypes is important cluster for the quantitative characters *viz.* branch/plant, seeds/pod and pod length (Table 5). Similarly, cluster IV is only important to pods/plant character. Cluster VI showed highest value of plant height and plot yield character so cluster VI is important for these two characters. Clusters were homogenous within and heterogenous across. The two way hierarchal dendrogram was framed using Ward's clustering method (Fig 2). This method is based on

Table 3. Trait relationship based on Pearson correlation coefficient in blackgram

Characters	Plant height	Branches/plant	Pods/plant	Seeds/pod	Pod length	Plot yield
Plant height	1	0.14	0.01	0.02	-0.03	-0.09
Branches/plant		1	0.71*	0.09	0.56*	0.61*
Pods/plant			1	0.21	0.49*	0.49*
Seeds/pod				1	0.19	0.02
Pod length					1	0.52*
Plot yield						1

* Significance at 1% level of probability

minimizing the loss of information from joining two groups. Similarly, constellation plot was also developed which also distributed genotypes in 7 clusters (Fig 3). Thus, the genotypes of cluster IV and VI can be used as agronomic base parent in the hybridization program with other genotypes to develop high yielding varieties. The genotypes belonging to different place of origin were distributed into same and different clusters indicated there was considerable amount of variability among the studied genotypes and lack of any relationship between the genetic and geographical diversity of the genotypes. The lack of correlation between agronomic performance and geographic origin is in accordance to the earlier reports (Amurrio *et al.* 1993, 1995; Ghafoor 2000). The magnitude of variation among the genotypes also directed the chance to use them through inter-genotypic improvement activities. Representative genotypes should be chosen from particular groups for hybridization programme. These results are corroborating to the earlier findings in black gram (Subramanian and Muthiah 2003; Neelavathi and Govindarasu 2010; Ghafoor *et al.* 2001, Ghafoor and Ahmad 2005; Ghafoor and Arshad 2008; Shafique *et al.* 2011). In addition, it also suggests that the genotypes within cluster may have ancestral relationship at some extent. Based on agronomic traits, the grouping of most of the advanced breeding lines along with released variety in I cluster revealed that only a portion of the genetic diversity of black gram has been exploited in varietal development program. It is suggesting that the genetic base of cultivated black gram should be broadened, involving diverse parents in the breeding programme (Laghetti *et al*. 1998, Ghafoor *et al.* 2001).

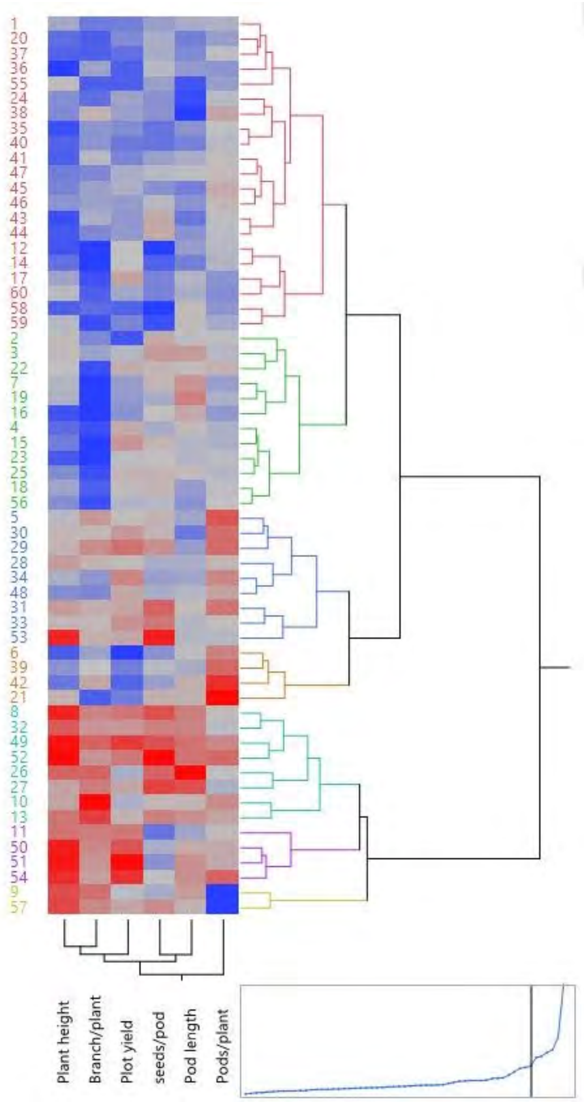

Fig. 2. Dendrogram of 60 genotypes of black gram based on 6 quantitative characters

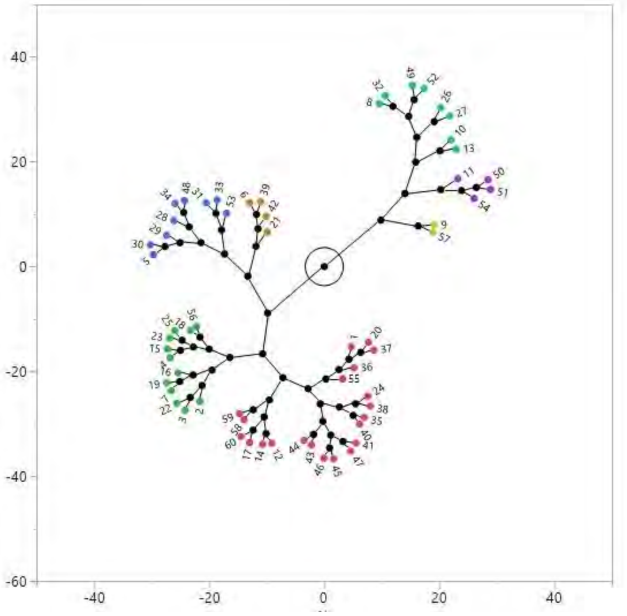

Fig. 3. Clustering of different blackgram genotypes using constellation Plot

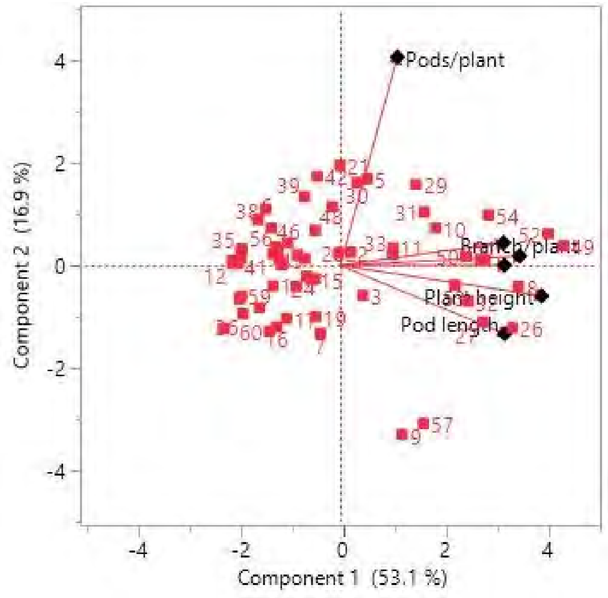

Fig. 4. The biplot of 60 genotypes of black gram based on PC1 and PC2.

Table 4. Distribution and frequency of 60 black gram genotypes into different cluster groups

Cluster	Number of genotypes	% contribution	Name of genotypes
I	**21**	35	AKU 10-6, KU 13-01, KU 96-7, NDUK 13-4, LBG-791, PU 09-37, RUG-88, RUG-89, RUG-90, RUG-92, RUG-93, RUG-95, RUG-96, RUG-87, RUG-97, RUG-98, RUG-99, SBC-47, Uttara, VBG 11-016 and VBG 11-31.
II	**12**	20	AKU 11-8, COBG 10-06, IU 02-1-3, MU-44, KUG-715, KUG-479, MU-06, NUL-244, Pant U 31, DKU-11, TU-67, PU 11-14
III	**9**	15	IPU 94-1, RUG-10, RUG-8, RUG-1, RUG-59, RUG-100, RUG-34, RUG-55, RUG-120
IV	**4**	6.66	IPU 94-3, RUG-91, RUG-94, NDUK 13-6
V	**8**	13.33	KPU 07-08, RUG-46, RUG-115, RUG-119, PU-1, PU-31, KPU 405, KU 96-3
VI	**4**	6.66	KPU 524-65, RUG-116, RUG-117, RUG-123
VII	**2**	3.33	KPU 129-104, UG-218.

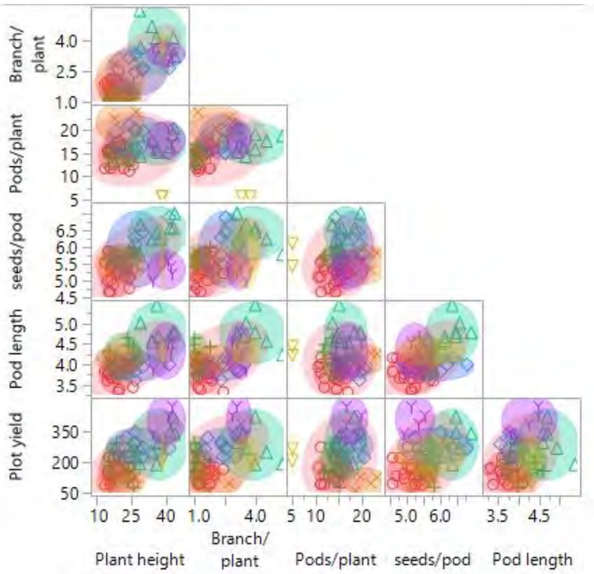

Fig. 5. Scatter plot matrix between different traits in blackgram genotypes

The Biplot diagram (Fig 4) graphically portrayed the relationship among yield and its attributes as it is important tool for graphical representation of association between traits. A less than 90° angle among vectors indicative of a positive correlation between yield attributing traits and vice versa. The close appearance between yield attributing traits on graph revealed positive association with yield through biplot analysis which confirmed the simple correlation study. Similarly, the scatter plot matrix is also a graphical tool used for illustrating the relationship between two variables (Fig 5). The pattern of scatter plot matrix of plot yield with plant height, pods/plant, seeds/pod and pod length showed positive relationship. On the contrary, branch/plant had slight scattered pattern which indicates comparatively weaker relationship.

Thus, the present investigation witnessed that abundant variability existing in given yield attributes of tested panel of blackgram genotypes. The significant positive relationship of seed yield with other traits suggesting indirect selection based on component traits would be helpful in improvement of the seed yield. The PCA analysis demonstrated significant variations among the traits with three major principal components contributing

Table 5. Cluster-wise mean values of characters in the studied black gram genotypes

Cluster	Count	Plant height	Branch/plant	Pods/plant	seeds/pod	Pod length	Plot yield
1	21	19.76*	1.60	14.60	5.24*	3.78*	155.42
2	12	22.16	1.28*	14.79	5.71	4.17	203.30
3	9	28.95	2.52	18.49	5.94	3.93	278.70
4	4	21.53	2.07	21.58**	5.48	4.13	101.66*
5	8	38.01	4.00**	17.20	6.43**	4.76**	285.62
6	4	41.51**	3.33	17.97	5.32	4.33	407.92**
7	2	39.71	3.66	5.66*	5.78	4.33	237.50

Note: **represents highest mean value, *represents the lowest mean value of the character.

more than 80 percent variation of total variation. The cluster analysis distributed the genotypes in seven distinct clusters. Moreover, the advanced breeding lines and released varieties refuge in same cluster registered that hitherto small portion of the available genetic diversity has been used in black gram varietal improvement program in India. At the end it may be concluded that selection of genotypes from different groups and their proper accommodation in urdbean hybridization programme would certainly increase the possibility of getting desired recombinants and also play crucial role in broadening the genetic base of blackgram. Thus, hybridization of these genetically divergent parents could also lead to the development of better promising blackgram varieties.

REFERENCES

Amurrio JM, De Ron AM and Escribano MR. 1993. Evaluation of *Pisum sativum* landraces from the Northwest of Iberian peninsula and their breeding value. Euphytica **66**: 1-10.

Amurrio JM, De Ron AM and Zeven AC. 1995. Numerical taxonomy of Iberian pea landraces based on quantitative and qualitative characters. Euphytica **82**: 195-205.

Anonymous. 2018. Project coordinator report (Mungbean and Urdbean) 2017-18. All India Coordinated Research Project on MuLLaRP, ICAR-IIPR, Kanpur.

Chauhan MP, Mishra AC and Singh AK. 2008. Genetic divergence studies in urdbean [*Vigna mungo* (L.) Hepper]. Legume Research **31**: 63-67.

Chauhan MP, Mishra AC and Singh AK. 2007. Correlation and path analysis in urdbean. Legume Research **30**: 205-208.

Dasgupta T and Das PK. 1984. Multivariate analysis and selection of parents for hybridization in blackgram. Philippine Agriculturist **57**: 86-92.

Dasgupta T and Das PK. 1985. Gene pool divergence and selection of parents for hybridization in blackgram. Bangladesh Journal of Agricultural Research **10**: 9-15.

Elangaimannan R, Anbuselvam Y and Karthikeyan P. 2008. Genetic diversity in blackgram [*Vigna mungo* (L.) Hepper]. Legume Research **31**: 57-59.

Ghafoor A, Ahmad Z, Hashmi NI and Bashir M. 2003. Genetic diversity based on agronomic traits and SDS-PAGE markers in relation to geographic pattern of blackgram [*Vigna mungo* (L.) Hepper]. Journal of Genetics & Breeding **57**: 5-4.

Ghafoor A and Ahmad Z. 2005. Diversity of Agronomic Traits and Total Seed Protein in Black gram [*Vigna mungo* (L.) Hepper]. Acta biologica Cracoviensia. Series botanica **47**: 69-75.

Ghafoor A and Arshad M. 2008. Multivariate analyses for quantitative traits to determine genetic diversity of blackgram [*Vigna mungo* (L) Hepper germplasm. Pakistan Journal of Botany **40**: 2307-2313.

Ghafoor A, Sharif A, Ahmad Z, Zahid MA and Rabbani MA. 2001. Genetic diversity in Black gram (*Vigna mungo* L. Hepper). Field Crops Research **69**: 183-190.

Ghafoor A. 2000. Genetic diversity and gene-action in *Vigna mungo* based on morphological and biochemical markers. Ph.D. dissertation, Quaid-I-Azam University, Islamabad, Pakistan.

Gupta S and Parihar AK. 2015. Broadening the genetic base of pulse crops. In: Pulses challenges and opportunities under changing climatic scenario. Proceeding of national conference on Pulses: Challenges & Opportunities under Changing Climatic Scenario. Pp 347.

Hadimani A, Konda CR, Nidagundi JM and Patil R. 2016. Genetic diversity analysis in blackgram [*Vigna mungo* (L.) Hepper] based on quantitative traits. Green Farming **7**: 598-601.

Jayamani P and Sathya M. 2013. Diversity in pod characters in blackgram [*Vigna mungo* (L.) Hepper]. Legume Research **36**: 220-223.

Katiyar PK and Dixit GP. 2010. Genetic divergence in Indian blackgram cultivars. Indian Journal of Agricultural Sciences **80**: 242-243.

Katiyar PK, Dixit GP, Gaurav K and Ayushi T. 2016. Bi-plot analysis for genetic diversity in blackgram [*Vigna mungo* (L.) Hepper]. Journal of Food Legumes **29**: 195-198.

Laghetti GBL, Pienaar S, Pasdulosi and Perrino P. 1998. Ecogeographical distribution of *Vigna* savi on Southern Africa and some area of Mediterrian basin. Plant Genetic Resources Newsletter **115**: 6-12.

Neelavathi S and Govindarasu R. 2010. Analysis of variability and diversity in rice fallow blackgram [*Vigna Mungo* (L.) Hepper]. Legume Research **33(3)**: 206-210.

Parihar AK, Dixit GP, Pathak V and Singh D. 2014. Assessment of the genetic components and trait associations in diverse set of fieldpea (*Pisum sativum*) genotypes. Bangladesh Journal of Botany **43**: 323-330.

Parihar AK, Dixit GP and Singh D. 2013. Multivariate analysis of various agronomic traits in grasspea (*Lathyrus* spp) germplasm. Indian Journal of Agricultural Sciences **83**: 570-575.

Shafique S, Khan MA, Nisar M and Rehman S. 2011. Investigation of genetic diversity in blackgram [*Vigna mungo* (L.) Hepper]. Pakistan Journal of Botany **43**: 1223-1232.

Shanmugam AS and Shreerangaswamy SR. 1982. Multivariate analyses of genetic divergence in blackgram (*Vigna mungo* (L.) Hepper). Madras Agricultural Journal **69**: 701-706.

Shivade HA, Rewale AP and Patil SB. 2011. Correlation and path analysis for yield and yield components in black gram [*Vigna mungo* (L.) Hepper]. Legume Research **34**: 178-183.

Sohela MH, Miaha MR, Mohiuddinb SJ, Sajjadul Islamc AKM, Rahmand MM and Haquee MA. 2016. Correlation and path coefficient analysis of Black gram (*Vigna mungo* L.). Journal of Bioscience and Agriculture Research **07**: 621-629.

Subramanian A and Muthiah A. 2003. Genetic diversity analysis in greengram and black gram Madras Agricultural Journal **90**: 481-484.

Umadevi M and Meenakshi NG. 2005. Correlation and path analysis for yield and yields components in black gram (*Vigna mungo* (L.) Hepper.) Madras Agricultural Journal **92**: 731-734.