Genetic Divergence Studies in Black Gram (*Vigna Mungo* (L.) Hepper)

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ABSTRACT

The experiment was conducted during 2017-2018 to estimate the genetic divergence, using 120 black gram genotypes for nine quantitative characters. Among the nineteen clusters, cluster I had maximum number of genotypes (62) followed by the cluster III (16 genotypes), cluster XIV (11 genotypes), cluster (9 genotypes). Clusters XV and XVII (4 genotypes) and cluster XVIII (2 genotypes). The clusters *viz.*, II, IV, V, VI, VII, VIII, IX, X, XII, XIII, XVI and XIX had one genotype each. The cluster XVII exhibited the maximum intra cluster distance. The maximum inter cluster distance was recorded between cluster XIX and IV. The maximum genetic divergence per cent was contributed by the trait number of clusters per plant. The cluster II and VI had the lowest mean value for days to 50% flowering and the cluster VII had the highest mean value for the trait and number of pods per plant.

Keywords: Black gram, clusters, genetic divergence, Biometrical traits

INTRODUCTION

Pulses are the universal crops rated as one among the important crops in the World. Globally these are grown in 22 million hectares of area with an annual production of 12-16 million tonnes (FAOSTAT, 2014). Among the pulses pigeon pea, black gram and green gram contributes majority of the total pulse production. India is the largest producer and consumer of black gram, cultivated in an area of about 3.26 million hectares with a production of 1.76 million tonnes (AICRP report, 2013). The cultivated black Gram belongs to the family Leguminosae, sub family Papilionaceae. It is a day neutral, warm season crop grown as mixed crop, cash crop, sequential crop and also grown as sole crop under residual moisture conditions after the harvest of rice crop. Black gram contains sulphur containing amino acids *viz.*, methionine and cysteine, as best source for human diet (Praveen *et al*., 2011). Black gram seeds contain 65 per cent carbohydrates and 25 per cent protein and are consumed as food where sprouts produced from urdbean can be used as vegetable a source of minerals and vitamins. The developments of modern breeding programmes are less in black gram compared to cowpea and mungbean crops (Ghafoor *et al*., 2001). The major disadvantage to achieve higher yield in black gram are low variability, poor harvest index, lack of appropriate videotapes for different cropping systems and susceptibility to biotic and a biotic stresses. Occurrence of narrow genetic base and non-availability of quality seeds of improved varieties are due to repeated usage of fewer parents with high degree of relatedness in crossing programmes. Genetic diversity is a pre-requisite for stabilizing the production for increasing yields in the face of disease epidemic and environmental variations in crops (Gupta *et al*., 2001).

Materials and Methods

The present investigation aimed within the study of genetic diversity using one hundred and twenty germplasm lines collected from National Bureau of Plant Genetic and Resources (NBPGR), New Delhi, Agricultural College and Research Institute Madurai

and Agricultural College and Research Institute, Killikulam. The field experiment was conducted at D block of Department of Plant Breeding and Genetics at Agricultural College and Research Institute, Killikulam during the year 2017-2018. During *Rabi* 2018 a set of one hundred and twenty genotypes of urdbean were evaluated in Randomized block Design (RBD) with two replications. Each genotype was raised in a single row of 3 meter length with a spacing of 30 x 10 cm. Observations were recorded on five randomly selected plants in each replication for nine quantitative characters *viz.*, days to 50 per cent flowering, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per plant, hundred seed weight (g), pod length (cm) and single plant yield (g). The genetic diversity was estimated by using Mahalanobis D^2 statistics (Mahalanobis, 1936) and the genotypes were grouped into different clusters following Tochers method as described by Rao (1952).

Results And Discussion
Genetic diversity analysis was carried by Mahalanobis method in one hundred and twenty black gram genotypes for nine quantitative characters and the genotypes were grouped in to nineteen clusters (Table 1 and Fig.1). Among the nineteen clusters, cluster I had maximum number of genotypes (62) followed by cluster III (16) cluster XIV (11) cluster XI (9) Clusters XV and XVII (4) and cluster XVIII (2). The clusters *viz.*, II, IV, V, VI, VII, VIII, IX, X, XII, XIII, XVI and XIX had one genotype each.

The intra and inter cluster distance among the nineteen clusters obtained are presented in Table 2. The maximum intra cluster distance was observed in the cluster XVII (17.76) followed by clusters *viz.*, XIV (15.07), cluster XV (14.31) and cluster III (11.61). No intra cluster values were recorded for twelve solitary clusters. The inter cluster distance ranged from 6.35 to 42.80. The maximum inter cluster distance was observed in clusters XIX and IV (42.80) followed by clusters *viz.*, XIX and XVI (41.50), XIX and IX (41.36) and XIX and XV (40.75). The discrimination of germplasm lines into many discrete clusters, suggested the presence of high degree of

genetic diversity. Earlier workers had reported the existence of high degree of genetic diversity in urdbean germplasm. (Shanthi *et al*. 2006 and Katiyar and Dixit, 2010), It is noted that the inter cluster distances was more than the intra cluster distances. Similar results were reported by Singh *et al*. (2001), Chauhan *et al*. (2008). Hence, magnitude of hetero sis is largely depends on the degree of genetic diversity in the parental lines. Least value of inter-cluster D^2 value was observed between the clusters VII and V (6.35) suggested that the genotype in one cluster is in close promixity with the genotype in the other cluster pair. Hence, genotype from these clusters may not be useful in breeding programmes (Konda *et al*., 2007).

The relative contribution of nine biometric characters for genetic divergence in black gram is represented in Table 3. The trait *viz.*, number of clusters per plant contributed maximum towards the genetic divergence (29.59 %) followed by single plant yield (27.44%), number of pods per plant (15.63 %), plant height (15.18 %), number of primary branches per plant (5.62 %), hundred seed weight (4.64%), days to 50 per cent flowering (1.40 %) and number of seeds per pod (0.50 %). Similar results were reported by Gowsalya *et al.* (2017) for eighty seven genotypes in urdbean into twelve clusters in urdbean,

The cluster mean for the nine characters studied is given Table 4. It revealed that the cluster II and VI with two genotypes (CO-6 and KKB14047) had the lowest mean value for days to 50 % flowering and hence these genotypes could be used as source for earliness. The highest mean values were recorded by the cluster XIX (number of pods per plant for 65.7) , cluster XII (plant height for 61.15 cm), Cluster XIX (number of clusters per plant for 37.30), cluster XV(single plant yield for 34.41 g), cluster VI (number of seeds per plant for 7.30), cluster XII (number of primary branches per plant for 6.00) and cluster I (hundred seed weight for 5.65 g) and Clusters XII (pod length for 5.23 cm). Hence, the genotypes present in the above said clusters would be utilized for hybridization programmes and that would result in getting transgressive segregants and exploiting genetic variation in future breeding programmes.

Table1. Composition of D^2 cluster for black gram genotypes

Clusters	Number of genotypes	Genotypes
I	62	IC436656, IC436676, VBG14003, VBG12039, KU11680, IC436536, ABG11030, IC436780, ABG11015, IC343812, IC343947, IC282002, IC436882, IC282004, IC436512, VBG11042, IC436545, IC436560, IC436565, IC343967, IC36604, IC36724, IC281992, IC436609, IC436720, RU155, IC436518, IC436627, ABG11032, IC436612, IC436676, KU12668, VBG10053, ABG11004, IC436869, KKB14054, IC436792, ABG11004, IC436547, IC436772, RU152, IC436524, IC436597, IC436922, VBG10024, IC343885, ADT-3, IC436784, IC436774, IC436635, IC436610, RU158, IC335331, IC343936, VBN-4, VBG11018, IC436652, IC436762, KKM-1, KKB14049, RU152
II	1	CO6
III	16	IC436765, KKB01453, ADT-6, KKB14038, KKB14051, KKB14020, IC343856, RU1515, KKB14043, IC436606, VBN6, IC343939, KKB14022, KKB14004, KKB14033, KKB14015
IV	1	IC436720
V	1	IC436758
VI	1	KKB14047
VII	1	IC436753
VIII	1	RU154
IX	1	RU151
X	1	IC436910
XI	9	RU153, RU15009, IC436621, RU1513, KKB14044, IC436852, KKB14009, IC343943, VBG12042
XII	1	VBG12034
XIII	1	RU1512
XIV	11	ADT5, RU1510,RU1516, KKB14001, KKB14002,KKB14004, KKB14052, KKB14003, VBG10010, KKB14034, KKB14048, KKB14004, KKB14002
XV	4	KKB14045, KKB14041, RU159, KKB14042
XVI	1	IC436508
XVII	4	KKB14046, VBG10027, IC436535, VBG11040
XVIII	2	IC436626, RU1511
XIX	1	KKB14049

Table2. Average inter and intra cluster D^2 values for black gram genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX
I	10.59	13.26	18.83	13.46	12.86	15.19	12.95	13.70	13.28	13.10	16.09	13.89	13.98	28.25	32.00	16.27	15.65	24.03	34.69
II		0.00	12.91	19.59	20.16	7.40	20.36	14.09	15.45	13.53	12.25	13.83	11.42	22.78	24.33	19.74	13.75	20.83	32.38
III			11.61	25.60	24.57	16.64	25.29	18.47	21.09	18.32	17.58	20.14	18.92	17.75	20.02	25.38	18.89	18.15	25.65
IV				0.00	11.05	18.94	12.21	14.48	11.10	11.00	17.96	17.64	21.21	36.14	37.83	19.69	20.93	27.52	42.80
V					0.00	22.34	6.35	16.89	14.80	16.51	21.92	17.86	20.28	32.96	38.59	16.44	19.33	25.66	38.55
VI						0.00	22.81	16.45	17.10	12.19	9.94	13.17	13.75	26.83	25.07	23.54	17.38	23.99	35.38
VII							0.00	18.60	15.00	17.43	22.23	18.68	19.39	34.11	39.73	14.40	19.73	28.91	39.25
VIII								0.00	8.16	13.11	17.48	19.93	17.85	28.74	31.29	16.51	15.21	22.10	37.75
IX									0.00	10.93	17.01	21.40	19.72	32.52	34.25	14.87	16.83	25.79	41.36
X										0.00	10.46	16.27	19.88	29.45	28.31	22.73	19.23	21.77	36.95
XI											11.33	15.73	18.37	27.71	25.32	25.41	20.10	23.37	35.18
XII												0.00	12.24	27.17	29.95	23.96	19.07	23.80	32.03
XIII													0.00	26.66	31.21	16.57	14.66	28.08	32.81
XIV														15.07	20.44	34.41	27.03	20.14	18.91
XV															14.31	40.75	31.64	23.12	26.25
XVI																0.00	16.66	32.96	41.50
XVII																	17.76	25.20	35.21
XVIII																		9.37	28.46
XIX																			0.00

Table3. Relative contribution of various characters to genetic divergence in black gram

Characters	Number of times ranked First	Contribution Percentage (%)
Days to 50% flowering	100	1.40
Plant height (cm)	1084	15.18
No. of primary branches per plant	401	5.62
No. of clusters/plant	2113	29.59
No. of pods/plant	1116	15.63
No. of seeds/ pod	36	0.50
100 seed weight (g)	331	4.64
Pod length (cm)	0	0.00
Single plant yield (g)	1959	27.44
Total	7140	100 %

Table4. Cluster mean for nine quantitative traits in black gram

Character Cluster	Days to 50 % flowering	Plant height (cm)	No. of primary branches per plant	No. of clusters/plant	No. of pods/plant	No. of seeds/ pod	100 seed weight (g)	Pod length (cm)	Single plant yield (g)
I	35.60	52.35	3.47	14.63	34.69	6.18	5.65	4.72	14.57
II	33.00	47.75	4.55	18.75	38.50	6.25	5.10	5.10	22.15
III	34.25	49.80	3.42	24.84	50.08	6.08	4.88	4.57	23.50
IV	37.00	59.05	3.25	8.75	19.00	6.16	4.55	4.30	14.70
V	40.50	56.30	2.25	15.30	26.00	6.60	5.15	4.88	9.00
VI	33.00	52.80	5.25	13.75	37.00	7.30	5.15	5.15	24.50
VII	37.50	54.30	2.00	12.25	29.00	5.15	5.45	5.00	8.95
VIII	34.00	44.75	3.25	16.25	27.00	6.80	3.60	3.60	18.55
IX	35.50	46.50	2.25	11.50	23.50	6.05	4.10	4.10	21.15
X	35.00	59.65	3.15	12.75	29.50	6.25	4.45	4.45	23.50
XI	34.11	58.06	4.36	13.80	36.81	6.24	4.87	4.84	25.42
XII	34.50	61.15	6.00	16.65	38.50	6.47	5.25	5.23	11.54
XIII	34.00	44.25	5.55	15.00	44.90	6.30	5.00	5.05	12.80
XIV	34.18	50.96	3.83	35.90	62.80	6.00	4.89	4.72	20.52
XV	34.50	57.89	4.82	31.09	61.29	6.10	4.87	4.55	34.41
XVI	37.00	34.30	2.30	11.45	33.00	6.00	4.60	4.60	11.40
XVII	36.00	42.08	3.84	18.35	37.03	6.66	4.86	4.73	16.58
XVIII	35.75	61.00	3.50	34.75	35.38	6.45	4.32	4.32	20.35
XIX	35.00	60.50	3.35	37.30	65.70	6.00	4.30	4.55	13.00
MEAN	35.28	52.28	3.70	19.76	38.37	6.26	4.79	4.65	18.24

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Fig 1, Clustering pattern of the studied genotypes in black gram by Tocher's method

Clustering by Tocher Method