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Genetic Diversity For Yield and its Components in Different Genotypes of the Blackgram {*Vigna mungo* (L.) Hepper}

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Abstract

The experimental material consisting sixty genotypes of Blackgram [Vigna mungo (L.) Hepper]" were subjected to genetic divergence by using D2 statistic.The genotypesgrouped into eight clusters by D2 analysis. Cluster VI consisted maximum accessions (12) followed by cluster II(10), cluster I (8), cluster VIII (7), cluster III, IV,VII, (6) and cluster V consisted 5 genotypes. At intra cluster level, maximum values were recorded for cluster VIII (35.77) followed by cluster II (30.81), cluster VI (28.70), cluster I (18.62). The average inter cluster values were maximum between cluster III and VIII followed by cluster VII and VIII. Cluster VIII showed maximum genetic divergence with III (84.28), cluster IV (80.77) and cluster V (66.36) distances revealing considerable amount of genetic diversity among the genotypes. Therefore, the genotypes falling in these clusters appeared to be divergent and might have different geographical/genetic origin hence could be gainfully utilized in blackgram breeding improvement programme.

Keywords -Yield attributes, Black gram, Divergence, D^2 analysis, Cluster

Introduction

Blackgram [*Vigna mungo* (L.) Hepper] is an annual, short duration, self pollinated, leguminous crop belong to family leguminoseae sub family Papilionaceae with a chromosome number of 2n=2x=22, it is commonly known as urd bean. Center of genetic diversity of blackgram is found in India (Zeven *et al*. 1982). It is important pulse crop of asia and grown extensively in India.

Pulses occupy a very significant and crucial position in Indian Agriculture after cereals and oilseeds. Besides being one of the important components of daily diet, pulses fix a large amount of atmospheric nitrogen in association with Rhizobium bacteria. Among the various pulses, blackgram is an important one which contains approximately 25-28% protein, 4.5-5.5% ash, 0.5-1.5% oil, 3.5-4.5% fibre and 62-65% carbohydrate on dry weight basis (Kaul, 1982). It contains sulphur containing amino acids, methionine and cysteine and also contains lysine, which are excellent component of balanced human nutrition.Due to highly nutritious and multipurpose nature of this crop, still it faces so many problems due to its narrow genetic base. A successful breeding programme is based on parents having more genetic diversity, may be used in hybridization breeding proramme. The genetic diversity between the genotypes is

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important as the genetically diverged parents can produce high heterotic effects (Mian and Bahl 1989). Knowledge of germplasm diversity among elite breeding materials has a significant impact on the improvement of crop plant.

Materials andMethods

Fifty six genotypes with four checks viz., (PU31, PU1, KPU405, KPU524-65) of blackgram were sown in three replication in a Randomized Block Design during *kharif* - 2017at the Botany field, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur, India. Each genotype was accommodated in one row plot of 4.0 m length with a spacing of 30 cm between rows and 10 cm between plants. All the recommended package of practices of zone IVA of Rajasthan were followed to raise a healthy crop. Observations were recorded on five randomly selected plants from each treatment in each replication for all the characters except days to 50 per cent flowering and days to maturity as they were recorded on plot basis in each replication for each genotype. The representative bulk sample from each entry in each replication was used for analysis of protein content. Mean value of 5 plants were used for statistical analysis.Genetic divergence was calculated for 15 characters by Mahalanobis D^2 statistics(1936).

Results and Discussion

Sixty genotypes were grouped into VIII clusters on the basis of observed distance among genotypes within a cluster as compared to genotypes in other cluster in Table 1. Cluster VI contains maximum number of genotypes i.e. 12 followed by 10 in cluster II, 8 in cluster I, 7 in cluster VIII, 6 in cluster III, IV and VII, 5 in cluster V. The clustering pattern revealed that, in general, genotypes from same origin showed no tendency to be in same cluster.

Looking to the pattern of genotypes distribution into different clusters in the present study, it appeared that geographical distance between the genotypes had no relation with the genetic divergence as the genotypes from same source had fallen into different clusters as well as the same cluster contained genotypes from different sources. These finding are in close agreement to earlier reported by Singh *et al.* (2012) and Gupta *et al.* (2016).

Table 1: Black gram genotypes included in each cluster

Clusters	Number of genotypes	Genotypes Included
I	8	KPU1079,KPU1084,KPU1088,KPU1097, KPU1107,Pant U40,KPU1115, KPUA14-146
II	10	KPU1078,KPU1094,KPU1095,KPU1101, KPU1104,KPU1124,KPU07-08,KPU52-87,KPU52-88, PU1
III	6	KPU1053, KPU1074,KPU1081,KPU1146,KPU1143,KPU1126
IV	6	KPU1070,KPU129-104, KPU1108,KPU514-

		75,KPU52-89,KPU1139
V	5	KPU1120, KPU1121, KPU1122, KPU12-1733,KPU96-3
VI	12	KPU1080,KPU1099,KPU1102,KPU1105,KPU1109, KPU1116,KPU1123,KPU1134,KPU1137,KPU1138, KPU1144, KPU405
VII	6	KPU1073, KPU1001,KPU1132,KPU1135,PU31,KPU524-65
VIII	7	KPU1072, KPU1147, KPU1148,KPU1098,KPU1027, KPU1125,KPU1128

Intra and inter cluster divergence:

As evident from table 2 at intra cluster level, maximum values were recorded for cluster VIII (35.77)followed by cluster II (30.81), cluster VI (28.70), cluster I (18.62). There were no intra- cluster distances in cluster III, cluster IV and cluster V and VII.

The average inter cluster values were maximum between cluster III and VIII followed by cluster VII and VIII. Cluster VIII showed maximum genetic divergence with III (84.28), cluster IV (80.77) and cluster V (66.36) distances revealing considerable amount of genetic diversity among the genotypes. Therefore, the genotypes falling in these clusters appeared to be divergent and might have different geographical/genetic origin hence could be gainfully utilized in blackgram breeding improvement programme. Singh *et al.* (2012) and Gupta *et al.* (2016) also reported same results in blackgram.

Thus, cluster VIII displayed high inter cluster distances from cluster III, cluster IV, cluster V. Therefore, crosses between such genotypes are expected to give desirable transgressive segregants.

Table 2: Average intra and inter-cluster distances in 60 genotypes of blackgram

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**18.62**	39.17	74.51	69.91	55.90	78.46	45.84	37.81
II		**30.81**	43.63	42.61	36.81	54.07	44.30	56.42
III			**0.00**	13.42	16.19	22.93	60.64	84.28
IV				**0.00**	19.50	25.73	66.60	80.77
V					**0.00**	30.68	73.90	66.36
VI						**28.70**	77.96	88.82
VII							**0.00**	62.00
VIII								**35.77**

Bold number = intra-cluster distance

Relative contribution of different characters:

Relative contribution of each of 14 characters towards total divergence was worked out using per cent I rank and some of D for each character over the pairs of genotypes (table 3). Trend of contribution of different characters was same in both the methods. Maximum contribution towards the total D using square of D was found to be from protein content (16.10) followed by pod length, cluster per plant, number of pods per cluster, seed yield per plant, days to 75 per cent maturity, plant height,days to flowering, biological yield per plant, pods per plant, seed per pod, primary branch per plant, harvest index.

Table 3 Relative contribution of different characters

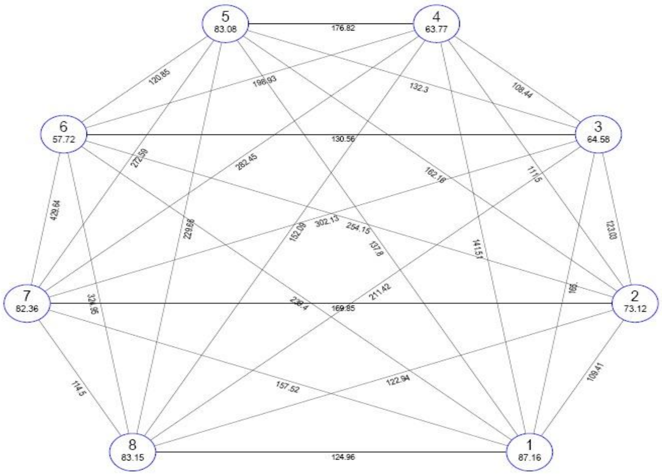
S. No.	Source	Times Ranked 1st	Contribution%
1	Days to 50 per cent flowering	45.00	2.54
2	Days to 75 per cent maturity	84.00	4.75
3	Plant height	76.00	4.29
4	No of primary branch per plant	18.00	1.02
5	Clusters per plant	215.00	12.15
6	Number of pods per cluster	144.00	8.14
7	Number of pods per plant	25.000	1.41
8	Pod length	228.00	12.88
9	Number of seeds per pod	20.00	1.13
10	100- Seed Weight	94.00	5.31
11	Biological yield/ per plant	29.00	1.64
12	Seed yield per plant	116.00	6.55
13	Harvest index %	15.00	0.85
14	Protein content %	285.00	16.10

Clusters means

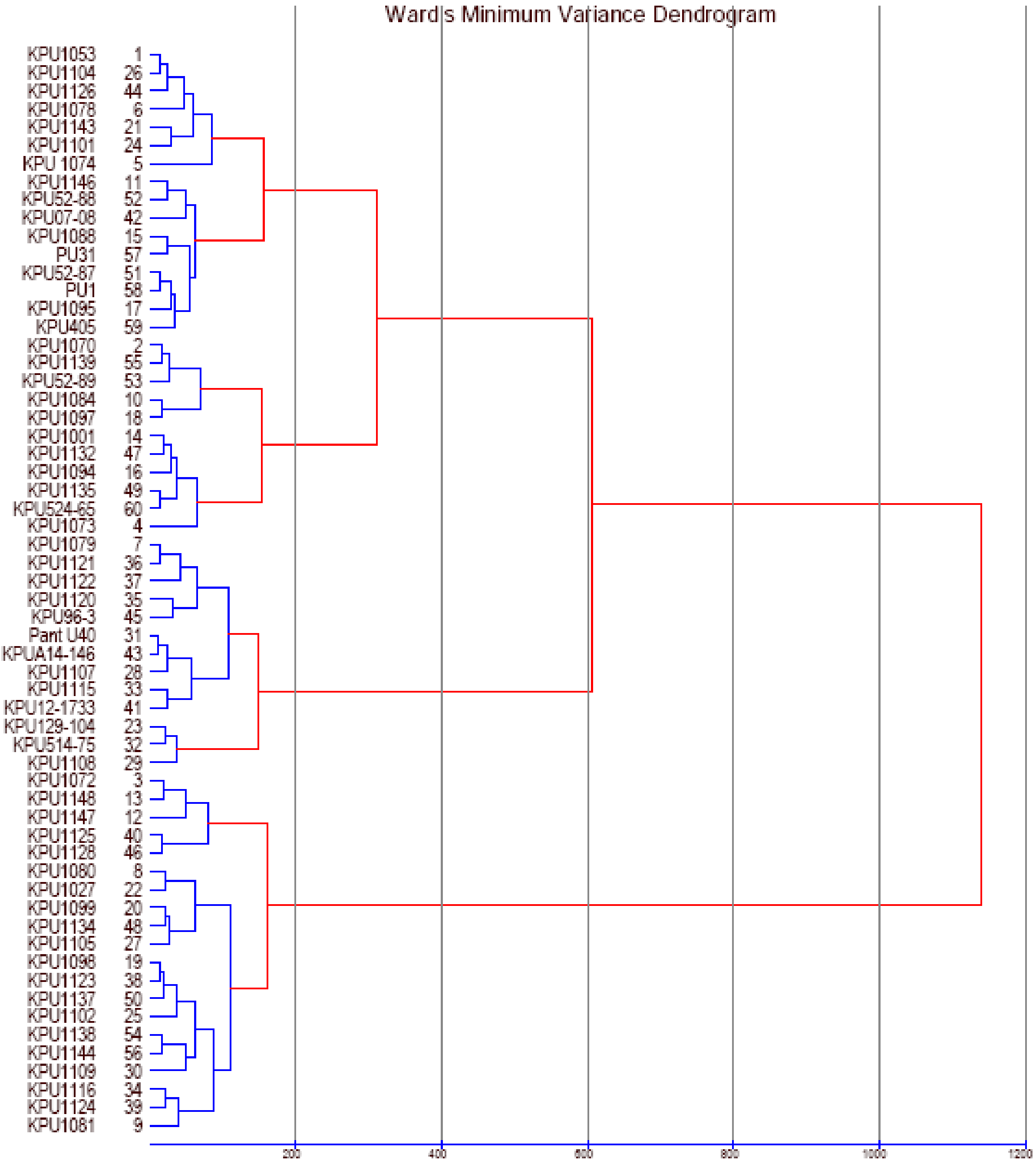
The cluster means (table 4.) indicated that cluster VI was having maximum seed yield per plant (5.97), cluster I showing highest harvest index (29.85), cluster IV maximum biological yield per plant (25.03),pod length (4.46), number of pod per plant (43.66), pod per cluster (16), 100-seed weight (5.66), cluster V shows earliest days to 50 per cent flowering (41), cluster VII shows earliest days to 75 per cent maturity (71), highest protein content (24.15), number of primary branch per plant (3.20), number of seed per pod (7.73), and cluster I have lowest plant height (19.30) and cluster VIII have highest number pod per cluster (3.11) therefore selection of genotypes for these characters may be made from these clusters. Higher mean values of different characters in different clusters was also reported by Gupta *et al.*(2016) and Gowsalya *et al.*(2017)

Table 4 Clusters means for different character in blackgram

Character	I	II	III	IV	V	VI	VII	VIII
Days to 50 per cent flowering	41.61	40.69	40.66	42.66	41.00	42.24	37.66	41.74
Days to 75 per cent maturity	76.22	75.80	77.00	80.00	80.00	76.60	71.00	77.07
Plant height	19.30	20.69	27.20	21.50	26.10	24.56	20.40	19.92
No of primary branch per plant	3.06	3.00	3.16	3.10	2.76	3.02	3.20	3.02
Clusters per plant	8.78	11.15	15.00	16.00	11.06	14.39	12.00	9.26
Number of pods per cluster	2.77	3.07	2.78	2.74	3.03	3.02	2.08	3.11
Number of pods per plant	24.61	33.57	43.00	43.66	42.66	43.46	26.33	27.96
Pod length	4.11	3.77	4.03	4.46	4.06	4.37	3.16	4.02
Number of seeds per pod	6.37	6.96	6.50	7.20	7.60	6.90	7.73	6.74
100- Seed Weight	4.19	5.27	5.60	5.66	5.00	5.30	4.66	3.86
Biological yield/ per plant	16.45	19.45	22.93	25.03	19.00	21.91	25.00	18.83
Seed yield per plant	4.80	5.41	5.53	5.17	4.83	5.97	4.53	4.68
Harvest index %	29.85	28.29	24.08	20.78	25.38	28.04	18.02	24.71
Protein content %	21.99	22.23	22.82	22.51	21.41	22.58	24.15	22.62



Euclidean² Distance (Not to the Scale)



Euclidean(Distance(NottotheScale)

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