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Genetic Diversity for Yield and Its Component Traits in Blackgram (*Vigna mungo*. L Hepper)

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Thirty eight genotypes were subjected to genetic divergence by using D_2 statistics. The genotypes were grouped into 7 clusters by D_2 analysis. Cluster I consisted of maximum accessions (32) followed by cluster II, III IV, V, VI, VII consisted of only 1 accession. The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Maximum intra cluster distance was observed in cluster I (56.58) indicating that some genetic divergence still existed among the genotypes. This could be made use of in the yield improvement through recombination breeding. Highest mean values exhibited no. of seeds per plant in cluster II (198.97), days to maturity in cluster VII (93.11), harvest index in cluster V (76.15) and plant height in cluster IV (69.59). The character contribution maximum towards diversity among the accessions were seed yield per plant (18.40%), followed by harvest index (14.32%), biological yield (11.98%), no. of pods per plant (10.76%), pod length (9.80%) and no. of seeds per plant (7.56%). These characters combining with early maturity were the major traits causing genetic divergence among the accessions. It was assumed that maximum mount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters.

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1. INTRODUCTION

It has been postulated that lack of genetic diversity is one of the basic causes for relatively poor success achieved in raising yield level in urdbean (*Vigna mungo* L. Wilczek). An assessment of the genetic diversity is an important first step in a program to improve crop yield. The proper estimate of nature and magnitude of diversity in a crop is essential to infer about extent of variation available for yield and its component traits. The selection of genetically divergent parents is expected to produce superior and desirable segregants following crossing [1]. The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programme. D_2 analysis has been found most effective and, therefore, widely used for the classification of parental lines for developing high yielding genotypes in black gram [2,3].

Yield is an important quantitative trait for any crop improvement programme. To increase production of blackgram there is need of developing high yielding varieties which requires a systematic breeding approach to be adopted. Assessment of variability is a first step in any breeding programme [4-7]. Greater the diversity in the material better are the chances of improvement, provided the heritability is high and genetic advance is more. Ultimate aim of any breeding programme is to get higher yield. Since, yield is a quantitative character and depends upon yield contributing traits, the selection is more effective when it is practiced simultaneously for the characters which have desired nature of association with the traits [8-11]. The present study was therefore, undertaken to estimate the amount of genetic diversity in thirty eight genotypes of black gram (*Vigna mungo* L. Hepper) and to identity genetic diversed parents for hybridization programmed at yield improvement in the crop.

2. METHODOLOGY

Thirty eight blackgram genotypes collected from diverse geographical origin were evaluated during kharif season 2019-2020 at experimental field of college farm in Sam Higginbottom University Agriculture, Technology and Science (SHUATS), Prayagraj, U.P. All the 38 genotypes were sown in Randomized Block Design with three replications each genotypes were sown in row of 1.5 m length with 30 cm row to row and 10 cm plant to plant distance ten competitive plants from each entry were randomly chosen to record the observations on days to 50% flowering, days to 50% pod setting, plant height, no. of primary branches per plant, days to maturity, no. pods per plant, pod length, no. of seeds per pod, no. of seeds per plant, biological yield, 100% seed weight, harvest index and seed yield per plant. The genetic divergence was estimated using mahalanobis' D_2 statistic [12] and genotypes were grouped into clusters following the Tocher's method as described by Rao [13].

3. RESULTS AND DISCUSSION

Thirty eight genotypes were found to be distributed in 7 clusters (Table 1 and Fig.1). Out of seven clusters, cluster I was the largest comprising of thirty two genotypes followed by cluster II, III, IV, V, VI, VII with one genotype each. The cluster II, III, IV, V, VI and VII were represented by single genotypes indicating high degree of heterogeneity among the genotypes. The assessment of genetic divergence of germplasm is essential to know the spectrum of diversity. In the present investigation, 38 genotypes of blackgram genotypes were considered for the assessments of genetic diversity by multivariate analysis as per Mahalanobis [12] concept of generalize distance considering 13 important quantitative characters. The values along the lines were inter cluster distances and the values within the circle were intra cluster distance. Maximum intra cluster distance was observed in cluster I (56.58) indicating that some genetic divergence still existed among the genotypes. High values of intra-cluster distance revealed that genotypes within the same cluster were quite diverse, hence selection of parents within cluster would also be effective and a good chance is there to develop a good segregates by hybridizing among parents within clusters. From the inter cluster D_2 seven clusters, it could be seen that the highest divergence occurred between cluster II and V (375.96) followed by cluster II and III (371.99), cluster III and VI (371.12) cluster V and VI (346.10), cluster VI and VII (305.04) that the crosses involving genotypes from these clusters

would give wider and desirable recombination. While the lowest was noticed between cluster III and V (41.44) followed by cluster II and VI (41.65), cluster III and VII (49.51), cluster IV and V (86.88) and cluster I and IV (99.48). Minimum inter cluster distance indicates that genotypes of these clusters had maximum number of gene complexes. The genotypes of these clusters may be used as parents in the crossing program to generate breeding material with high diversity. The results are in accordance with Solomon et al. [2]. The cluster means for each of 13 characters were presented in Table 3. From data it could be seen that considerable differences existed for all the characters under study. The data indicated that the cluster mean for days to 50% flowering was highest in cluster II, VII (46) and lowest in cluster VI (43.20), days to 50% pod setting was highest in cluster I (58.41) and lowest in cluster VI (54.20), plant height was highest in cluster VI (69.59) and lowest in cluster III (15.07), no. of primary branches per plant was highest in cluster VI (3.41) and lowest in cluster VII (1.95), days to maturity was highest in cluster VII (93.11) and lowest in cluster VI (88.53), no. of pods per plant was highest in cluster II (37.21) and lowest in cluster VII (5.43), pod length was highest in cluster V (5.50) and lowest in cluster VII (3.26), no. of seeds per plant was highest in cluster II (6.49) and lowest in cluster VII (3.33), no. of seeds per plant was highest in cluster II (198.97) and lowest in cluster VII (14.90), biological yield was highest in cluster VI (44.92) and lowest in cluster V (5.02), 100 seed weight was highest in cluster V (5.51) and lowest in cluster VII (3.26), harvest index was highest in cluster V (76.15) and lowest in cluster VI (40.46), seed yield per plant was highest in cluster II (20.30) and lowest in cluster V (3.83). The results indicated that selection of genotypes having high values for particular trait could be used in the hybridization programme for improvement of that character. The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times each of the yield component characters appeared first in rank and its respective percent contribution towards genetic divergence was presented in Table 4. Among the yield attributing traits the maximum contribution towards divergence was made by seed yield per plant (18.40%) by taking 129 times ranking first, followed by harvest index (14.32%) by 101 times, no. of pods per plant (10.76) by 76 times. The pattern of distribution of

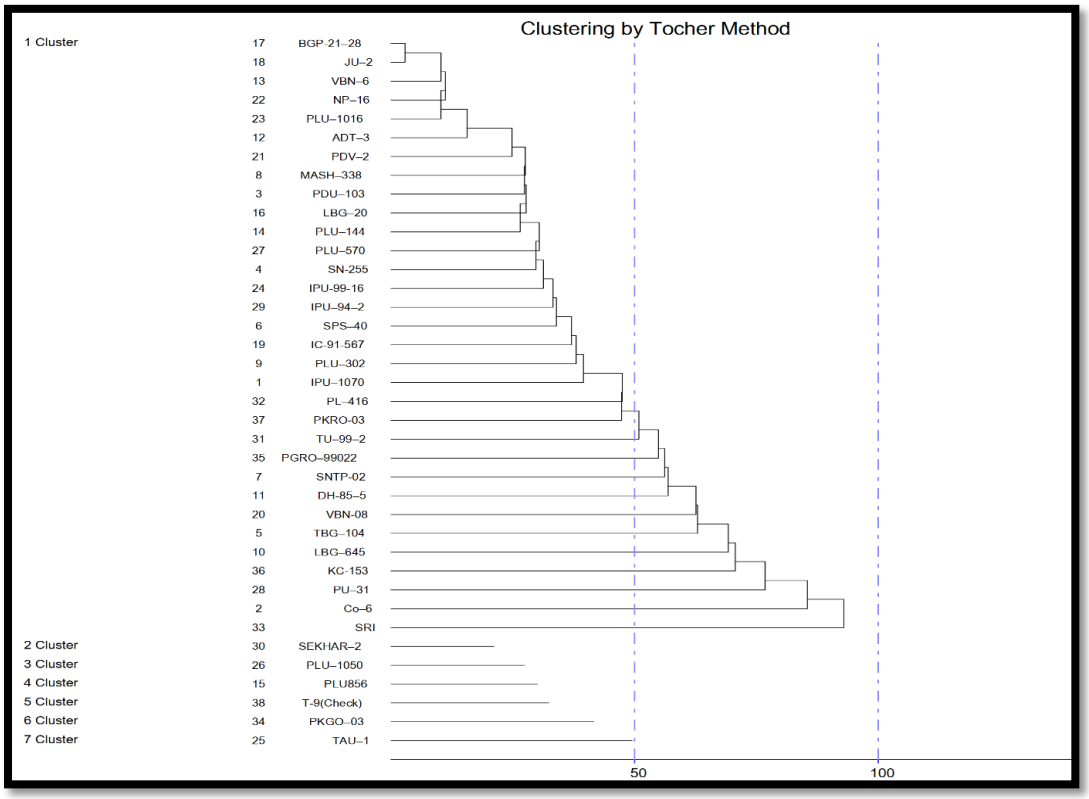

Fig. 1. Dendrogram showing distribution of thirty-eight genotypes of blackgram

Table 1. Distribution of 38 blackgram genotypes into different clusters based on D_2 statistic

Cluster	No. of genotypes	Genotypes
I	32	BGP-21-28, JU-2, VBN-6, NP-16, PLU-1016, ADT-3, PDV-2, MASH-338, PDU-103, LBG-20, PLU-144, PLU-570, SN-225, IPU-99-16, IPU-94-2, SPS-40, IC-91-567, PLU-302, IPU-1070, PL-416, PKRO-03, TU-99-2, PGRO-99022, SNTP-02, DH-85-5, VBN-08, TBG-104, LBG-645, KC-153, PU-31, Co-6, SRI.
II	1	SEKHAR-2
III	1	PLU-1050
IV	1	PLU856
V	1	T-9 (Check)
VI	1	PKGO-03
VII	1	TAU-1

Table 2. Cluster distance using Tocher method among thirty-eight genotypes of blackgram

Cluster Distances - Tocher method							
	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**
Cluster 1	56.58	146.41	123.23	99.48	117.35	145.13	111.48
Cluster 2		0.00	371.99	292.92	375.96	41.65	290.24
Cluster 3			0.00	145.90	41.44	371.12	49.51
Cluster 4				0.00	86.88	232.55	127.13
Cluster 5					0.00	346.10	105.41
Cluster 6						0.00	305.04
Cluster 7							0.00

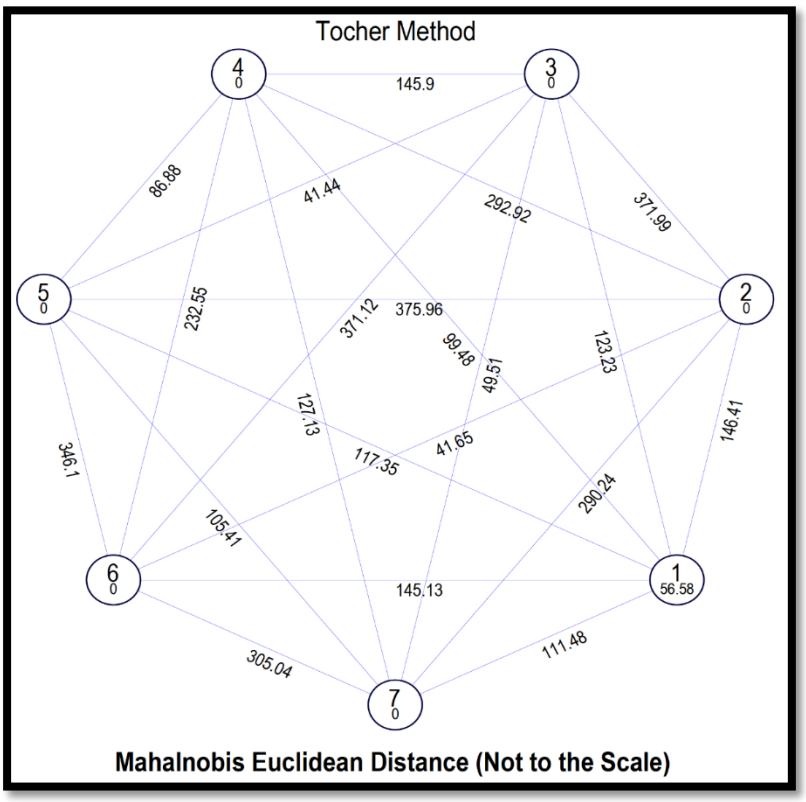

Fig. 2. Graphical representation of cluster distances and means among thirty-eight genotypes of blackgram

Table 3. Cluster mean using Tocher method among thirty-eight genotypes of blackgram

	Cluster Means: Tocher Method												
	Days to 50% flowering	**Days to 50% pod setting**	**Plant height (cm)**	**Number of primary branches per plant**	**Days to maturity**	**Number of pods per plant**	**Pod length (cm)**	**Number of seeds per pod**	**Number of seeds per plant**	**Biological yield (g)**	**100 Seed weight (g)**	**Harvest index (%)**	**Seed yield per plant (g)**
Cluster 1	45.18	58.41	43.61	2.58	90.92	20.66	4.32	5.58	94.99	18.39	4.32	57.97	10.60
Cluster 2	46.00	57.80	43.67	3.25	92.54	37.21	4.40	6.49	198.97	38.88	4.40	52.76	20.30
Cluster 3	45.40	56.80	15.07	2.28	90.63	7.38	3.68	4.83	29.15	7.11	3.69	68.03	4.78
Cluster 4	44.60	55.80	69.59	3.25	89.87	8.72	4.40	5.66	40.68	10.07	4.40	64.66	6.51
Cluster 5	44.80	55.80	33.11	3.16	90.06	19.28	5.50	5.33	84.65	5.02	5.51	76.15	3.83
Cluster 6	43.20	54.20	51.02	3.41	88.53	35.60	4.08	4.99	147.82	44.92	4.08	40.46	18.04
Cluster 7	46.00	57.60	31.74	1.95	93.11	5.43	3.26	3.33	14.90	11.08	3.26	69.19	7.66

Table 4. Percent contribution towards Genetic Divergence among thirteen characters of blakgram genotypes

Source	Contribution %	Times ranked 1st
Days to 50% flowering	2.00	14
Days to 50% pod setting	3.20	23
Plant height (cm)	4.65	33
Number of primary branches per plant	2.50	18
Days to maturity	3.11	22
Number of pods per plant	10.76	76
Pod length (cm)	9.80	69
Number of seeds per pod	5.40	38
Number of seeds per plant	7.56	53
Biological yield (g)	11.98	84
100 Seed weight (g)	6.32	44
Harvest index (%)	14.32	101
Seed yield per plant (g)	18.40	129

genotypes into various clusters indicates that geographical diversity having no parallelism with clustering pattern which was in agreement with earlier reports in blackgram [14,15]. The genotypes belonging to different clusters having maximum divergence can be successfully utilized in hybridization programmes to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters [16]. However, for a practical plant breeder, the objective is not high heterosis but also to achieve high level of production. To improve any particular trait donor for hybridization could be chosen from an appropriate cluster and that should be utilized in breeding Programme.

4. CONCLUSION

It was concluded that based on the mean performance of 38 genotypes of blackgram, SEKHAR-2 (17.30 g) was found superior in terms of seed yield per plant followed by VBN-08 (17.23 g), PKGO-03 (17.04 g), TBG-104 (16.85 g) and PU-31 (16.09 g). The genotype SN-255 took minimum days to fifty percent flowering and minimum days to maturity. Hence can be considered as early variety compared rest of the genotypes. PLU-1016 took minimum days to pod setting. On the basis of analysis of variance significant difference was recorded for all the seed yield and its components indicating presence of large variability in the genotypes. The magnitude of GCV and PCV recorded highest (46.94 and 48.79) number of seeds per plant. High heritability associated with high genetic advance was observed for number of seeds per plant (93 and 87.04) suggesting that there was greater role of additive gene action in inheritance. Maximum number of genotypes were grouped into cluster I which include 32 genotypes. The highest inter cluster distance (375.96) was found between cluster II and V. Results pertaining to inter and intra cluster distances clearly indicates that there is a wide genetic diversity I the population under study crosses involving most divergent clusters would be expected to manifest maximum heterosis and release of desirable recombinants in segregating generations. Genotypes belonged to these clusters may be used as parent to produce transgressive segregants. Among the lines, SEKHAR-3, VBN-08, PKGO-03, TBG-104 and PU-31 these genotypes utilized in future hybridization program.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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