

Genetic diversity analysis in greengram and blackgram

A. SUBRAMANIAN AND AR. MUTHIAH

Dept. of Pulses, Centre for Plant Breed. & Genetics, Tamil Nadu Agrl. Univ., Coimbatore- 641 003, Tamil Nadu

Abstract: Genetic divergence of 80 genotypes of greengram and blackgram was studied by using principal component analysis (PCA). Clustering based on PCA scores separated the genotypes into seven clusters. Appropriateness of the clustering pattern was indicated by sequential "F" test. Intra cluster distance was narrow, which indicated that cluster composition was fairly homogenous. Pattern of clustering was such that greengram and blackgram genotypes separated into distinct clusters. This indicated that both greengram and blackgram have evolved into two distinct species. Average intercluster distance was more among the blackgram genotypes. This indicated high degree of genetic among the 40 blackgram genotypes.

Key words : Greengram, Blackgram, Genetic diversity, PCA

Introduction

Greengram (*Vigna radiata* (L.) Wilczek) and Blackgram (*V. mungo* (L.) Hepper) are the most important pulse crops, which are widely cultivated and consumed. Many breeding efforts have been carried out to improve the yield level of these crops and to break the yield plateau. One of the strategies for yield improvement is to cross diverse parents, as heterosis is known to depend on the extent of genetic diversity between parents. Study of genetic diversity helps in selection of diverse parents for their use in hybridization. This study was undertaken with an objective of studying the genetic diversity in a germplasm of greengram and blackgram genotypes and also to study the genetic relationship between the two species.

Materials and Methods

Seeds of 40 genotypes each of greengram and blackgram were obtained from the Department of Pulses, Tamil Nadu Agricultural University. These were raised during 1997 at Millet Breeding Station, Tamil Nadu Agricultural University in a randomized block design with three replications. Each genotype was sown in three single row plots, each of three-meter length with spacing of 45 cm x 30 cm. Package of practices in the crop production guide were followed.

Observations of nine morphological traits viz. plant height, number of primary branches, number of clusters, number of pods per plant, pod length, pod yield per plant, 100 seed weight,

seed yield per plant and number of seeds per plant, were recorded by selecting five plants randomly from each replications. Principal Component Analysis (PCA) (Boyce, 1969) was done and the principle component scores generated were used for clustering of genotypes.

Results and Discussion

As a primary step in the present study, genetic divergence was studied in a germplasm of 40 genotypes each, of greengram and blackgram, by Principal component analysis. It was found that the genotypes clearly separated into seven clusters.

Appropriateness of these clusters was tested by sequential "F" test, which revealed that the seven-cluster arrangement was most appropriate. The cluster strength varied from 22 individuals in cluster-I to one individual in cluster-V. The pattern of distribution of genotypes was such, that greengram and blackgram formed separate clusters. Greengram genotypes were grouped in clusters-III, IV and VII, while blackgram genotypes were grouped in cluster-I, II, V and VI (Fig.1 and Table 1).

Estimation of cluster means, standard deviation, standard error and coefficient of variation indicated that genotypes of cluster-IV had taller plants, more number of seeds per pod, lengthy pods, highest seed yield and more seeds per plant (Table 2).

Table 1. Distribution of genotypes in clusters (PCA)

Cluster number	Number of genotypes	List of genotypes
I	22 (Blackgram)	P-133/3, P-133/83, P-133/56, P-133/51, P-81, PLS-364/92, CO-2/1, Pant-U-6, PLS-365/54, AC-43, VZM-189/3, P-226, P-133/13, P-169, T-9, PDU-3, P-123, Lam.BG-295, LU-162, U-7, CTM, TMV-1
II	11 (Blackgram)	P-69, AC-149, P-200/1, PLS-365/83, CO-4, KM-2, VZM-189/76, AC-291, VZM-189/1, Krishna, Mithiulundu
III	12 (Greengram)	LM-36, LM-205, LM-222, 1732/2, LM-32, LM-125, MDU-3179, V-1972, AC-147, PLS-326, PLS-308, LM-18
IV	12 (Greengram)	VBN-1, PLS-274, MDU-1387, PLS-318, PLS-265, PLS-284, Paiyur-1, LM-336, PLS-294, LM-216, MDU-3385, LM-179
V	1 (Blackgram)	Small leaf
VI	6 (Blackgram)	CO-5, AC-303, P-217, AB-15/1, Cotton leaf
VII	16 (Greengram)	PLS-267, PLS-275, LM-346, LM-352, AC-254, PLS-262, AC-192, PLS-280, MDU-2010, PLS-267/1, ADT-1, AC-164, PLS-272, PLS-317/2, MDU-3405, PLS-312

Table 2. Mean values of intracluster (in bold) and the intercluster distances in greengram and blackgram germplasm

Cluster	I	II	III	IV	V	VI	VII
I	1.311						
II	2.684	1.266					
III	3.476	3.810	1.706				
IV	5.527	3.784	3.790	2.294			
V	5.68	5.588	6.504	6.864	0.00		
VI	4.415	1.994	4.925	3.294	5.523	1.419	
VII	3.204	4.673	2.267	5.239	6.563	5.876	1.656

The intra cluster distance ranged from 0.00 to 2.29 (Table 3). The narrow range of intra cluster distances suggested that cluster compositions were fairly homogenous. Inter cluster distance ranged from 1.994 to 6.864. Dendrogram constructed using the principal component scores by non-hierarchical method indicated that the clusters I, II, V and VI formed the first subgroup, while the clusters III, IV and VII formed second subgroup.

The separation of greengram and blackgram genotypes into two distinct groups was tested by Ward's (1963) hierarchical cluster analysis

using principal component scores. The result indicated that Ward's hierarchical clustering method and non-hierarchical cluster analysis go hand in hand in indicating the distinctness of the two groups of genotypes.

Prior to 1960, it was considered that the two taxa *Vigna radiata* and *Vigna mungo* would be variants of one single species (Verdcourt 1970). However, Indian workers Sen and Ghosh (1960), Dana (1966) and De and Krishnar (1966) demonstrated the existence of incompatibility barriers when the two taxa were crossed. De and Krishnan (1966) based on pachytene

Table 3. Cluster means, standard deviation, standard error and coefficient of variation of ten characters in greengram and blackgram germplasm

Cluster	No. of genotypes	Para-meter	Plant height (cm)	No. of primary branches	No. of clusters	No. of pods/plant	Pod length (cm)	No. of seeds/pod	Pod yield (gms)	Seed yield (gm)	Total no. of seeds	100 seed weight (gm)
I	22	Mean	31.23	2.56	7.15	17.98	5.20	6.35	7.72	4.99	88.86	5.54
		SD	5.70	0.65	1.43	2.88	0.38	0.51	1.81	1.35	20.59	0.51
		SE	1.22	0.11	0.30	0.61	0.08	0.11	0.38	0.28	4.39	0.109
		C.V%	18.25	21.09	20.00	16.02	7.31	8.03	23.44	27.05	23.17	9.21
II	11	Mean	40.97	3.00	10.61	27.76	5.43	6.82	12.62	8.03	133.61	5.90
		SD	4.87	0.58	1.29	3.26	0.37	0.66	1.85	1.53	20.05	0.51
		SE	1.46	0.175	0.388	0.98	0.11	0.02	0.558	0.46	6.04	0.15
		C.V%	11.89	19.33	12.16	11.74	6.81	9.68	14.66	19.05	15.00	8.64
III	12	Mean	34.42	1.89	6.36	24.22	6.87	11.31	9.05	5.72	159.11	3.73
		SD	7.74	0.63	2.02	5.73	0.45	1.09	1.98	1.29	39.11	0.52
		SE	2.34	0.189	0.61	1.73	0.136	0.32	0.59	0.389	11.79	0.16
		C.V%	22.49	33.34	31.76	23.66	6.55	9.64	21.88	22.55	24.58	13.94
IV	12	Mean	49.60	3.64	10.83	31.06	7.10	11.25	15.19	9.59	233.81	3.78
		SD	12.72	0.77	2.52	4.18	0.62	0.93	3.95	1.99	71.51	0.49
		SE	3.83	0.23	0.76	1.26	0.18	0.28	1.19	0.60	21.56	1.48
		C.V%	25.64	21.15	21.38	13.46	8.73	8.28	27.02	20.75	30.58	12.96
V	1	Mean	25.17	4.00	18.33	38.00	3.50	6.33	6.39	2.37	99.57	2.39
		SD	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		SE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		C.V%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
VI	6	Mean	39.64	4.11	12.61	35.00	7.11	5.38	15.79	5.56	9.56	171.61
		SD	6.57	0.66	1.64	3.77	0.50	0.25	2.50	0.30	1.71	27.57
		SE	2.66	0.27	0.67	1.54	0.20	0.10	1.02	0.12	0.69	11.25
		C.V%	16.42	16.05	13.00	10.77	7.03	4.65	15.83	5.39	17.88	16.06
VII	16	Mean	27.86	2.82	5.04	12.65	10.83	6.73	6.10	3.54	3.90	112.83
		SD	5.04	0.90	1.49	2.15	1.06	0.93	1.41	0.60	0.94	27.45
		SE	1.26	0.22	0.37	0.54	0.26	0.23	0.35	0.15	0.24	6.86
		C.V%	18.09	31.91	29.56	16.99	9.78	13.82	23.11	16.95	24.10	24.33

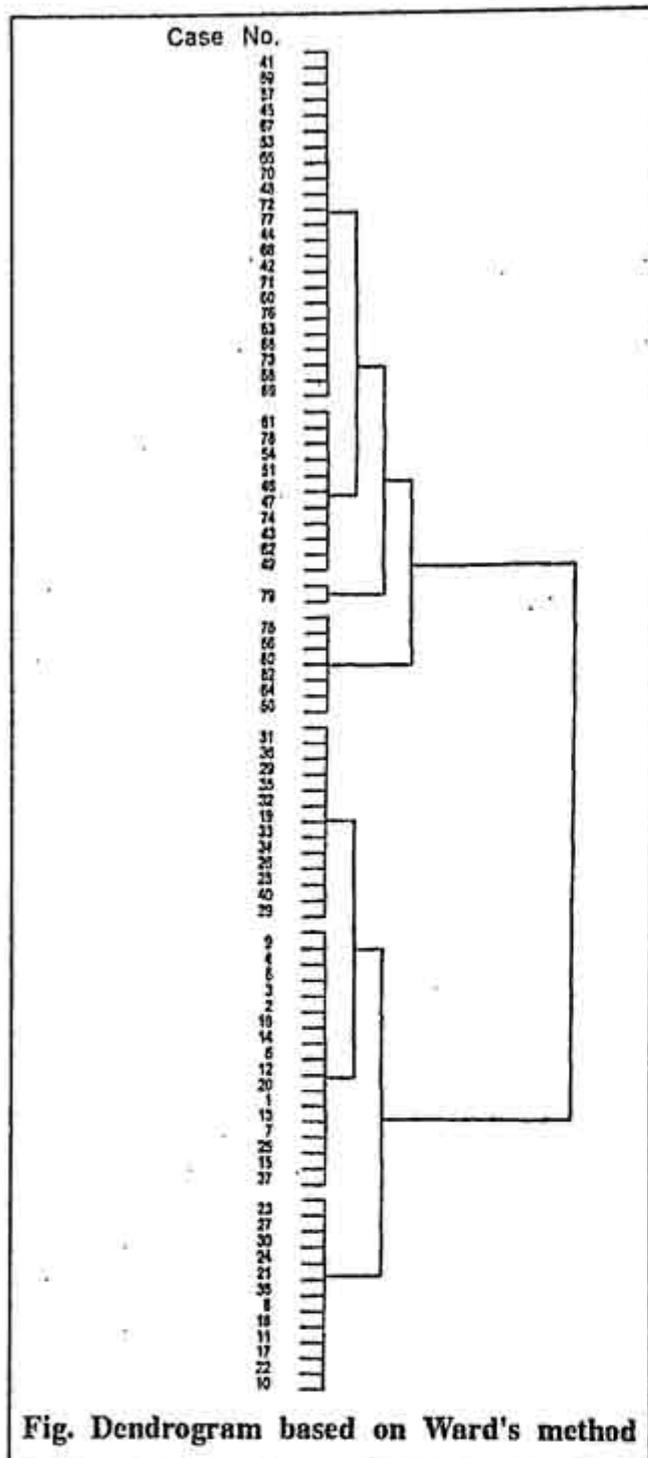


Fig. Dendrogram based on Ward's method

analysis of meiotic chromosomes of these two species and of their F_1 hybrids revealed that *V. mungo* is more recent and has been derived from *Vigna radiata* through a deletion that had occurred in chromosome 10 and a duplication in chromosome 4. These results as well as the results derived from the cluster analyses by Lukokhi (1975), Watt and Marechal (1977), Shanmugam and Sree Rangasamy (1984) and Ganesh Ram (1993) strongly favour the fact that *Vigna radiata* and *Vigna mungo* have evolved into two distinct species.

The average inter cluster distance among blackgrams was greater than that of greengram, which indicated that genetic diversity among the blackgram genotypes was greater. This is in accordance with the results reported by Shanmugam *et al.* (1984). PCA also indicated that intra cluster distance was the greatest in the case of greengram when compared to blackgram. This may be because of the diverse nature of genotypes selected. The clustering pattern was observed to be independent of geographical location.

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