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STUDIES ON GENETIC DIVERGENCE OVER ENVIRONMENTS IN MUNGBEAN (*VIGNA RADIATA* (L.) WILCZEK)

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ABSTRACT

Forty nine mungbean genotypes were studied in three environments (kharif, rabi uplands, and rabi rice fallows) to understand the genetic diversity and study the influence of genotype–environment interactions. Considerable genetic diversity was recorded in the material studied. Clustering pattern of the genotypes was influenced by the environment. The genotypes studied fell into 14, 11 and 8 clusters in the three environments, respectively, indicating the importance of studying the material in more than one environment. No relation between geographic diversity and genetic diversity was observed. The parentage had no effect on the clustering pattern except in rice fallows. Shoot dry weight at harvest and pods/plant were the common characters differentiating the clusters in all the environments. Based on per se performance and intercluster distances, LGG 424 and LGG 442 were considered to be genetically diverse parents and may be used in hybridization to achieve rare recombinants and transgressive segregates.

Key words: Genetic divergence, genotype x environment interactions; mungbean.

Creation of variability and selection of superior recombinants among the variants are the major objectives of any plant breeding programme. One of the constraints listed for lack of breakthrough in mungbean production has been the lack of genetic variability for high yield potential [1]. Selection of diverse parents belonging to distant groups leads to a wide spectrum of gene combinations for quantitatively inherited traits [2]. Multivariate analysis with D^2 technique measures the amount of genetic diversity in a given population in respect of several characters considered together. Any genetic investigation carried out on the quantitative characters becomes complicated when more than one environment is considered because of the change in the gene expression that may occur with change in the environments. Hence the present investigation has been carried out in three distinct environments involving 49 genotypes of mungbean to identify genetically diverse parents and also study the influence of environment on character expression and clustering pattern.

MATERIALS AND METHODS

The experimental materials comprising 49 diverse genotypes of mungbean drawn from different centres were grown in a simple lattice design with two replications under three environments: kharif, 1988; rabi uplands 1987–88; and rabi rice fallows, 1987–88 at the Regional Agricultural Research Station, Lam, Andhra Pradesh, India. Each genotype was grown in four rows, each of 5.0 m length, with the spacing of 30 cm between rows and 10 cm between plants. The crop was raised under rainfed conditions following the recommended package of practices (ZREAC, 1987–88) kharif and rabi upland fallows, while the crop was raised entirely on residual moisture and fertility in rice fallows. Observations were recorded on 10 randomly selected plants in each genotype per replication for 13 characters.

STATISTICAL ANALYSIS

Analysis of variance and covariance of plot means were carried out for all the characters. The original mean values were transformed to uncorrelated variables using pivotal condensation method and dispersion matrix. The D^2 values were calculated by taking the sum of squares of the difference between pairs of corresponding values, taking two at a time for all the 1176 combinations. The significance of D^2 values was tested, treating them as χ^2 values at $P = 0.05$ at 624 degrees of freedom. The genotypes were grouped into a number of clusters, following the Tocher's method (cf. [3]).

RESULTS

Analysis of variance revealed highly significant differences among the genotypes for all the characters under all the environments studied. The Wilk's test revealed highly significant differences between the genotypes for the aggregate of the 13 characters. D^2 values ranged from 42.8 to 7784.6 in kharif, from 66.1–5953.0 in uplands, and from 64.0–5697.9 in rice fallows. The genotypes fell into different clusters. The number of clusters varied from 8 in rice fallows to 14 in kharif. In no case all the genotypes derived from one region grouped together into one cluster. The number of genotypes in each cluster also varied with the environment. Maximum number of genotypes were included in a particular cluster (III) in rice fallows. In contrast, the number of clusters containing single genotypes were high in kharif (7), followed by rice fallow (5) and uplands (3). Distribution of genotypes into different clusters was at random and was not influenced by parentage in kharif and uplands, while in rice fallows, both parents and their derivatives were included in the same cluster. Double and multiple cross derivatives, viz., $DC_1 \times DC_2$—4S B-5B, LGG 444, LGG 434, $DC_1 \times DC_2$—1SB-SB in kharif, and LGG 444 and LGG 441 in uplands formed separate clusters.

The average intra- and intercluster distances are presented in Tables 1, 2 and 3 for kharif, upland and rice fallows, respectively. The highest intercluster distance of 6986.0 was observed between clusters VIII and X in kharif; 5748.1 in rabi uplands between clusters I and VIII; and 5697.9 in rice fallows between clusters V and VII. The intracluster distance was also high in kharif (542.0) compared to rabi upland (475.5) and rice fallows (429.5).

Table 1. Average intracluster (in bold) and intercluster D^2 values among 14 clusters of mungbean in kharif, 1988

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**542.0**	2074.0	2389.7	750.7	3022.8	1282.2	1041.8	3744.6	2210.4	1424.9	3789.0	2003.9	1094.5	1804.1
II		**539.7**	1727.6	1526.3	881.8	1988.3	3289.2	1176.5	947.2	3845.7	1197.4	1857.8	964.9	804.2
III			**280.8**	3154.5	2837.3	2621.4	3217.4	1365.9	834.2	6684.0	2231.8	1516.7	1049.0	2527.4
IV				**490.7**	2030.2	1178.8	1814.5	3387.7	2425.6	1181.6	2826.8	2523.0	1233.5	924.0
V					**394.3**	3294.3	4951.8	1014.1	1622.9	3270.8	2322.1	1954.2	1606.1	1070.2
VI						**399.5**	1271.7	3706.4	2298.0	1569.2	2393.3	3011.7	1569.2	2255.3
VII							**467.0**	4946.7	2844.3	2253.8	4904.4	2456.1	1387.1	3517.9
VIII								**0.0**	1046.1	6986.0	1878.9	1619.2	1668.1	2494.5
IX									**0.0**	5133.9	2116.4	707.2	942.4	2161.9
X										**0.0**	5024.6	5416.3	2926.7	2585.0
XI											**0.0**	4190.4	1473.9	1589.5
XII												**0.0**	1491.5	2977.3
XIII													**0.0**	1486.0
XIV														**0.0**

The mean values for 13 different characters in the various clusters are presented in Tables 4, 5, and 6 for the three environments, respectively. Significant differences between the cluster means were observed in all the environments. The genotypes constituting single-genotype clusters possessed either very high or very low mean performance for one or more characters. The cluster means for various characters showed appreciable differences under all circumstances.

Table 2. Average intracluster (in bold) and intercluster D^2 values among 11 clusters of mungbean under rabi uplands, 1987–88

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**65.6**	2247.2	1483.2	1391.2	1390.4	628.0	2436.5	5748.1	2164.5	2904.9	2480.8
II		**357.2**	1165.1	920.6	724.8	2018.4	839.2	1246.2	2298.2	980.4	799.2
III			**407.1**	769.5	1991.9	814.3	1688.8	3368.2	1142.9	767.6	942.8
IV				**435.6**	1664.6	1020.5	1110.0	2503.7	1861.2	1026.7	1036.0
V					**390.3**	3008.2	1426.9	1949.4	3367.6	1516.9	1527.0
VI						**237.4**	1973.2	3935.3	1942.1	1024.6	1167.2
VII							**382.2**	1261.4	2800.7	1542.3	862.5
VIII								**475.5**	5170.5	1540.7	2175.6
IX									**0.0**	1749.6	1756.1
X										**0.0**	626.0
XI											**0.0**

Table 3. Average intracluster (in bold) and intercluster D^2 values among 8 clusters of mungbean under rabi rice fallows, 1987–88

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**381.7**	771.3	660.8	665.8	1402.3	895.1	2145.0	732.7
II		**429.5**	695.2	1071.7	639.0	722.4	3108.2	1502.0
III			**422.5**	765.9	1215.5	232.9	3044.0	928.6
IV				**0.0**	2438.0	1506.2	1403.6	1419.8
V					**0.0**	951.1	5697.9	2076.9
VI						**0.0**	3986.8	1685.0
VII							**0.0**	2904.7
VIII								**0.0**

DISCUSSION

The clustering pattern of the genotypes showed that genetic diversity was not related to geographic diversity. In no case all the genotypes from one state grouped into one cluster. The explanation for the genotypes for the same geographical origin falling into different

Table 4. Cluster means for various characters of mungbean in kharif 1988

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per plant	Pod length (cm)	Seeds per pod	1000-seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
I	40.0	69.9	82.3	1.73	4.79	28.1	7.12	11.7	32.6	24.1	26.6	2.48	9.55
II	32.8	63.4	81.9	1.56	4.81	25.8	7.10	10.6	33.4	20.7	26.2	2.37	8.35
III	33.0	63.2	92.2	1.63	5.38	33.7	7.85	12.3	36.0	29.8	25.9	2.73	11.97
IV	39.7	69.2	78.3	1.60	4.86	26.8	7.17	10.9	32.8	20.3	23.4	2.39	8.26
V	30.7	61.0	66.4	2.05	5.15	22.8	6.97	10.7	33.0	18.7	24.7	2.40	7.59
VI	36.0	66.0	82.9	1.44	4.64	28.2	7.40	10.7	34.4	20.1	26.9	2.35	8.71
VII	42.3	72.3	91.0	2.13	4.77	33.0	7.27	12.0	35.7	29.4	24.9	2.79	11.75
VIII	30.0	61.5	66.9	1.98	4.95	26.0	7.60	12.5	33.7	21.6	28.3	2.65	8.88
IX	32.0	62.0	81.8	1.29	4.52	32.0	7.00	10.6	32.0	28.1	26.6	2.75	11.27
X	44.0	74.0	81.6	1.84	4.44	24.5	7.15	9.6	35.2	18.8	27.5	2.44	7.45
XI	32.5	62.5	94.3	2.09	4.82	24.0	7.80	9.8	32.0	17.4	27.4	2.24	6.95
XII	34.0	64.0	67.8	2.21	4.67	29.0	6.95	12.4	32.5	30.5	24.2	2.76	12.25
XIII	37.0	67.0	89.7	1.82	4.18	24.5	7.60	12.2	33.0	22.6	27.7	2.25	9.23
XIV	34.0	64.5	85.8	1.81	4.97	23.0	6.60	10.8	32.5	16.7	24.2	2.21	6.70

Table 5. Cluster means for various characters of mungbean in rabi uplands 1987–88

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per plant	Pod length (cm)	Seeds per pod	1000-seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
I	44.7	73.0	72.0	1.47	4.33	26.6	6.72	10.3	32.2	20.4	26.5	2.62	8.22
II	35.4	65.0	46.9	1.82	3.83	21.6	6.88	10.1	32.5	15.8	26.8	2.41	6.42
III	35.6	65.8	52.3	1.91	4.23	26.7	6.97	10.3	34.1	20.8	26.2	2.63	8.45
IV	38.6	68.3	57.0	1.83	4.67	27.5	6.75	10.1	33.0	18.5	25.0	2.62	8.09
V	32.7	62.7	45.8	1.92	5.18	20.7	6.53	9.5	26.4	15.3	25.7	2.33	6.25
VI	37.5	66.8	64.6	1.45	3.69	22.5	6.75	10.2	31.7	20.3	26.5	2.55	8.72
VII	39.7	69.2	57.0	1.45	3.71	19.1	6.87	10.3	37.6	15.2	24.6	2.19	6.27
VIII	34.2	64.2	39.7	1.20	4.37	17.4	6.78	9.8	31.5	10.8	26.2	2.10	4.90
IX	37.0	66.5	51.5	1.88	4.83	30.0	8.85	10.8	40.0	22.1	27.0	2.65	9.02
X	32.0	62.0	48.2	2.09	5.50	25.0	6.90	10.3	36.2	19.2	24.8	2.54	8.10
XI	38.0	68.0	42.0	1.48	4.16	23.5	7.10	11.0	36.0	20.7	22.5	2.40	8.43

clusters can be found in the wide genetic divergence in the features created through selection and genetic drift. Murthy et al. [4] in Brassica, Murthy and Anand [5] in linseed; Arunachalam and Ram [6] in sorghum; Singh and Bains [7] in cotton; Gupta and Singh [8], and Malhotra et al. [9] in mungbean have also indicated that geographic diversity cannot always be used as an index of genetic diversity.

All the 49 genotypes of mungbean studied could be grouped into varying number of clusters in three different environments. The variation in the clustering pattern of genotypes could be due to differences in the environments studied, thereby emphasizing the importance of multi-environment studies for quantitative assessment of genetic diversity. High magnitude of genotype–environmental interaction observed in the present study is a linear function of the environments. Variation in clustering pattern in different environments was also observed in mungbean by Rao and Suryawanshi [10]. The distribution of genotypes into clusters was random and the parentage had no effect in majority of environments. In contrast, Gupta and Singh [8] reported that parentage had a definite effect on the clustering pattern in mungbean. The deviations recorded in the present study may be attributed to the differences in the environments and the materials used.

The factors responsible for differentiation at the intra- and intercluster levels were different in different environments, as indicated by the cluster means for various characters. This also explains the profound influence of environment on character expression. In all the environments, shoot dry weight and pods/plant contributed maximum to the cluster

Table 6. Cluster means for various characters of mungbean in rabi rice fallows, 1987–88

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per plant	Pod length (cm)	Seeds per pod	1000-seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
I	45.8	75.9	38.2	1.48	3.70	16.6	6.82	10.7	32.8	12.7	25.5	2.39	5.05
II	46.8	77.7	41.7	1.55	4.31	20.4	7.10	11.9	31.8	15.8	26.1	2.48	6.75
III	47.7	77.2	40.2	1.82	4.42	19.2	6.55	10.9	38.6	15.8	24.2	2.57	6.30
IV	45.5	75.0	37.9	1.65	4.10	18.0	7.80	10.2	39.5	13.0	26.8	2.40	5.20
V	45.5	75.5	37.8	0.80	4.10	20.0	6.20	12.5	30.0	17.4	27.1	2.80	7.00
VI	45.0	74.5	48.5	0.90	3.60	17.0	6.50	10.7	29.7	18.5	26.0	2.20	6.37
VII	44.0	74.0	41.2	1.20	3.90	16.0	9.70	10.3	34.5	13.7	21.0	2.40	5.50
VIII	45.5	75.5	38.0	0.90	3.70	13.0	5.90	10.1	35.5	10.6	21.2	2.35	4.22

differentiation. Based on per se performance, inter- and intracluster distances over all the three environments, two genotypes, i.e. LGG 441 and LGG 442 were found to genetically more diverse from others.

REFERENCES

1. S. Ramanujam. 1978. Biometrical basis for yield improvement in mungbean. *In*: Proc. 1st Intern. Mungbean Symp. (ed. R. Cowell). AVRDC, Taiwan: 210.

2. H. K. Jain. 1981. Evolving a new production technology of pulses. Pulse Crops Newsl., **1**: 1–2.

3. C. R. Rao. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York: 236–272.

4. B. R. Murthy, J. B. L. Mathur and V. Arunachalam. 1965. Self-incompatibility and genetic divergence in *Brassica campestris* var. Sarson. Sankhya (B), **27**: 271–278.

5. B. R. Murthy and I. J. Anand. 1966. Combining ability and genetic diversity in some varieties of *Linum usitatissimum*. Indian J. Genet., **26**: 21–36.

6. V. Arunachalam and Jawahar Ram. 1967. Geographic diversity in selection to genetic divergence in cultivated sorghum. Indian J. Genet., **27**: 369–380.

7. R. B. Singh and S. S. Bains. 1968. Genetic divergence for gining outturn and its components in upland cotton (*Gossypium hirsutum* L.). Varieties obtained from different geographic locations. Indian J. Genet., **28**: 262–268.

8. M. P. Gupta and K. B. Singh. 1970. Genetic divergence for yield and its components in green gram. Indian J. Genet., **30**: 212–221.

9. V. V. Malhotra, Sukhdev Singh and K. B. Singh. 1974. Relation between geographic diversity and genetic divergence and the relative role of each character toward maximizing divergence in greengram. Indian J. agric. Sci., **44**: 811–815.

10. S. K. Rao and Suryawanshi. 1988. Genotype x environment interactions in the genetic diversity of urd germplasm collections. Legume Res., **11**: 15–20.