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Research Note

Genetic Diversity Studies under Moisture Stress Condition in Mungbean (*Vigna radiata* (L.) Wilczek)

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Abstract

Genetic divergence among thirty one mungbean genotypes grown under moisture stress condition induced during pod filling stage was estimated using Mahalanobi's D^2 statistic and total of eleven clusters were obtained. Cluster I and cluster II contained the highest number of eight genotypes followed by cluster VII with six genotypes. The highest intra cluster distance was observed for cluster VIII (808.83) and the lowest was observed for cluster VII (354.57) and cluster III, cluster IV, cluster V, cluster VI, cluster IX, cluster X and cluster XI showed zero intra cluster distance. While the highest inter cluster distance was observed between cluster VII and cluster IX (7351.35). Days to maturity contributed maximum towards diversity. Cluster X recorded the highest mean for seed yield per plant followed by days to 50% flowering, days to maturity, 100 seed weight, SCMR and chlorophyll content. Therefore, it was concluded that more emphasis should be given on cluster X for selecting genotypes as parents for crossing with genotypes of other clusters which may produce new recombinants with desired traits

Keywords
Mungbean, D^2 analysis, diversity.

Mungbean (*Vigna radiata* (L.) Wilczek) is an important pulse crop in India and occupies third rank after pigeon pea and chickpea. It is cheap and rich source of protein containing 23-25 per cent, high lysine content and rich in amino acids, minerals and vitamins. However, its production potential was reduced due to abiotic stress like drought. Many breeding programmes have been initiated to develop drought tolerant/ resistant varieties in mungbean. However, the progress is not significant as the drought is a complex phenomenon and always coupled with moisture and high temperature stresses. Therefore, systematic efforts are needed to breed the cultivars by thorough understanding of the mechanisms of drought at various developmental, physiological, biochemical and molecular levels.

The current demand to develop high yielding and drought tolerant genotypes necessitated an immediate need to breed suitable high yielding varieties under drought conditions. In order to reach this goal, drought tolerance and high yield is essential to identify and concentrate on the important traits that could contribute to optimum yields under drought. Hence, choosing genetically diverse parents will enable the expansion of genetic base and development of superior genotypes. Keeping this in view, the present study was understand to estimate the genetic diversity on yield and drought contributing characters using Mahalanobi's D^2 statistic.

The experimental material for the present investigation consisted of thirty one mungbean genotypes obtained from Regional Agricultural Research Station, Lam, Guntur and Agricultural Research Station, Madira. The experiment was conducted in randomized block design (RBD) with three replications during summer, 2013-14 at wet land farm, Sri Venkateswara Agricultural College, Tirupati. The salient features of thirty one mungbean genotypes were presented in Table 1. Each genotype was sown in three rows of 4 m length with a spacing of 30 cm between rows and 10 cms between plants within rows. In the present study, moisture stress was induced during pod filling stage by withholding irrigation for fifteen days. Observations were recorded on five randomly selected plants per replication for traits namely plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 seed weight, harvest index, SPAD chlorophyll meter reading (SCMR), Relative Water Injury (RWC), Relative Injury Percentage (RI), Chlorophyll content and Specific Leaf Area (SLA). Whereas, traits days to 50 % flowering and days to maturity observations were recorded on plot basis. The mean values for each trait over the replications were subjected to the analysis of variance. Estimates of genetic divergence was done by following Mahalanobi's D^2 (1936) analysis and based on the D^2 values the thirty one genotypes were grouped into different clusters following Tocher's method as suggested by Rao (1952).

The analysis of variance showed significant differences between mungbean genotypes for all the characters studied and hence considered for estimation of D^2 values clustering. All the 31 genotypes were grouped into eleven clusters (Table 2 and Fig 1). The maximum number of genotypes were included in cluster I and cluster II (eight genotypes), followed by cluster VIII (six genotypes) and cluster IV (two genotypes). While the cluster III, cluster IV cluster V, cluster VI, cluster IX, cluster X and cluster XI were solitary clusters consisting of one genotype each. The pattern of group constellation indicated significant variability among the genotypes as observed from the clusters. It is to be note that, the genotypes of the same origin were distributed into different clusters indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes. Similar findings were also reported by Manivannan *et al.* (1998), Arpita Das *et al.* (2010) and Rahim *et al.* (2010) in mungbean. This kind of genetic diversity recorded among the genotypes belonging to the same geographic origin but distributed in different clusters might be due to difference in adoption, selection criteria, selection pressure and environmental condition. The factors other than the geographical diversity may be attributed for inclusion of different genotypes in the same cluster. The variation might be due to the fact that the ecotypes in a particular habitat could have been evolved with different objectives and varied local needs, thus, giving importance to different characters.

The inter cluster distance ranged from 357.97 (cluster IV and VI) to 7351.35 (cluster VII and IX) (Table 3). Maximum distance was observed between the cluster VII and IX (7351.35) and was closely followed by VII and XI (6997.32). The genotypes in these clusters may serve as potential parents and crossing between these genotypes may result in novel recombinants that may be best suited for drought condition. Manivannan *et al.* (1998) and Patel and Patel (2012) made similar study in mungbean to identify genotypes resulting in heterotic expression for yield components.

Cluster III recorded the highest mean for number of seeds per pod and Specific Leaf Area (SLA) (Table 3). Cluster IV recorded highest mean value for SCMR. Cluster V recorded highest mean values for number of clusters per plant, number of pods per plant and Relative Water Content (RWC). Similarly, cluster VIII registered maximum values for number pods per cluster, while cluster IX for days to 50% flowering, harvest index; cluster X for days to 50% flowering, days to maturity, 100 seed weight, SCMR, chlorophyll content and seed yield per plant and cluster XI for plant height. Inter crossing the genotypes from these clusters could be suggested to generate wide range of variability subsequently followed by effective selection for these characters.

The selection and choice of parents mainly depends upon contribution of characters towards divergence and the contribution towards genetic divergence is represented in table 5. It was observed that among all the traits, days to maturity contributed maximum (49.03%) to the diversity by taking first rank in 228 times out of 465 combinations, followed by number of pods per cluster (34.19% with 159 times ranked first), 100 seed weight (11.61% with 54 times ranked first) and seed yield per plant (5.16% with 24 times ranked first). On contrary, days to 50% flowering, plant height, number of clusters per plant, number of pods per plant, number of seeds per pod, harvest index, SCMR, RWC, Relative Injury, chlorophyll content and Specific Leaf Area had negligible contribution towards genetic divergence.

It is well known that crosses between divergent parents usually produce greater heterotic effect and transgressive segregants in further generations than closely related ones. However, for a practical plant breeding, the objective is not only high heterosis but also to achieve high level of production coupled with drought tolerance in this present study. Considering the importance of characters towards total divergence, the present study indicated that hybridization programme may be initiated between ML 145 X MGG 295 (cluster VII X cluster IX) in order to get transgressive segregants for drought tolerance since, these genotypes showed maximum diversity among themselves with desirable drought parameters (high SCMR, high RWC, low RI% and low SLA). Similarly, the crosses between genotypes VG 7098A X MGG 295 (cluster VII X cluster IX), ML 145 X WGG 2 (cluster VII X cluster XI) and VG 7098A X WGG 2 (cluster VII X cluster XI) could be suggested for the exploitation of transgressive segregants for high yield coupled with drought tolerance.

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Table 1. Salient features of mungbean genotypes

S. No	Name of the Genotype	Salient features
1	AKM 9904	Bold and dull green coloured seed. Tolerant to ABLS (Angular Black Leaf Spot), PM (Powdery Mildew) and Multiple disease resistance. High yielding.
2	ASHA	Derivative of K 851 and L 24- 2. Small shiny green seed. Tolerant to YMV.
3	COGG 974	Medium duration. Bold and dull green seed. Tolerant to ABLS.
4	EC-396117	Early maturing variety. Very bold and shiny green seed. Tolerant to PM.
5	GVIT-203	Medium duration variety. Green shiny pods with small seeds.
6	IPM-02-03	Derivative of IPM 99-125 and PUSA BOLD 2. Large seeded. Resistant to YMV.
7.	IPM-02-19	Bold and dull green colour seed. Resistant to YMV.
8	KM-8-657	Bold and shiny green seeds.
9	KM-122	Very bold and dull green colour seed. Resistant to powdery mildew.
10	LGG 407	Mutant from pant mung-2. Medium duration. Seeds are medium bold and shiny green. Resistant to YMV and tolerant to ABLS and root rot diseases.
11	LGG 410	Derivative of ML-26-10-3-40 and KR-48. Photo insensitive. Shiny green seed. Resistant to YMV and tolerant to ABLS.
12	LGG 450	Mutant from pant mung-2. Semi erect inhabit and shiny green seed. Resistant to pre harvest spouting, YMV, Powdery mildew and tolerant to ABLS.
13	LGG 460	Derivative of LAM M-2 and ML-267. Early maturity, short plant type, photo insensitive and shiny green coloured seeds. Resistant to YMV.
14	LGG 528	Medium duration. Small and shiny green seed.
15	MGG 295	Derivative of CO-3 and PIMS 4. Seed medium bold and dull dirty green color. Resistant to ABLS, root rot, PM and tolerant to YMV.
16	MGG 347	Synchronous maturity. Bold and dark green colour seed. Resistant to YMV and tolerant to Cercospora, PM, Thrips and Stemfly.
17	MGG 350	Medium duration variety. Medium size and shiny green colour seed.
18	MH-3-18	Bold and shiny green colour seed. Resistant to YMV.
19	MH-565	Bold and shiny green colour seed. Resistant to YMV.
20	ML-145	Medium size and shiny green colour seed. Resistant to YMV.
21	ML-267	Derivative of ML-1 and LM-287. Small shiny light green seed. Tolerant to YMV.
22	PM 110	Bold and dull green coloured seed. Resistant to YMV.
23	PUSA 9531	Selection from NM 9473. Small shiny seed. Resistant to YMV and tolerant to Jassids and Whitefly.
24	PUSA VISHAL	Long Pod length with bold seed. Resistant to YMV and tolerant to Jassids and Whitefly.
25	RMG-492	Bold and shiny green colour seed. Resistant to BLS.
26	TLM-7	Bold and dull green colour seed. Resistant to YMV.
27	TM-96-2	Shiny green bold seed, pigmented seedlings and synchronous in maturity. Suitable for rice fallows. Resistant to PM and Cercospora Leaf Spot.
28	VG-6197A	Medium duration maturity. Bold and shiny green seed. Resistant to YMV.
29	VG-7098A	Early maturing variety. Bold and dull green colour seed.
30	WGG-2	Derivative of W15-70 and PUSA 101. Medium bold and shiny green seed. Resistant to PM, YMV and tolerant to ABLS and root rot diseases.
31	WGG-37	Early maturity and erect trifoliate leaves. Green shiny pods with globular and shiny green coloured seed.

Table 2. **Cluster composition of thirty one mungbean genotypes (Tocher's method) under moisture stress condition**

Cluster No.	No. of genotypes	Genotypes
I	8	COGG 974, LGG 410, LGG 528, LGG 460, PUSA 9531, ML-267, AKM 9904, KM-122
II	8	IPM-02-03, MH-3-18, TLM-7, MH-565, EC 396117, IPM-02-19, PM 110, ASHA
III	1	WGG 37
IV	1	TM 96-2
V	1	RMG 492
VI	1	LGG 407
VII	2	ML-145, VG 7098A
VIII	6	KM-8-657, PUSA VISHAL, LGG 450, GIVT-203, MGG 350, MGG 347
IX	1	MGG 295
X	1	VG-6197A
XI	1	WGG 2

Table 3. Intra cluster (diagonal) and inter-cluster distances for eleven clusters in mungbean under moisture condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	495.06 (22.25)	1601.60 (40.02)	807.13 (28.41)	2497.00 (49.97)	1656.49 (40.70)	2313.61 (48.10)	4422.25 (66.50)	2413.76 (49.13)	975.31 (31.23)	2282.93 (47.78)	1658.93 (40.73)
Cluster II		600.74 (24.51)	1011.88 (31.81)	1184.74 (34.42)	1018.25 (31.91)	1040.06 (32.25)	1617.65 (40.22)	3677.21 (60.64)	3524.79 (59.37)	1584.04 (39.30)	3738.09 (61.14)
Cluster III			0.00 (0.00)	1672.81 (40.90)	693.79 (26.34)	2073.89 (45.54)	2955.00 (54.36)	2114.16 (45.98)	1330.79 (36.48)	559.32 (23.65)	1386.82 (37.24)
Cluster IV				0.00 (0.00)	623.00 (24.96)	357.97 (18.92)	655.36 (25.60)	2193.05 (46.83)	4490.34 (67.01)	1548.42 (39.35)	4197.74 (64.79)
Cluster V					0.00 (0.00)	857.90 (29.29)	1416.77 (37.64)	1787.59 (42.28)	2843.02 (53.32)	912.64 (30.21)	3205.82 (56.62)
Cluster VI						0.00 (0.00)	879.12 (29.65)	2972.43 (54.52)	4697.73 (68.54)	2624.51 (51.23)	5184.00 (72.00)
Cluster VII							354.57 (18.83)	4637.61 (68.10)	7351.35 (85.74)	2366.82 (48.65)	6997.32 (83.65)
Cluster VIII								808.83 (28.44)	2223.12 (47.15)	2510.01 (50.10)	2171.56 (46.60)
Cluster IX									0.00 (0.00)	2974.61 (54.54)	724.15 (26.91)
Cluster X										0.00 (0.00)	2248.66 (47.42)
Cluster XI											0.00 (0.00)

Table 4. Mean performance of the clusters with respect to different characters under moisture stress condition

Character / Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	100-seed weight	Harvest index	SCMR	RWC	Relative injury (%)	SLA	CC	Seed yield
Cluster I	42.58	65.33	39.30	4.79	2.19	9.79	8.33	3.16	20.97	41.25	72.64	14.31	102.60	1.91	3.43
Cluster II	40.83	63.46	29.93	4.42	2.52	9.42	8.33	3.76	24.36	43.73	73.36	14.09	102.69	1.73	3.45
Cluster III	42.00	63.33	38.09	5.33	2.45	14.67	9.33	4.33	27.34	42.13	73.97	10.70	120.49	1.49	4.61
Cluster IV	41.67	63.67	32.43	4.33	3.72	8.33	8.00	3.58	18.12	44.84	75.47	15.23	109.82	1.78	2.82
Cluster V	40.33	63.33	35.33	6.00	3.43	18.33	8.00	3.52	30.55	44.65	76.14	10.19	100.17	1.38	5.04
Cluster VI	42.33	67.00	29.85	4.33	3.54	11.67	8.00	2.67	24.34	42.70	75.13	12.55	108.55	1.76	2.57
Cluster VII	40.00	64.17	25.37	5.17	3.77	9.83	8.17	3.91	22.82	44.54	74.75	11.28	103.35	1.61	3.46
Cluster VIII	41.89	65.22	46.48	5.50	3.83	10.50	7.78	3.27	26.42	43.40	74.46	16.42	91.99	1.56	3.61
Cluster IX	43.33	65.00	47.53	3.67	2.11	10.33	8.00	3.31	33.17	40.35	71.59	19.44	110.67	1.09	4.31
Cluster X	43.33	68.00	36.48	5.67	2.84	8.33	9.00	5.31	25.89	44.84	73.65	16.52	114.32	2.06	5.26
Cluster XI	41.00	64.67	48.37	4.67	2.16	11.67	8.67	4.88	19.84	40.09	71.58	18.36	89.74	1.09	3.13

Table 5. Contribution of different quantitative characters to diversity in mungbean under moisture stress condition

Character	Times ranked first	Contribution (%)
Days to 50% flowering	0	0.00
Plant height (cm)	0	0.00
Days to maturity	228	49.03
No. of clusters/ plant	0	0.00
No. of pods/ cluster	159	34.19
No. of pods/ plant	0	0.00
No. of seeds/ pod	0	0.00
100 seed weight (g)	54	11.61
Harvest index (%)	0	0.00
SPAD	0	0.00
Relative Water Content (%)	0	0.00
Relative Injury (%)	0	0.00
Chlorophyll content	0	0.00
Specific leaf area (cm^2 g^{-1})	0	0.00
Seed Yield (g)	24	5.16

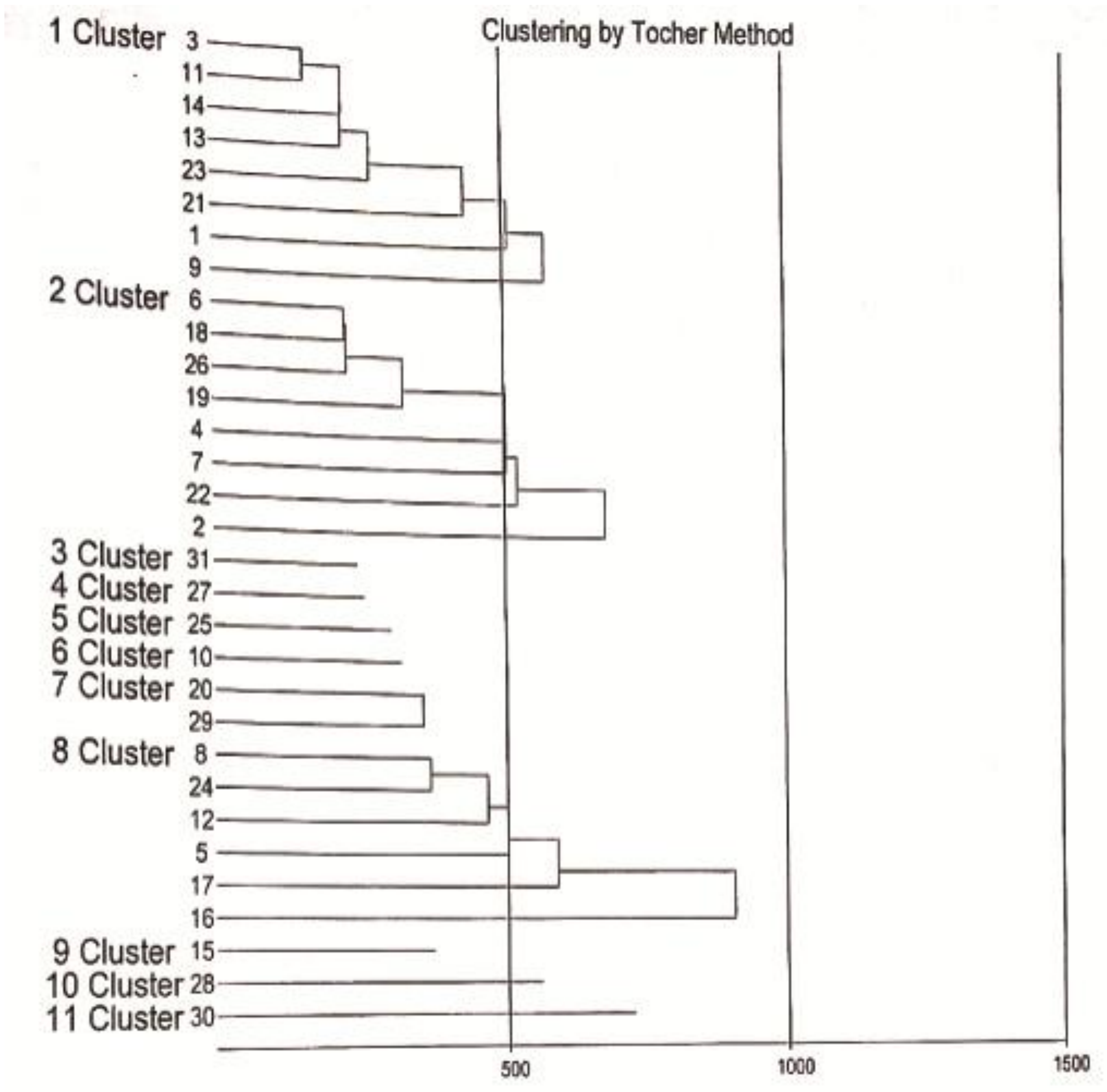

Fig. 1 Dendrogram of thirty one mungbean genotypes obtained through Tocher's method of classification under moisture stress condition