Indian J. Genet., **61**(1): 50-52 (2001)

Genetic diversity in a germplasm collection of mungbean (*Vigna radiata* L. Wilczek)

R. S. Raje* and S. K. Rao

Department of Plant Breeding and Genetics, J. N. Agricultural University, Jabalpur 482 004

(Received: September 1997; Revised: October 2000; Accepted: December 2000)

Abstract

Two hundred germplasm lines, along with six commercial varieties of mungbean were evaluated over four diverse environments for seed yield and its components. The genotypes were grouped into seven clusters. Genetic diversity was found to be unrelated to geographical diversity. On the basis of this analysis, genetically diverse genotypes with desirable level of particular characters have been identified and crossing programme has been suggested.

Key words : Mungbean, genetic diversity, clustering behaviour

Introduction

In mungbean, most of the studies on genetic diversity based on D^2 statistic [1-3] have been carried out with a limited number of genotypes that too evaluated in a single environment, only one study [4] involved more than one environment in assessment of genetic diversity. In the present investigation D^2 analysis of mungbean germplasm lines which originated from different states of India has been carried out by using mean values of the genotypes for different characters over four environments to draw clear inferences on the clustering pattern of the genotypes and to identify precisely the true genetically diverse parents for a hybridization programme.

Materials and methods

The experimental material for the present study consisted of 200 germplasm lines of mungbean from different states in India procured from the NBPGR (Amravati centre) along with six commercial varieties as checks (Table 1). These 200 germplasm lines along with the six commercial checks were grown in RCBD with two replications under four environments created by sowing the material on two different dates in summer (28.2.1994 and 17.3.1994) and also in late *kharif* (21.9.1994 and 5.10.1994) at JNKVV Research Farm, Jabalpur. The soil type for summer season was heavy whereas that for late *kharif* it was light. Each genotype was sown in single row plot of 2m length with row to row spacing of 30 cm. Observations were recorded on 10 randomly selected plants from each genotype in each replication for 15 characters. Mean values of 10 plants were used for statistical analysis. Mahalanobis D^2 analysis [5] was used to estimate genetic divergence among the 206 genotypes. Grouping of genotypes into various clusters was carried out following Tocher's method [6]. Genotypes were also evaluated for disease reaction to YMV (yellow mosaic virus) on the basis of 0-9 scale in each environment and mean values of disease scores of each genotype over the environments was used to identify the resistant genotypes.

Table 1. Source of genotypes included in the study

S.No.	Source (State)	Number of entries
1.	Andhra Pradesh	9
2.	Bihar	44
3.	Delhi	2
4.	Exotic	8
5.	Gujrat	20
6.	Haryana	11
7.	Himachal Pradesh	6
8.	Jammu and Kashmir	8
9.	Karnataka	3
10.	Madhya Pradesh	19
11.	Orissa	2
12.	Maharashtra	24
13.	Punjab	14
14.	Rajasthan	16
15.	Tamil Nadu	3
16.	Uttar Pradesh	10
17.	West Bengal	1

Checks: J 45; Malvia local - 52; PSM 1060; PS-105; PB; K-851

---

*Present address: Department of Plant Breeding and Genetics, SKN College of Agriculture, Jobner, 303 329.

Results and discussion

All the germplasm lines were classified into 7 clusters (Table 2). Cluster 1 comprised of 186 genotypes followed by cluster II eleven genotypes, cluster III four genotypes, cluster IV-two genotypes and cluster V, VI and VII each had a single genotype.

Table 2. Inter and intra cluster distances (D^2) of different clusters based on seed yield and its components pooled over environments

Cluster	Cluster						
	I	II	III	IV	V	VI	VII
I	**12.90**	39.74	34.17	93.54	40.48	55.59	52.08
II		**16.92**	81.18	42.43	49.32	39.55	30.79
III			**15.65**	128.79	98.52	63.55	84.03
IV				**14.04**	87.96	45.98	35.78
V					**0.0**	104.75	45.73
VI						**0.0**	60.29
VII							**0.0**

Table 3. Character means of various clusters for seed yield and its components

Character/Cluster	I	II	III	IV	V	VI	VII
Days to 50% flowering	48.25±0.16	50.20±0.71	42.71±1.28	52.06±1.50	59.62±2.36	43.50±2.04	49.75±3.04
Days from flowering to maturity	32.88±0.25	31.39±1.00	34.34±1.86	30.37±2.17	26.25±3.43	34.12±3.74	29.37±3.76
Days to maturity	81.10±0.18	81.51±0.69	77.06±1.03	82.43±1.58	85.57±3.87	77.62±2.63	79.12±2.05
Plant height (cm)	42.27±0.22	37.95±0.92	31.06±1.30	22.28±0.97	47.93±4.10	17.27±1.85	31.05±2.48
Primary branches/plant	0.60±0.01	0.32±0.04	1.05±0.18	0.13±0.03	0.35±0.08	0.58±0.20	0.21±0.04
Clusters/plant	3.69±0.03	1.92±0.08	4.61±0.25	1.04±0.17	1.62±0.44	1.99±0.17	1.08±0.43
Pods/cluster	3.81±0.01	3.47±0.09	3.92±0.08	2.20±0.25	2.98±0.46	3.91±0.31	2.17±0.56
Pods/plant	14.10±0.12	7.25±0.30	17.96±0.93	3.39±0.46	6.52±1.37	7.52±0.37	4.10±1.74
Pod length (cm)	6.47±0.01	7.43±0.10	6.11±0.08	70.6±0.13	6.13±0.13	6.62±0.17	7.16±0.32
Seeds/pod	6.67±0.02	6.05±0.14	6.20±0.22	6.42±0.26	6.55±0.65	5.81±0.27	6.58±0.75
Seeds/plant	94.76±0.98	45.18±2.21	110.80±6.49	23.61±3.47	47.63±9.02	43.26±1.70	30.87±15.86
100-seed weight (cm)	3.34±0.01	1.97±0.07	2.70±0.05	4.98±0.18	3.52±0.12	4.60±0.23	3.86±0.32
Seed yield/plant (g)	3.11±0.03	1.97±0.09	2.95±0.16	1.13±0.21	1.70±0.34	1.98±0.08	1.21±0.57
Biological yield/plant(g)	9.52±0.08	7.47±0.29	8.27±0.57	6.30±1.03	10.21±1.20	5.17±0.46	6.97±0.79
Harvest index (%)	33.35±0.21	27.11±1.08	37.46±1.28	22.41±3.52	16.81±2.67	39.60±2.61	14.88±6.42

The mean values for different characters of seven clusters indicated the superior expression of some characters in different clusters (Table 3). Cluster III had genotypes having the highest values for days from flowering to maturity, primary branches/plant, clusters/plant, pods/cluster, pods/plant and seeds/plant and lowest mean values for days to 50% flowering, days to maturity and pod length. Cluster I had genotypes having the highest values for seeds/pod and seed yield/plant. Cluster II had genotypes having longer pod length. Bolder seed sized genotypes were observed in cluster IV. Cluster V comprised of genotypes having taller plant height, high biological yield/plant and later flowering and maturity. Cluster VI had genotypes having high harvest index.

Clustering pattern revealed that genotypes from different states and even the exotic lines were grouped into a single cluster e.g. cluster II contained two genotypes from Rajasthan, three genotypes from Bihar, two genotypes from Maharashtra, one genotype from Gujarat, one genotype from Haryana, one genotype from MP and one exotic genotype. Similarly genotypes from the same state included in the different cluster. These facts suggested that genetic diversity was not directly related to geographical diversity.

Genotypes having desirable specific level for particular character have been identified from specific clusters (Table 4).

Genetically diverse genotypes from different clusters have been identified on the basis of intercluster distances and *per se* performance for hundred seed weight, plant height and pod length. On the basis of intercluster D^2 values, cluster means for component characters, mean performance of genotypes over environment, component complementation and disease reaction to YMV it is suggested to use the hybridization programme as given in Table 5.

Table 4. Genotypes from different cluster having desirable specific level of particular character

Genotype	Cluster	Desirable trait(s)	Resistance to YMV
PLM-32	I	Seeds per pod (7.22)	Resistant
PLM-477	I	Harvest index (40.6%)	Resistant
PLM-156	I	Seeds per pod (8.75)	Resistant
IC-19413	I	Days from flowering to maturity (37.75)	Resistant
EC-5478	I	Seed yield per plant (5.26g)	Resistant
PLM-90	I	Seeds per plant (148.18)	Resistant
PLM-20	I	Primary branches per plant (1.43)	Resistant
IC-53728	I	Pods/cluster (4.27)	Resistant
PLM-169	II	Pod length (6.91 cm)	Resistant
PLM-261	II	Pod length (7.12 cm)	Resistant
IC-610	II	Pod length (8.22 cm)	Resistant
PLM-509	II	100 seed weight (4.47 g)	Moderately resistant
EC-16563	II	100 seed weight (5.12g)	Resistant
PLM-618	III	Days to 50% flowering (41.0)	Resistant
PLM-661	III	Days to maturity (74.75) and harvest index (42.17%)	Resistant
PLM-333	III	Clusters per plant (5.22) and pods per plant (21.47)	Moderately resistant
PLM-214	III	Pods per plant (19.37)	Resistant
PLM-75	IV	Pod length (7.0 cm)	Moderately resistant
EC-5551	IV	100 seed weight (5.35 g)	Resistant
PLM 263	V	Biological yield/plant (19.21 g)	Resistant
EC-13077-2	VI	Harvest index (39.6%)	Resistant
PLM-336	VII	Lower plant height (31.05 cm)	Moderately resistant

Table 5. Suggested hybridization programme

S.No.	Proposed crosses
1	PLM 214 (cluster III) × EC 5551 (Cluster IV)
	PLM-333 (cluster III) × PLM 75 (Cluster IV)
2	PLM-263 (Cluster V) × EC-13077-2 (Cluster VI)
	PLM-214 (Cluster III) × PLM-263 (Cluster V)
	PLM-333 (Cluster III) × PLM-263 (Cluster V)
	PLM-20 (Cluster I) × PLM-75 (Cluster V)
	PLM-20 (Cluster I) × EC-5551 (Cluster IV)
	PLM-32 (Cluster I) × PLM-75 (Cluster V)
	PLM-32 (Cluster I) × EC-5551 (Cluster IV)
5	PLM-75 (Cluster IV) × PLM-263 (Cluster V)
	EC-5551 (Cluster IV) × PLM-263 (Cluster V)
6	PLM-333 (Cluster III) × PLM-336 (Cluster VII)
7	PLM-116 (Cluster III) × PLM-333 (Cluster III)
	PLM-169 (Cluster II) × PLM 333 (Cluster III)
	PLM-261 (Cluster II) × PLM-333 (Cluster III)

References

1. **Renganayaki K. and Sreerangaswamy S. R**. 1991. Genetic divergence in *Vigna* species. Indian J. Pulses Res., **4**: 159- 164.
2. **Satyan B. A., Siddaraju I. G. and Amarnath K. C.** 1991. Genetic divergence in greengram (*Vigna radiata* L. Wilczek). Mysore J. Agric. Sci., **25**: 18-25.
3. **Chandra N., Mehra R. B. and Chaturvedi S. N.** 1993. Genetic diversity in mungbean. Indian J. Pulses Res., **6**: 123-126.
4. **Naidu N. V. and Satyanarayana A.** 1991. Studies on genetic divergence over environments in mungbean (*Vigna radiata* L. Wilczek). Indian J. Genet., **51**: 454-460.
5. **Mahalanobis P. C.** 1936. On generalised distance in statistics. Proc. Nat. Inst. Sci., (India) : 12-49.
6. **Rao C. R.** 1952. Advanced statistical methods in biometrical research, Ed 1, pp 390-395. John Wiley and sons Inc., New York.