Indian J. Pl. Genet. Resources 13(3): 230-233, 2000

GENETIC DIVERSITY FOR SEED YIELD IN A LARGE COLLECTION OF CLUSTERBEAN (*Cyamopsis tetragonoloba* (L) Taub.)

JIBAN MITRA, S. NATARAJAN, R. K. JAIN AND U. P. SINGH[1], Indian Grassland and Fodder Research Institute (IGFRI), Western Regional Research Station, Avikanagar 304 501, (Rajasthan);
[1]IGFRI, Jhansi 284 003 (Uttar Pradesh)

Two hundred thirty.one Yermplasm lines of clusterbean (*Cyamopsis tetragonoloba*) were evaluated alone with three checks for seed yield and its components in augmented design. Pods per plant exhibited highest variability and contribution to divergence. This trait was also significantly and positively correlated with seed yield which indicates its importance as selection criteria. Following non-hierarchical Euclidean analysis, all the 234 genotypes were grouped into 12 clusters with variable number of genotypes. The highest genetic divergence was observed between cluster V and IX, whereas cluster III and VIII were closest one. On the basis of genetic divergence and mean performance eight diverse and superior genotypes, being exceptionally good for one or more traits and reasonable for others in comparison to checks, were selected and these genotypes may be useful in multiple crossing or diallel selective mating system to recover transgressive segregants.

Key words: *Cyamopsis tetragonoloba,* clusterbean, genetic diversity, seed yield

Clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.), commonly known as guar, is one of the most important kharif legumes grown for green fodder, vegetables, green manuring and seed purpose. Now-a-days it has been emerged as an industrial crop due to importance of its seed as a source of industrial gum, guar meal for animal, nutritional protein to meet human dietary and other uses (Joshi and Arora, 1993). A limited number of varieties have been released in this crop that is also keeping the importance of its fodder value in mind. Thus, breeding a high seed yielding genotype is need of the hour. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop to exploit transgressive segregation has been emphasized (Murty and Arunachalam, 1966 and Bhatt, 1970). But information on genetic diversity in clusterbean, particularly for attributes of seed yield is lacking and hence, the present experiment was aimed at assessment of its genetic diversity for seed yield and its components.

MATERIALS AND METHODS

The experimental materials comprising two hundred thirty-one genotypes collected from different parts of Rajasthan and three checks (Bundel Guar 1, Bundel Guar 2, HG 75) were evaluated in augmented design with 11 blocks in kharif, 1999 at Research Farm, Western Regional Research Station (IGFRI), Avikanagar, Rajasthan. Each block contained 21 different test genotypes (germplasm) and the three checks. Each genotype was sown in a two-row plot of 3 in long with row to row and plant to plant spacing of 30 cm and 15 cm, respectively. After every 10th germplasm line the checks were sown in each block. Recommended agronomic practices were followed to raise a good crop. The data on seed yield and its components were recorded on 10 plants for each genotype and their mean values were subjected to statistical analysis.

Adjusted mean value for all the characters of 231 test genotypes and the estimates of different mean squares were obtained following Federer (1956) and Peterson (1985) and used for subsequent analysis. The mean, range, phenotypic coefficient of variation (%) (PCV), genotypic coefficient of variation (%) (GCV), heritabilty (%) and correlation coefficient were estimated as per standard statistical procedures (Panse and Sukhatme, 1954). The non-hierarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973) was conducted to group the genotypes into different clusters and to estimate the intra- and inter-cluster distances.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes indicating the scope of selection for high (seed) yielding genotypes. Considerable range was observed for all the characters (Table 1). Pods per plant showed the highest GCV and PCV followed by clusters per plant, whereas seeds per pod showed the lowest ones. Accordingly, pods per plant exhibited highest heritability. Again, pods per plant showed significant, positive correlation with seed yield per plant (Table 2). However, clusters per plant, seeds per plant and 100 seed weight also had significant, positive association with seed yield. Pods per plant and clusters per plant were significantly and positively correlated. Thus, pods per plant should be given importance during selection for high seed yield.

Table 1. Estimate of different genetic parameters for attributes of seed yield in clusterbean

Character	Range	Mean	PCV (%)	GCV (%)	Heritabilty (%)
Clusters/plant	5.30-54.40	25.46	60.29	45.64	57.32
Pods/plant	9.40-156.20	66.38	67.18	53.44	63.28
Seeds/pod	5.30-10.90	8.38	14.82	10.41	49.38
Pod length (cm)	4.20-9.10	5.54	20.18	13.96	47.89
100-seed wt (g)	2.13-4.65	3.27	35.11	20.65	34.72
Seed yield/plant (g)	1.26-64.32	16.22	57.26	32.02	31.28

Table 2. Correlation coefficients among seed yield and its components in clusterbean

Character	Pods/ plant	Seeds/ pod	Pod length	100-seed wt	Seed yield/ plant
Clusters/plant	0.51**	0.19	- 0.01	0.06	0.52**
Pods/plant		0.21	0.11	0.1	0.63**
Seeds/pod			0.33*	-0.17	0.33*
Pod length				0.12	0.12
I 00-seed wt					0.43**

*, **: Significant at 5% & 1% level of significance

Based on non-hierarchical Euclidean cluster analysis, the 234 genotypes were grouped into 12 clusters with variable number of genotype (Table 3) revealing the presence of considerable amount of genetic diversity in the material. Cluster III had the maximum number of 49 genotypes followed by cluster VIII with 27 genotypes. These two clusters accounted for sufficient (76) genotypes reflecting narrow genetic diversity. The similarity in base material from which these have been evolved might be the cause of genetic uniformity. The members of cluster V and IX exhibited maximum divergence indicating greatest diversity between genotypes belonging to these two clusters followed by VI and VII, whereas cluster III and VIII were closest one with minimum genetic distance (Table 4). The average intra-cluster distance in cluster V was maximum suggesting that the genotypes in this cluster were relatively more diverse among themselves, whereas closeness among the genotypes in cluster XII was indicated. However, in all cases, the inter-cluster distances were greater than the intra-cluster distances implying the degree of genetic diversity present among the genotype between clusters.

Cluster mean also indicated substantial variation among different cluster as well as superiority of different cluster for different

Table 3. Grouping of clusterbean genotypes into 12 clusters

Cluster No.	No. of Genotypes	Genotypes
I	24	AVKG 9, 19, 20, 24, 26, 30, 40, 60, 68, 78, 101, 126, 138
II	6	AVKG 2, 15, 33, 80, 117, 202
III	49	AVKG 1, 5, 10, 18.21, 25, 27, 29, 34,37, 38, 44, 46, 54, 55, 61, 62, 69, 75, 89, 97, 113, 114, 116, 118, 119, 121, 124, 132, 159, 167, 168, 171, 173, 179, 190, 191, 194, 197, 198, 199, 208, 212, 217, 221, 2221, 225, 2271, 229
IV	21	Bundel Giiar 1,AVKG 7, 11, 17, 28, 41, 45, 53, 70, 86, 87, 93, 98, 110, 115, 125, 131, 143, 149, 166, 193
V	26	AVKG 12, 23, 32, 56, 63, 74, 81, 94, 104, 105, 123, 130, 142, 156, 160, 163, 180, 183, 186, 189, 195, 196, 209, 211, 223, 228
VI	8	AVKG 71, 83, 91, 99, 137, 141, 148, 224
VII	18	AVKG 4, 13, 16, 35, 36, 51, 66, 82, 129, 133, 134, 140, 154, 177, 187, 216, 219, 226
VIII	27	Bundel Guar 2, AVKG 8, 31, 47, 52, 57, 64, 72, 77, 84, 95, 100, 103, 106, 107, 111, 112, 127, 144, 157, 165, 169, 181, 192, 204, 206, 218
IX	13	AVKG 6, 39, 48, 67, 88, 90, 122, 135, 147, 151, 174, 188, 213
X	22	HG 75, AVKG 14, 42, 43, 58, 65, 73, 85, 92, 108, 109, 120, 139, 146, 153, 161, 176, 182, 200, 205, 207, 230
XI	6	AVKG 49, 76, 128, 152, 162, 215
XII	14	AVKG 3, 22, 50, 59, 79, 96, 102, 136, 150, 155, 175, 184, 201, 220

Table 4. Estimates of intra- (diagonal value) and inter-cluster distances of 12 clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	2	4.75	8.56	6.84	5.14	7.58	5.85	8.56	6.84	11.84	13.75	8.51
II		4.25	9.62	8.62	4.91	7.14	5.25	8.78	13.66	11.46	15.64	7.98
III			2.21	9.48	8.07	7.86	4.80	4.32	11.32	9.63	6.25	11.22
IV				6.27	8.85	5.88	7.12	13.16	14.12	12.36	6.85	8.87
V					9.92	17.25	21.65	12.39	39.87	15.62	13.34	16.95
VI						6.92	24.12	7.89	20.06	11.42	10.68	22.34
VII							5.25	6.75	23.66	13.25	12.60	17.12
VIII								2.16	13.25	11.25	9.30	6.25
IX									6.23	9.66	11.25	20.12
X										2.98	4.96	5.25
XI											2.66	4.66
XII												1.01

characters (Table 5). Cluster V showed the highest mean for both clusters per per and pods per plant, whereas cluster IX, XII, VII and VI had the maximum seeds per pod, pod length, 100-seed weight and seed yield per plant, respectively. The differential contribution to total divergence was observed in different seed attributes (Table 5). The germplasm lines were divergent (for seed attribute) mainly on the basis of pods per plant and clusters per plant as these two traits contributed largely to divergence as compared to other traits.

The data on inter-cluster distance and performance of the genotypes was used to select genetically diverse and agronomically superior genotype among 231 genotypes. The genotypes, exceptionally good in respect of one or more character and at least comparable in respect to

Table 5. Cluster mean and contribution to total divergence of different attributes of seed yield

Character	Cluster mean												Contribution to total divergence (%)
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	
Clusters/plant	24.69	19.26	30.16	25.12	34.56	22.19	29.66	20.12	28.76	26.33	20.46	24.20	27.64
Pods/plant	60.18	70.26	71.22	65.66	74.83	71.33	61.23	63.19	65.21	62.49	71.94	59.02	40.44
Seeds/plant	8.32	8.93	9.42	8.44	8.01	7.86	8.22	8.06	8.97	8.06	8.11	8.71	6.78
Pod length (cm)	5.61	5.26	5.05	5.64	4.96	6.04	5.61	5.13	5.04	5.71	6.01	6.42	7.94
100-seed wt(g)	3.06	3.01	3.61	3.22	2.98	3.51	3.72	3.26	3.41	3,06	3.33	3.50	5.10
Seed yield/plant(g)	10.56	18.22	20.17	17.59	16.19	24.32	17.27	18.29	12.78	14.36	11.64	14.01	12.10

Table 6. Diverse and superior genotype with desirable characters selected from different clusters

Sl. No.	Genotype	Cluster No.	Dsireable characters
1	AVKG 63	V	Clusters/plant,Pods/plant,Seed yield/plant
2	AVKG 189	V	Pods/plant,100-seed wt
3	AVKG 137	VI	100-seed wt,Seed yield/plant
4	AVKG 51	VII	Pods/plant,100-seed wt,Seed yield/plant
5	AVKG 187	VII	Pods/plant,100-seed wt,Seed yield/plant
6	AVKG 39	IX	Seeds/pod,100-seed wt
7	AVKG 122	IX	Seeds/pod,Seed yield/plant
8	AVKG 201	XII	Pods/plant,Pod-length

others to the checks, were deemed desirable. On this basis, eight genetically diversed and superior genotypes were selected (Table 6). They belonged to different five clusters. Intermating of divergent (groups would lead to greater opportunity for crossing over which releases latent variability by breaking linkage (Thoday, 1960) and progenies derived from diverse cross are expected to show broad spectrum of genetic variability, providing a greater scope for isolating trangressive segregates in the advanced generation. So, these genotypes may be used in a multiple crossing programme or in diallel selective mating system to recover transgressants. Furthermore, the trait, pods per plant may be used as a selection criteria in segregating generations as it showed the highest GCV heritability (%), contribution to the total divergence as well as significant, positive correlation with seed yield/plant.

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