Annals of Arid Zone 49(2): 145-147, 2010

Short Communication

Diversity Analysis in Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.]

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Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.], locally known as guar, belongs to family Leguminoseae, is a multipurpose drought-tolerant crop grown primarily in India and Pakistan for feed, green fodder, vegetable, green manure and grain purposes. The findings that clusterbean seed endosperm could be a source of industrial gum brought this little known arid legume crop paved its way to be the crop of major prominence. The nature and magnitude of genetic divergence in a population is essential for selection of diverse parents which upon hybridization leads to a wide spectrum of gene recombination for quantitatively inherited traits (Singh *et al.*, 2005). Therefore, the present study was undertaken to assess genetic diversity available in released varieties and a few breeding lines of clusterbean so as to identify diverse parents for hybridization programme.

A total of 28 genotypes of clusterbean, including 14 released varieties/cultivars, eight advanced entries and six mutant lines, were evaluated in randomized block design with three replications during kharif 2008 at research farm of Agricultural Research Station, Mandor, Jodhpur. Each genotype was sown in six rows of 4 m length. Distance between rows was 30 cm while plant-to-plant distance within row was 15 cm. The crop was raised under rainfed condition and all cultural operations were done as and when required. The data were recorded on five competitive plants, taken randomly from each plot, for plant height, branches per plant, number of pods per plant, seeds per pod and 100-seed weight, whereas seed yield, fodder yield, days to 50% flowering and days to maturity were observed considering whole plot. The data were subjected to analysis of variance following standard methods. Clustering was performed as per the procedure of Ward's minimum variance method (Ward, 1963).

The analysis of variance revealed significant differences among the genotypes for all the characters depicting sufficient variability in the experimental material, but such analysis is unable to explain the extent of genetic diversity. For this, a hierarchical cluster analysis of Ward's minimum variance method were used to produce a dendrogram showing successive fusion of individuals which exhibited a clear cut 2-, 4- and 6-cluster partition (Fig. 1). For the 2-cluster partition, the groups were designated as A and B having 21 and 7 entries, respectively. Entries of group A were earlier in flowering and maturity, dwarf, having more branches and pods per plant, higher number of seeds per pod, higher 100-seed weight, more seed yield and lower fodder yield compared to the entries of group B. For the 4-cluster partition, each A and B group was sub-divided into two sub-groups, which designated as A I, A II, B I and B II. When 6-cluster partition was considered, the sub-groups A I and B II each were further sub-divided into two clusters. Finally based on Euclidean^2 cluster analysis, 28 genotypes were accommodated into six clusters with variable numbers of genotypes revealing the presence of considerable diversity. Number of genotypes was the maximum in cluster I (10) followed by eight in cluster III, three each in clusters I and IV, and two each in clusters V and IV.

There was no association between clustering pattern and geographical origin of the varieties. It has been often postulated that geographical distribution reflects genetic diversity (Joshi and Dhawan, 1966). But in present study, in spite of different geographical origin of the varieties HG 365 and HG 563 (Haryana), Naveen (Delhi), RGM 112, RGC 1003, RGC 1017 and RGC 1066 (Rajasthan) and GG 2 (Gujarat) were accommodated in a single cluster I indicating their close affinity. This showed geographical distribution does not necessarily exhibit genetic divergence. These results are in accordance to those reported in different crops (Arora *et al.*, 2005; Prakash *et al.*, 2008). On the other hand, nine varieties (RGM 112, RGC 936, RGC 986, RGC 1002, RGC 1003, RGC 1017, RGC

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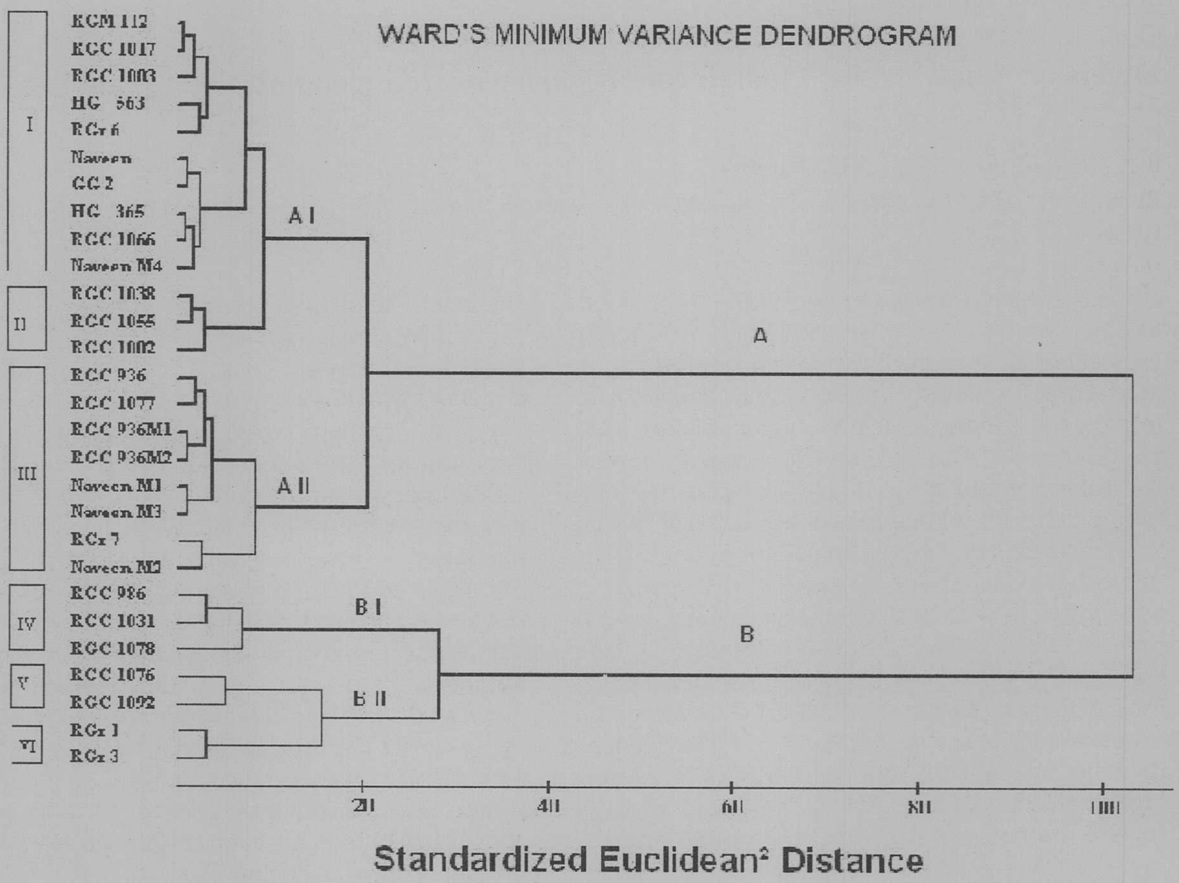

Fig. 1. Dendrogram showing clusterbean genotypes in different clusters.

1031, RGC 1038 and RGC 1055) belonging to Rajasthan fell into four different clusters. This implied that genetic material from the same geographical region might also have greater diversity. Thus, it may be wrong to generalize that all the varieties sharing common geographical origin would always have low diversity among them. In this study, a complex situation occurred which supported the view that geographical origin and genetic divergence do not follow the same trend as also noted by Pathak *et al.* (2009). With regard to mutant lines, one out of four of Naveen and both of RGC 936 were accommodated in clusters along with their respective progenitor, showing their affinity to their parent lines.

Intra and inter-cluster Euclidean^2 distances are depicted in Table 1. The maximum intra-cluster distance was observed in cluster V (10.4) indicating wide genetic diversity within the genotypes of the cluster. The highest inter-cluster distance was observed between clusters II and IV (47.5) followed by clusters III and IV (41.6), and clusters I and IV (41.4) exhibiting wide diversity between genotypes of these cluster pairs. The crosses between genotypes of these diverse clusters might

Table 1. Average intra- and inter-cluster values among eight clusters in clusterbean

Cluster	I	II	III	IV	V	VI
I	4.8	7.7	9.4	41.4	19.6	23.5
II		4.5	10.1	47.5	20.1	34.2
III			6.2	41.6	22.6	30.6
IV				10.1	31.9	19.7
V					10.4	19.8
VI						6.3

Table 2. Cluster means for different characters in clusterbean

Clusters	Days to flowering	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pod	100-seed weight (g)	Fodder yield (kg ha^{-1})	Seed yield (kg ha^{-1})
I	40.4	82.3	45.6	1.47	17.6	7.6	2.39	1287	300
II	40.1	81.8	41.7	1.82	18.8	7.6	2.63	1034	259
III	40.5	82.2	50.3	2.47	22.7	7.1	2.47	1400	301
IV	48.2	96.6	57.7	1.71	9.0	6.0	2.46	2222	107
V	45.2	85.5	50.7	1.60	17.8	6.3	2.15	880	121
VI	47.5	92.0	63.1	0.47	13.6	7.4	2.31	1505	196

result into greater variability and desirable recombinants (Arunachalam *et al.*, 1984).

The diversity was further supported by the appreciable variation among the cluster means for different characters (Table 2). The cluster III, which had eight genotypes, showed the highest mean values for many characters, such as branches per plant, pods per plant and seed yield while genotypes of cluster II were earliest in flowering and maturity, and had maximum 100-seed weight and highest seeds per pod. Entries of cluster IV were late in maturity and superior for fodder yield. Genotypes of these clusters would offer a good scope of improvement for desirable traits through hybridization and selection.

The characters contributing the most divergence should be given more importance for the purpose of effective selection and the choice of parents for hybridization. Amongst the nine characters studied, plant height (41.8%) contributed the maximum towards the total divergence followed by seed yield (25.4%), 100-seed weight (15.6%) and fodder yield (15.6%). Since, plant height, seed yield, 100-seed weight and fodder yield contributed maximum towards the divergence therefore, direct selection of these traits may help in guar improvement.

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