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Geeta Vishnoi
M.Sc. Research scholar,
Department of Plant Breeding
and Genetics College of
Agriculture SKRAU, Bikaner,
Rajasthan, India

AK Sharma
Professor, Department of Plant
Breeding and Genetics College of
Agriculture SKRAU, Bikaner,
Rajasthan, India

Pawan Kumar
Ph.D Research scholar,
Department of Plant Breeding
and Genetics, Rajasthan
Agricultural Research Institute,
SKNAU, Jaipur, Rajasthan,
India

Manoj Kumar
Ph.D Research scholar,
Department of Plant Breeding
and Genetics, Rajasthan
Agricultural Research Institute,
SKNAU, Jaipur, Rajasthan,
India

Correspondence

Geeta Vishnoi
M.Sc. Research scholar,
Department of Plant Breeding
and Genetics College of
Agriculture SKRAU, Bikaner,
Rajasthan, India

Genetic diversity for yield and its component traits in cluster bean (*Cyamopsis tetragonoloba* (L.) Taub.)

Geeta Vishnoi, AK Sharma, Pawan Kumar and Manoj Kumar

Abstract

30 genotypes of clusterbean were studied for genetic divergence analysis utilizing Mahalanobis D² technique. Genetic divergence analysis revealed that genotypes could be grouped into 6 clusters. The cluster I was the largest and consisted of 16 genotypes followed by cluster II with 10 genotypes and cluster III, IV, V and VI had solitary genotype. Therefore, selection and intercrossing of genotypes involved in these clusters would be useful for inducing variability in the respective characters. Average intra and inter-cluster D² values among 30 genotypes revealed that cluster I recorded maximum intra cluster distance followed by cluster II revealing thereby the existence of diverse genotypes in these clusters. While, inter cluster differences were maximum between cluster II and cluster IV followed by II and V, IV and VI, I and VI and I and III indicating that the genotypes from these clusters can be selected for future breeding programme to produce heterotic hybrids.

Keywords: clusterbean, D² technique, Genetic divergence, Cluster

1. Introduction

Clusterbean, (*Cyamopsis tetragonoloba* (L.) Taub) commonly known as Guar, is a drought and high temperature tolerant deep rooted summer annual legume of high social and economic significance. The qualities of the crop like high adaptation towards erratic rainfall, multiple industrial uses and its Importance in cropping system for factors such as soil enrichment properties, low input requirement, etc have made the guar one of the most significant crops for farmers in arid areas in India. Guar meal and seeds are the source of high protein and nutritious feed to the cattle. It is one of the most important and potential vegetable cum industrial crop grown for its tender pods and endospermic gum (30-35 %). Guar seeds are mainly used for extraction of endospermic gum having good binding properties and have high demand in food industry as an ingredient in products like sauces and ice creams etc. In agriculture, guar gum is used as water retainer, soil aggregate and anti-crusting agent. In petroleum industry, it is used as gelling and thickening agent. Rajasthan occupies first position in area and production of guar in the country. In Rajasthan, it is cultivated on 4.56 million hectare area with the production of 2.02 million tonnes and productivity is 447 kg/ha (Anonymous, 2014) [1]. In Rajasthan, Bikaner is the leading district both in terms of area (29.1 per cent) and production (19.04 per cent). The districts like Hanumangarh (19.0 per cent), Sriganganagar (19.03 per cent), Churu (7.35 per cent), Jodhpur (5.97 per cent) and Jhunjhunu (3.85 per cent) are the major guar producing districts of the state.

Materials and Methods

The experimental material comprised of 30 genotypes of cluster bean selected on the basis of their diverse geographical origin and wide variation in morphological characters. The experiment was laid out in randomized block design with three replications during *kharif* 2014 at Agronomy Farm, College of Agriculture, Bikaner. Each plot comprised of two rows of 4 meter length, the spacing between row to row and plant to plant was 30 cm and 10 cm, respectively. Normal and uniform cultural operations were followed to raise a good crop. The observations were recorded on the basis of five randomly selected plants from each replication for ten character *viz.*, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, biological yield per plant, harvest index and seed yield per plant while days to 50% flowering and days to maturity were recorded on plot basis. The collected data was subjected to statistical analysis using Mahalanobis D² statistic to assess genetic divergence. The genotypes were grouped on the basis of minimum generalized distance using the Tocher's methods Rao (1952).

Results and discussion

Analysis of variance revealed significant difference among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Based on D2 values, 30 genotypes were grouped into six clusters (Table

1). This suggested the presence of high degree of divergence in the material studied. Maximum number of genotypes accommodated in the cluster I (16). Cluster II had (10) genotypes and remaining cluster (III, IV, V and VI) were mono genotypic.

Table 1: Composition of clusters

Clusters	Number of genotypes	Composition of cluster
I	16	GG 2, CAZG 04-01, RGE 07, HG 365, HG 563, BG 2, HG 884, HG 258, FGB 2 R1, HGS 891, HG 382, GAUG 9406, GG 1, HG 75, BG 1, HG 119
II	10	RGC 1017, RGC 1055, RGC 1038, RGC 1003, RGC 1033, RGC 471, RGC 1002, RGC 986, RGC 936, HG 832
III	1	BG 3
IV	1	FS 277
V	1	RGC 197
VI	1	RGC 1066

The clustering pattern of the genotypes showed that geographical diversity was not related with genetic diversity. Gipson and Balkishnan (1992) [2] and Singh *et al.* (2005) [6] also reported that there is no association between genetic diversity and geographical diversity. The genotypes namely BG 3, FS 277, RGC 197 and RGC 1066 belong to different cluster indicating wide diversity from set, as well as from each other. Results obtained in the present study are in accordance with the findings of Singh *et al.* (2002) [4] which grouped 107 genotypes into 8 clusters; Kumar *et al.* (2014) [3] accounted 30 genotypes into 5 clusters. Intra cluster distance was highest in cluster I followed by cluster II (Table 2). The intra cluster distance was not observed in cluster III, IV, V and VI as these clusters had only one genotypes each. The high intra cluster distance values revealed the presence of genetic diversity between the genotypes which were grouped together in these clusters. Hence, there is a lot of scope for exchange of genes among the genotypes within these clusters. The highest inter cluster existence was observed between cluster II and cluster IV followed by II and V, IV and VI, I and VI and I and III indicating that the genotypes from these clusters can be selected for hybridization to produce heterotic hybrids. The inter cluster differences were minimum between

cluster III and IV, suggesting that the genetic constitution of these genotypes in one cluster as in close proximity with the genotypes in other cluster pair. The cluster mean values (Table 3) for seed yield, harvest index and number of seeds per pod were highest in case of cluster VI with one genotype (RGC 1066). The cluster mean values for number of branches per plant, number of clusters per plant, number of pods per cluster and number of seeds per pod were highest in case of cluster II with 10 genotypes. While cluster III with one genotype (BG 3) registered highest mean values for biological yield and seed yield per plant. Hence, suggesting quite different genetic makeup of the genotypes included in these clusters and important role of these characters in the genetic divergence.

Table 2: Average intra (in bold) and inter cluster D² value

Clusters	I	II	III	IV	V	VI
I	5.62	8.85	6.50	7.61	8.59	9.33
II		4.82	9.21	11.34	9.76	7.73
III			0.00	5.29	7.10	8.45
IV				0.00	6.75	9.56
V					0.00	6.29
VI						0.00

Table 3: Mean values for yield and its components in various clusters

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per cluster	Number of seeds per pod	Pod length (cm)	100-Seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
I	45.73	89.35	63.93	2.94	7.46	2.97	4.88	4.46	3.24	35.62	21.32	7.52
II	43.83	85.80	56.17	4.25	10.27	4.38	6.56	4.93	3.61	39.05	25.21	9.76
III	46.67	82.67	80.73	2.33	8.53	2.97	4.20	3.60	3.11	48.93	20.50	10.02
IV	45.67	83.67	85.67	1.80	6.57	2.63	3.77	4.52	3.10	29.31	25.52	7.45
V	45.67	86.67	86.17	1.03	8.57	3.63	6.10	5.44	3.67	47.64	20.60	9.76
VI	45.00	72.33	55.07	1.40	9.50	4.27	7.55	4.54	3.49	38.16	26.73	10.19

Contribution of individual character towards total divergence was calculated as per method given by Singh and Choudhury (1979) [5] and has been presented in. The relative contribution of various characters indicated (Table 4) that the characters like seed yield per plant (18.39%) towards total divergence which was followed by plant height (16.78%), number of seeds per pod (13.33%), harvest index (12.18%) and number of branches per plant (12.18%). While number of clusters per plant (8.74%), number of pods per cluster (8.51%), biological

yield per plant (3.68), days to maturity (2.99%), pod length (1.84%) and days to 50 per cent flowering (1.38%) had low value of character contribution towards total divergence. The characters *viz.*, seed yield per plant, plant height, number of seeds per pod, harvest index and number of branches per plant was the major contributing characters in total about 72.86 per cent of the total divergence. Thus, these five characters are important and should be considered while selecting genetically diverse genotypes.

Table 4: Contribution of different characters towards total divergence

Characters	Number of times appearing in first ranking	Per cent contribution
Days to 50% flowering	6	1.38
Days to maturity	13	2.99
Plant height (cm)	73	16.78
Number of branches per plant	53	12.18
Number of clusters per plant	38	8.74
Number of pods per cluster	37	8.51
Number of seeds per pod	58	13.33
Pod length (cm)	8	1.84
100- Seed weight (g)	0	0.00
Biological yield per plant (g)	16	3.68
Harvest index (%)	53	12.18
Seed yield per plant (g)	80	18.39

Conclusion

The highest inter cluster distance was observed between cluster II and cluster IV followed by II and V, IV and VI, I and VI and I and III respectively. Thus, crossing between genotypes of cluster II and IV might provide good chance for transgressive segregates in the segregating generations and may end up in some promising genotypes. Cluster mean for different clusters indicated that cluster VI had high mean values for seed yield, harvest index and number of seeds per pod. Cluster II was also good source of number of branches per plant, number of clusters per plant, number of pods per cluster and number of seeds per pod. Cluster III was the best source of biological yield and seed yield per plant.

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