Research Article

GENETIC DIVERSITY FOR YIELD AND ITS CONTRIBUTING TRAITS IN GUAR (*Cyamopsis tetragonoloba* L. Taub.)

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Abstract- A set of thirty genotype of cluster bean were studied for genetic divergence analysis utilizing Mahalanobis D^2 technique. The analysis of data revealed that significant difference was observed among the genotypes for all the traits. Based on the genetic distance (D2 value), the thirty genotypes were grouped into 8 clusters. Of the 8 clusters, cluster I was largest with 14 genotype followed by cluster IV with 7 genotypes while Cluster II, Cluster III, Cluster V and Cluster 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. Minimum inter-cluster distance was present between clusters I and cluster VII. The intra-cluster distance was maximum in cluster III followed by cluster II and cluster IV.

Keywords- Cluster bean, D^2 technique, Genetic divergence, Cluster.

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Introduction

Guar is an important legume crop of dry land agriculture. It grows well in soils with low fertility in the arid and semi-arid areas of the tropics and subtropics where the rainfall is scanty. The green pods of the crop are used as a green vegetable for human consumption while plant is used as fodder for cattle feed, meal (hull+seed coat) for non -ruminants.

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 tones and productivity is 447 kg/ha [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 among the genotypes significantly different sowing wide genetic divergence among them. Based on D2 values, 30 genotypes were grouped into eight clusters [Table-1].This suggested the presence of high degree of divergence in the material studied. Maximum number of genotypes accomated in the cluster I (14). Cluster IV had 8 genotypes; cluster VII and VIII had 2 genotypes and remaining cluster (II, III, V,VI) were mono genotypic.

The clustering pattern of the genotypes showed that geographical diversity was not related with genetic diversity. [2,3] also reported that there is no association between genetic diversity and geographical diversity. The genotypes namely HGC 365, RGr 12-5, RGC 471 and RGM -115 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 [4] which grouped 45 genotypes into 8 clusters; [5] accounted 45 genotypes into 15 clusters. Intra cluster distance was highest in cluster VIII followed by cluster I and IV [Table-2]. The intra cluster distance was not observed in cluster II, III, 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 V and cluster VII followed by VI and VII indicating that the genotypes from these clusters can be selected for hybridization to produce heterotic hybrids. The inter cluster differences were minimum between cluster II and III, 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 and plant height were highest in case of cluster VII with 2 genotypes (RGr 13-4, RGr 13-5). The cluster mean values for Days to flowering, number of pods per cluster, number of seeds per pod and 100 seed

weight were highest in case of cluster VIII with 2 genotypes (RGC 1066, RGC 197).The cluster mean values for Days to Maturity was highest in case of cluster II with 1 genotype (HGC 365) and for pod length in case of cluster I with 14 genotypes. While cluster V with 1 genotype (RGC 471) registered highest mean values for Number of branches per plant, Number of cluster per plant, biological yield and Harvest index. Hence, suggesting quite different genetic makeup of the genotypes included in these clusters and important role of these characters in the genetic divergence.

Table-1 *Composition of clusters*

Clusters	Number of genotypes	Composition of cluster
I	14	RGC 1033, RGC 1003, RGC 1038, RGC 1031, RGC 986, RGC 1017, RGC 1002, RGC 1055, RGr-13-2, RGr-12-03, RGC 936, CAZG 302, CAZG 307, HG 2-20
II	1	HGC 365
III	1	RGr-12-5
IV	8	RGr-13-3, RGr-12-1, RGr-13-1, GUAG 9703, HGS 26-05, RGM 114
V	1	RGC 471
VI	1	RGM 115
VII	2	RGr-13-4, RGr-13-5
VIII	2	RGC 1066, RGC 197

Table-2 *Average intra (in bold) and inter cluster D^2 value*

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**8.54**	9.64	9.75	10.84	11.22	10.48	17.52	15.07
II		**0.00**	6.23	6.92	15.39	10.05	17.09	17.03
III			**0.00**	7.09	15.82	11.13	13.02	13.65
IV				**7.18**	16.77	10.64	16.08	17.78
V					**0.00**	10.76	22.43	17.94
VI						**0.00**	19.28	19.78
VII							**6.86**	14.87
VIII								**9.74**

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	44.52	90.50	101.46	5.50	17.75	3.98	6.63	5.64	3.55	39.79	25.62	10.18
II	44.00	93.33	78.53	5.00	16.27	3.73	5.73	5.15	3.62	30.70	22.58	6.87
III	45.67	92.67	93.00	4.03	12.60	4.27	5.73	5.62	3.23	34.52	22.17	7.61
IV	45.02	92.42	97.23	5.28	14.00	3.43	5.77	4.86	3.30	35.88	22.04	7.78
V	45.33	91.00	104.80	8.10	20.63	5.40	7.53	5.77	3.60	40.07	26.34	10.53
VI	44.00	93.00	109.40	8.00	14.53	4.67	5.33	4.50	3.50	30.68	24.95	7.63
VII	44.17	92.67	132.75	2.10	10.95	4.57	6.53	5.44	3.39	34.78	22.83	38.75
VIII	45.67	87.33	109.82	1.08	15.50	5.70	8.03	5.77	3.78	37.41	25.05	9.45

Contribution of individual character towards total divergence was calculated as per method given by [6] and has been presented in [Table-4]. The relative contribution of various characters indicated [Table-4] that the characters like Number of branches per plant (33.79%) had highest contribution towards total divergence which was followed by harvest index (29.66%) and number of cluster per plant (10.80%). While Days to 50 per cent flowering (1.15%), 100 seed weight (0.92%) and biological yield per plant (0.92%)had low value of character contribution towards total divergence.

The characters *viz.,* Number of branches per plant, harvest index and number of cluster per plant was the major contributing characters in total about 74.25 per cent of the total divergence. Thus, these three characters are important and should be considered while selecting genetically diverse genotypes.

Conclusion

The highest inter cluster existence was observed between cluster V and cluster VII followed by VI and VII, cluster II and cluster VII and cluster III and cluster V 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. The cluster mean values for seed yield and plant height were highest in case of cluster VII with 2 genotypes (RGr 13-4, RGr 13-5). Cluster VIII with 2 genotypes (RGC 1066, RGC 197) was also good source of Days to flowering, number of pods per cluster, number of seeds per pod and 100 seed weight. Cluster V with 1 genotype (RGC 471) was the best source of Number of branches per plant, Number of cluster per plant, biological yield and Harvest

index.

Table-4 *Contribution of different characters towards total divergence*

Characters	Number of times appearing in first ranking	Percent contribution
Days to 50% flowering	5	1.15
Days to maturity	12	2.76
Plant height (cm)	23	5.29
Number of branches per plant	147	33.79
Number of clusters per plant	47	10.80
Number of pods per cluster	10	2.30
Number of seeds per pod	21	4.83
Pod length (cm)	14	3.22
100- Seed weight (g)	4	0.92
Biological yield per plant (g)	4	0.92
Harvest index (%)	129	29.66
Seed yield per plant (g)	19	4.37

Author Contributions: All author equally contributed

Conflict of Interest: None declared

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