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GENETIC DIVERSITY STUDIES IN GUAR (*CYMOPSIS TETRAGONOLOBA* L.) GENOTYPES

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ABSTRACT

The field experiment was conducted in College of Agriculture, University of Agriculture and Horticultural Science, Shivamogga, Karnataka. The experiment was composed of 81 guar genotypes collected from Regional research station, Jodhpur, NBPGR, New delhi with 2 replications and recorded observations on ten agromorphological traits. The genetic material exhibited wide range of genetic diversity for all the traits studied and grouped into ten different clusters. The maximum intra cluster distance was observed in cluster IX indicates that genotypes are having diverse genetic architecture. The maximum inter cluster distance was recorded between cluster VII and cluster X, indicating the presence of wide range of variability among the genotypes of the cluster. The percent contribution towards genetic diversity was highest from grain yield per hectare (41.3 %) followed by grain yield per plant (23.52%). On the basis of inter cluster distances and per se performance observed in the present study a hybridization programme involving genotypes for a specific trait may be selected using cluster mean values.

INTRODUCTION

Guar [*Cyamopsis tetragonoloba* (L.) Taub.] [2n=14], is an under exploited versatile and multipurpose legume vegetable of arid and semiarid regions cultivated for feed, fodder and manure. It is commonly known as guar, chavlikayi, guari, khutti etc. Although cluster bean is a minor crop but due to its better and finer guar gum qualities it is considered as an important cash crop for industrial gum production (Hymowitz, and Matlock (1963); Pathak and Singh., 2010). 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. Further in textile and juice industry, guar gum is used for sizing and as a thickener and stabiliser. In paper industry, it is used for improving quality of paper board by enhancing dry and wet strength and for enhancing sizing degree. Guar gum has also greater utility in pollution control and acts as absorbent in waste water treatment in textile industry as a flocculating and exchanging agent [Mahalanobis, 1936].

Despite the importance of this crop, only limited breeding work has been done and very little attention has been given for its genetic improvement in the past, in order to enhance the productivity levels of cluster bean. Information on the nature and magnitude of genetic diversity present in the genotypes is a pre-requisite. Parents to be selected on the basis of combing ability and F1 heterosis for developing high yielding varieties through hybridization. Literature available on the nature and magnitude of genetic diversity in cluster bean crop indicates that the studies in this kind are scanty and not properly documented. Therefore, an attempt in the present investigation was made a major objective to study the degree of genetic diversity in set of 81 genotypes collected from NBPGR, RRS, Jodhpur, Rajasthan, for 10 biometrical traits.

MATERIALS AND METHODS

Genetic evaluation of guar accessions on the basis of agromorphological traits was performed in field of department of genetics and plant breeding, College of Agriculture, Shivamogga. Genotypes were obtained from NBPGR, RRS, Jodhpur, Rajasthan. Experiment was conducted as per Randomized Complete Block Design with plot size of 1.8 m² during August, 2014. 4m length row per genotype with spacing 30 X 10 cm was followed. All agronomical practices were followed as per package of practices.

Ten quantitative traits viz., days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters per plant, seeds per pod, pods per plant, 100-seed weight, seed yield per plant and seed yield per ha, were taken into consideration for estimating genetic diversity. The mean values of five plants were taken for the analysis of genetic divergence following Mahalanobis. The genotypes were grouped into different clusters following Tocher's method as described by Rao, 1953.

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RESULTS AND DISCUSSION

Genetic diversity is the basic requirement for successful breeding programme. Collection and evaluation of germplasm lines and genotypes of any crop is a pre-requisite for any programme and provides a greater scope for exploiting genetic diversity. The multivariate analysis (D^2) is a powerful tool to measure the genetic divergence within a set of genotypes (Murthy, and Arunachalam., 1966).

The genotypes were grouped into 10 clusters indicating large amount of genetic diversity among the genotypes (Table 1).

Cluster VI was the largest (17 genotypes) followed by clusters VII (16 genotypes), cluster I (11 genotypes), IX (10 genotypes), II and IV each had seven genotypes, X cluster had six genotypes and rest of the clusters had three genotypes except

cluster III had only one distinct genotype these results indicates that the architecture of one line is entirely differs from others (Sachin *et al.*, 2014). Grouping of accessions by multivariate method in the present study is of practical value to the breeders. Representative accessions may be chosen from particular cluster for genetic base enhancement (Manivnnan., 2013). In this clustering pattern cluster III had only one diverse genotype *viz.*, IC-420332 was shown better yield than check used in the experiment.

Cluster V (IC-311431, IC-311444, IC-311449) and VIII had three genotypes (IC-311392, IC-415106, IC-415161) This pattern of clustering mostly demarcated the gum yielding genotypes. However majority of the genotypes from different origins are clustered into same cluster, while some other members fell into different cluster these are suggesting that the breeding

Table 1: Grouping of guar genotypes

Group	No. of Genotypes	Genotypes
I	11	IC-42181, IC-421814, IC-311392, IC-311393, IC-311431, IC-311440, IC-370490, IC-373438, IC-402296, IC-402298, IC-415145
II	7	IC-325758, IC-325800, IC-325806, IC-325811, IC-402295, IC-415148, IC-415153
III	1	IC-415146
IV	7	IC-325038, IC-329033, IC-329036, IC-370496, IC-370502, IC-415102, IC-415123
V	3	IC-311403, IC-311432, IC-311438
VI	17	IC-311417, IC-323992, IC-325821, IC-324020, IC-324008, IC-370509, IC-370563, IC-370516, IC-373497, IC-373557, IC-402293, IC-415112, IC-415115, IC-415125, IC-415131, IC-415151, IC-415154
VII	16	IC-421817, IC-311449, IC-325743, IC-325757, IC-325819, IC-325832, IC-329062, IC-373467, IC-373480, IC-402301, IC-402303, IC-415108, IC-415110, IC-415128, IC-415135, IC-415157
VIII	3	IC-421816, IC-370563, IC-415137
IX	10	IC-311444, IC-325846, IC-370478, IC-373427, IC-402299, IC-402302, IC-402304, IC-415109, IC-415140, IC-415138
X	6	IC-324023, IC-329030, IC-369838, IC-415106, IC-415118, IC-415142

Table 2: Average intra (in bold) and inter cluster distances of guar

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	24.25	52.54	47.04	80.53	59.00	47.23	256.71	120.15	220.25	101.92
II		18.30	127.11	187.56	135.98	100.25	454.91	224.22	392.65	67.44
III			0.00	30.46	67.67	46.44	119.80	112.20	109.02	224.10
IV				38.57	70.46	73.83	98.10	102.48	93.76	256.06
V					0.00	81.93	195.66	17.88	135.14	154.50
VI						49.38	225.41	143.55	211.90	160.50
VII							0.00	198.45	49.27	554.90
VIII								0.00	118.35	246.60
IX									38.80	492.93
X										0.00

Table 3: Per cent contribution of quantitative traits towards genetic diversity

Source	Times ranked 1st	% Contribution
DFF	31	0.96
DM	65	2.01
PH	377	11.64
C/P	52	1.6
P/P	199	6.14
G/P	15	0.46
B	349	10.77
100 SW (gm)	10	0.31
GY/P	762	23.52
GY/ha (kg)	1338	41.3

lines are selecting for hybridization in breeding programme (Ravi *et al.*, 2013). Grouping of genotypes based on agromorphological characters is not always associated with their geographical origin. Our results are in accordance with the findings of Brahmi *et al.*, 2004; Pervaiz *et al.*, 2010; Pathak *et al.*, Rai *et al.*, 2012; Sultan *et al.*, 2012; Grish *et al.*, 2012 and Kumar *et al.*, 2013 whose results given conclusion that there is no or less correlation between geographic location and genetic diversity in guar.

Average intra- and inter-cluster distances (D^2 values) among 10 clusters are given in Table 2. The value of intra-cluster distance for cluster III (3 genotypes), V (3 genotypes) and X were had zero as these had very few numbers of genotype in

Table 4: Cluster mean values for 10 biometrical characters in guar.

Clusters	DFF	DM	PH	C/P	P/P	G/P	B	100 SW	GY/P (gm)	GY/ha (kg)
I	35.56	97.80	70.33	12.41	66.70	4.91	3.68	3.42	287.64	2121.42
II	37.67	96.33	46.15	9.70	43.08	4.30	1.55	3.44	135.09	806.46
III	34.50	103.00	70.20	19.80	89.30	5.80	2.90	3.40	457.77	3346.60
IV	38.09	97.91	84.10	15.67	88.69	5.84	4.90	3.41	495.92	3826.36
V	41.00	100.00	92.50	15.30	72.00	5.50	13.80	3.85	367.50	3007.95
VI	35.20	95.20	85.77	17.09	103.77	4.63	4.52	3.08	394.02	2468.87
VII	40.00	100.00	89.70	15.50	114.00	5.70	4.30	3.53	616.50	5771.47
VIII	42.00	102.50	96.30	15.25	72.00	6.00	18.52	3.35	446.50	3506.42
IX	42.67	99.63	80.52	22.47	90.27	6.90	10.67	3.80	611.95	5485.27
X	33.50	94.50	93.00	5.50	16.20	4.80	2.30	3.65	77.82	724.71

DFF: Days to fifty per cent flowering, DM: Days to maturity, PH: Plant height, C/P: Clusters per plant, P/P: Pods per plant, G/P: Grains per pod, B: Branches, 100SW: 100 Seed weight, GY/P: Grain yield per plant, GY/ha: Grain yield per hectare

their cluster. While considering the other clusters, the intra-cluster distance varied from 18.30 to 49.38 and did not transgress the limits of any of the inter-cluster distances. Cluster II had lowest intra-cluster distance of 18.30 and cluster VI accounted for highest intra-cluster distance of 49.38.

The highest inter cluster distance was found between cluster VII and cluster X (554.90) followed by cluster IX and X (492.93), cluster II and VII (454.91) and cluster II and IX (392.65). The inter cluster distance of all other clusters with cluster X showed higher values when compared to the inter cluster distances between other clusters. The least inter cluster distance was found between cluster V and VII (17.88).

The maximum distances between clusters are the right choice of diverse parents for hybridization programme (Girish and Gasti., 2012; Singh, Chaudhary *et al.*, 2005) The contribution of various traits to the genetic diversity worked out from their rank, maximum contribution (41.3%) was from Grain yield per hectare followed by seed yield per plant (23.52 %) and least contribution of 0.96 % from days to fifty percent flowering (Table 3). The mean value for all the characters are presented vide Table 4. Cluster VII had highest mean value for grain yield per hectare (5771.47 kg) and lowest value was from (724.71 kg) cluster X. The highest mean value for grain yield per plant was recorded by cluster VII (616.50 gm) and the lowest was recorded by cluster X (77.82). The highest mean value was recorded for the character of clusters per plant from cluster IX (22.47) and the lowest value of 5.50 recorded from cluster X. Maximum number of pods per plant was observed from cluster VII (114.00) and minimum of 16.20 from cluster X. Cluster IX had maximum number of seeds per pod (6.90), while cluster II recorded minimum number of seed (4.30). Maximum days to attain fifty percent flowering was recorded from cluster IX (42.67 days) and lowest from cluster X and III each with the value of 33.50 and 34.50 days. Cluster III took maximum days for maturity (103.00 days) and cluster X was recorded with minimum days (94.50 days). Maximum 100 seed weight of 3.85g and 3.80 were recorded in the cluster of V and cluster IX. Cluster VI was recorded minimum of 3.08g. Cluster IX had maximum cluster mean values for number of characters *viz.*, number of clusters per plant, number of grains per pod and seed yield per plant showing its superiority over other clusters. Greater manifestation of heterosis is expected in cross combinations involving the parents from the most divergent clusters. Similar results were obtained by Pathak *et al.*, 2009; Girish *et al.*, 2012 and Rai *et al.*, 2012.

Cluster bean which is a self-pollinated crop though there is a potential for obtaining hybrid vigor by implementing hybridization programme between the genotypes of distinct group to obtain superior genotypes from the segregating generation.

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