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Genetic diversity of guar germplasm (*Cyamopsis tetragonoloba* (L.) Taub) by different methods

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Abstract

Analysis of Variation through Augmented design revealed significant mean sum of squares for days to 50% flowering and seed yield per plant. The mean square due to checks vs varieties was significant for no. of primary branches, no. of clusters per plant, no. of seeds per pod and seed yield per plant indicating that the test entries were significantly different from checks for these characters. Genetic Divergence in 97 genotypes of guar germplasm was studied using Mahalanobis D^2 statistic and Principal component Analysis. On the basis of D^2 statistic eight clusters were obtained and cluster IV and VII are the most divergent. Principal component analysis (PCA) identified 5 Principal Components (PC's) with eigen value more than one which contributed 78.84 per cent of cumulative variance. The Genotypes IC 116685 (29), IC 116712 (36) and IC 384766 (65) were more divergent from the both the methods D^2 statistic and Principal component Analysis and could be used as donors in hybridization programme for obtaining wide spectrum of variation.

Keywords: Augmented design, genetic diversity, cluster distance and principal component analysis

Introduction

Guar (*Cyamopsis tetragonoloba* L.) is mainly grown in arid and semi arid regions of India. The qualities of the crop like high adaptation towards erratic rainfall, multiple industrial uses and its importance in soil enrichment, low input requirement etc. have made the guar one of the most significant crops for farmers in arid and drought conditions in India (Geeta Vishnoi *et al.* 2017) [3]. Ananthapuramu is one of the drought-prone district in the rain shadow area of Andhra Pradesh. The annual average rainfall of the district is 546 mm. Most of the northern parts of the district receive rainfall in the range of 500 to 575 mm whereas the most of the southern parts receive in the range of 575 to 650mm. The normal rainfall for the SWM period is 338 mm which is 61.2% of the total rainfall for the year. The rainfall for NEM period is 156 mm, which is 28.3% of annual rainfall (October to December). The remaining months (March, April, May) are warm and dry, when the normal daily max. temperature ranges between 29^0C and 42 ^{0}C. The months of November, December and January are cool when the min. temperature is around 17.2 ^{0}C.

As guar is mainly grown in arid and drought conditions, there is a need to improve for its yield and various other traits suit to specific agro-ecological conditions. Therefore, the evaluation of germplasm will provide information to know extent of variability in this crop. It has been well known that genetically diverse parents are likely to yield desirable gene recombinants to produce high heterotic effect. Hence the present investigation was undertaken to assess the nature and the magnitude of genetic diversity in guar genotypes through different methods *i.e* D^2 statistic and Principal component analysis (PCA).

Material and Methods

The present investigation was carried out with 95 genotypes of guar germplasm from NBPGR, New Delhi grown in augmented design (Federer, 1956) [1] with two checks during *kharif* 2016 at Agricultural Research Station, Ananthapuramu (ANGRAU), A.P, India. Each genotype was sown in a single row of 4m length with a spacing of 30 x 10 cm. Ten uniform size plants per genotype were selected and tagged for recording the observations *viz.* days to 50% flowering, days to maturity, Plant height, no. of primary branches per plant, no. of pods per cluster, no. of clusters per plant, pod length, no. of pods per plant, no. of seeds per pod, 100 seed weight and seed yield per plant.

The Augmented design presumes checks as fixed effects whereas the new entries as random effect. It is highly useful in early testing of huge number of test entries/ accessions when the replication is not practically possible or amount of seed is very limited as well as in case of unequal plot size. It saves time and money without compromising on the precision of critical comparisons among treatments. The present study was undertaken to analyse the pattern of variation for yield and its component traits in a core set of germplasm accessions representing diverse growth habits as well as pod and seed characters. The data was analysed using D^2 statistics (Mahalanobis, 1928) [6] and Principal component Analysis (Jackson, 1991) [4].

Results and Discussion

Augmented block design is used for evaluation of large set of germplasm suitable for different aspects of crop breeding. The ANOVA (Table 1) revealed significant mean sum of squares for days to 50% flowering and seed yield per plant. The block effects were significant for days to 50% flowering, days to maturity, plant height, no.of primary branches, no.of seeds per pod, seed weight and seed yield per plant. Similarly the mean square due to checks vs varieties was significant for no.of primary branches, no.of clusters per plant, no. of seeds per pod and seed yield per plant indicating that the test entries were significantly different from checks for these characters. The results were in accordance with findings of Iram Saba *et al*, 2017 [3].

On the basis of D^2 analysis the 97 genotypes were grouped into 8 clusters (Table 2 and Fig 1). Cluster III was largest with 42 genotypes followed by cluster I (27), cluster II (14), cluster V (5), cluster IV (4), cluster VI (3), cluster VII (1) and cluster VIII (1). Mean intra cluster and inter cluster D^2 values are presented in table 3. The intra cluster D^2 values ranged from 0 to 256.8. Maximum intra cluster distance was found in cluster VI (256.8) and it was lowest in cluster VIII and VII. The lowest inter-cluster value was observed between Cluster VII and cluster VIII (215.25) and highest inter cluster value was observed between cluster IV and cluster VII (2288.5). Among the eight clusters cluster IV and VII were the most divergent to other clusters and could be used as donors in hybridization programme for obtaining wide spectrum of variation. Kuma Pawan *et al* 2017 [5], Shabarish Rai and Dharmatti 2013 [7], Vikas Kumar *et al.* 2014 [8], Geeta Vishnoi *et al.* 2017 [3] reported similar results.

Cluster IV had highest mean value for maximum of six characters *viz.* no. of pods per cluster, no. of clusters per pod, pod length, no. of pods/ plant, no. of seeds per pod and seed yield per plant (Table 4).

Principal component analysis (PCA) identified 5 Principal Components (PC's) (Table 5) with eigen value more than one which contributed 78.84 per cent of cumulative variance. The first Principal Component (PC $_1$) contributed maximum towards variability (27.71) with significant loading of all traits except for no.of primary branches and 100 seed weight (Table 6). The second Principal Component (PC $_2$) described 18.19 per cent of the total variance and reflected highest loading for no.of primary branches (0.41) where as the fourth (PC$_4$) showed highest loading for 100 seed weight (0.49).

The three PCA scores were plotted in graph to get the 3D (Fig 2) scattered diagram. This 3D plot clearly indicated clustering of genotypes IC 116712 (36), IC 116685 (29), IC 384849 (88), IC 384784 (71) towards positive side of PC1 axis. The genotypes IC 11384811 (76), IC 384803 (74), IC 384804 (75), IC113618 (12) were placed towards positive portion of PC$_2$ axis. Genotypes belonging to common cluster have fallen nearer to each other and vice versa. Genotypes IC 116685 (29) and IC 116712 (36) were fallen far apart from IC 384766 (65) which reflect the more diversity and the same results were obtained by both the diversity methods. D^2 analysis also showed IV (1C 116692 (31), 1C 116708 (35), 1C 116685 (29), 1C 116712 (36)) and VII 1C 384766 (65) as more divergent groups. These genotypes are better for obtaining desirable segregants.

Table 1: Analysis of variance of Augmented block design for 11 quantitative traits in guar (*Cyamopsis tetragonoloba* (L.) Taub.)

Augmented R.B.D. ANOVA												
	DF	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of primary branches**	**No of pods/ cluster**	**No. of clusters/ plant**	**Pod length (cm)**	**No. of pods/ plant**	**no of seeds/ pod**	**100 seed weight (g)**	**Seed yield / Plant (g)**
Block (ignoring Treatments)	3	29.81 **	84.21*	216.98*	7.89 *	2.12	0.25	2.48	101.72	8.46 *	1.37**	16.45 **
Treatment (eliminating Blocks)	96	6.01 *	13.62	89.37	3.56	1.45	1.79	0.30	44.30	1.05	0.1	2.80 *
Checks	1	2.00	28.13	55.13	0.5	0.13	1.13	0.13	28.13	2.00	0.01	0.32
Checks+Var vs. Var.	95	6.05 *	13.46	89.73	3.60	1.47	1.80	0.30	44.47	1.04	0.10	2.82 *
ERROR	3	0.67	4.46	19.13	0.83	0.46	0.79	0.34	22.13	0.33	0.03	0.27
Block (eliminating Check+Var.)	3	6.67 *	2.12	5.80	0.17	0.80	1.13	0.27	2.13	0.33	0.01	0.05
Entries (ignoring Blocks)	96	6.73 *	16.18	95.97	3.80	1.50	1.76	0.37	47.41	1.30	0.14	3.31 *
Checks	1	2.00	28.13	55.13	0.5	0.13	1.13	0.13	28.13	2.00	0.01	0.32
Varieties	94	6.85 *	16.17	97.30	3.7	1.52	1.43	0.37	47.54	1.26	0.14	3.10 *
Checks vs. Varieties	1	0.66	4.99	11.46	8.89 *	0.31	33.73**	0.96	53.95	4.97 *	0.27	26.31 **
ERROR	3	0.67	4.46	19.13	0.83	0.46	0.79	0.34	22.13	0.33	0.03	0.27

Table 2: Distribution of 97 guar (*Cyamopsis tetragonoloba* (L.) Taub.) genotypes in different clusters by Tocher's method.

Cluster	**No. of Genotypes**	**Genotypes (S.no.)**
I	27	1C 116694 (32), 1C 329038 (58), 1C 113640 (18), 1C 127882 (52), 1C 384760 (61), 1C 113616 (11), 1C 113624 (13), 1C 127795 (43), 1C 103200 (4), 1C 113659 (21), 1C 113614 (10), 1C 113666 (22), 1C 116667 (24), 1C 384844 (85), 1C 127831 (50), 1C 41352 (3), 1C 127810 (47), 1C 127790 (41), 1C 127799 (45), 1C 113634 (16), 1C 127884 (53), 1C 116677 (25), 1C 127798 (44), 1C 127792 (42), 1C 116706 (34), 1C 127886 (54).
II	14	1C 127786 (40), 1C 384759 (60), 1C 384758 (59), IC 1038 (1), 1C 127775 (39), 1C 113630 (14), 1C 384774 (69), 1C 12776 (38), 1C 113657 (20), 1C 113633 (15), 1C 384873 (93), 1C 249696 (55), 1C 41346 (2), 1C 116680 (27).
III	42	1C 127803 (46), 1C 384855 (89), 1C 384876 (95), 1C 113649 (19), 1C 127860 (51), 1C 384770 (66), 1C 116686 (30), 1C 127741 (37), 1C 384875 (94), 1C 384773 (68), 1C 113635 (17), 1C 384835 (81), 1C 384863 (90), 1C 384772 (67), 1C 384765 (64), 1C 384825 (80), 1C 384845 (86), 1C 384762 (62), 1C 127828 (49), 1C 384813 (77), 1C 384764 (63),

		1C 384800 (73), 1C 384839 (83), 1C 384786 (72), 1C 384875 (94), 1C 384837 (82), 1C 384847 (87), 1C 113607 (9), 1C 384821 (79), 1C 384778 (70), 1C 113601 (8), 1C 113588 (5), 1C 384871 (92), 1C 116656 (23), 1C 116682 (28), 1C 113595 (7), 1C 116703 (33), 1C 113590 (6), 1C 384784 (71), 1C 384840 (84), 1C 116679 (26), 1C 384869 (91),
IV	4	1C 116692 (31), 1C 116708 (35), 1C 116685 (29), 1C 116712 (36)
V	5	1C 384803 (74), 1C 113618 (12), 1C 384811 (76), 1C 384804 (75), 1C 127826 (48)
VI	3	1C 384819 (78), 1C 384849 (88), 1C 329030 (57)
VII	1	1C 384766 (65)
VIII	1	1C 249697 (56)

Table 3: Intra (bold) and inter-cluster average divergence (D^2) values of 8 clusters from 97 genotypes

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**	**Cluster 8**
Cluster 1	103.22	244.75	313.90	939.05	258.70	637.20	542.50	300.10
Cluster 2		135.79	546.90	1308.50	370.00	1187.00	255.80	313.00
Cluster 3			141.00	383.80	354.80	352.60	1200.00	935.70
Cluster 4				70.80	1052.00	431.10	2289.00	2012.00
Cluster 5					242.90	704.6	784.30	526.30
Cluster 6						256.80	2035.00	1399.00
Cluster 7							0	215.30
Cluster 8								0

Table 4: Mean values of clusters based on D^2 analysis from 97 accessions of guar (*Cyamopsis tetragonoloba* (L.) Taub.).

	Days to 50% flowering	**Days to maturity**	**Plant Height**	**No.of primary branches/pl.**	**No. of pods/cluster**	**No. of clusters/plant**	**Pod length (cm)**	**no. of pods per plant**	**no. of seeds per pod**	**100 seed weight (g)**	**seed yield/plant (g)**
Cluster 1	27.06	72.09	54.19	2.74	5.19	5.41	4.87	21.70	7.59	3.36	4.17
Cluster 2	26.86	72.29	43.79	3.29	5.43	6.29	5.02	26.43	7.50	3.51	4.70
Cluster 3	29.48	76.19	62.95	2.90	5.98	6.02	5.33	31.38	8.00	3.30	5.06
Cluster 4	26.75	72.75	74.50	0.25	6.75	6.50	6.10	42.25	9.25	3.33	7.83
Cluster 5	32.20	81.00	53.40	2.60	5.00	5.00	5.42	23.60	7.00	3.38	3.22
Cluster 6	29.33	76.67	75.33	0.00	5.00	4.67	5.43	26.00	8.00	3.13	2.97
Cluster 7	23.00	68.00	33.00	3.00	3.00	6.00	4.80	21.00	9.00	2.55	2.60
Cluster 8	25.00	70.00	43.00	0.00	4.00	4.00	5.80	12.00	6.00	3.30	1.30

Table 5: The Eigen values, Percent variability and Cumulative per cent variability for 5 Principal components

	PC1	**PC2**	**PC3**	**PC4**	**PC5**
Eigene Value (Root)	3.05	2.00	1.49	1.19	0.94
% Var. Exp.	27.71	18.19	13.59	10.83	8.52
Cum. Var. Exp.	27.71	45.90	59.49	70.32	78.84

Table 6: Character loading of 5 Principal components of 97 genotypes of guar (*Cyamopsis tetragonoloba* (L.) Taub.)

		PC 1	**PC 2**	**PC 3**	**PC 4**	**PC 5**
1	Days to 50% flowering	0.35	0.38	0.39	0.14	0.23
2	Days to maturity	0.35	0.40	0.40	0.12	0.14
3	Plant height (cm)	0.38	-0.15	0.19	-0.02	-0.28
4	No.of primary branches	0.09	0.41	-0.45	-0.14	0.36
5	no of pods/cluster	0.34	-0.09	-0.23	0.28	-0.39
6	No.of clusters/plant	0.28	0.20	-0.50	0.24	-0.02
7	Pod length (cm)	0.27	-0.30	0.25	-0.30	-0.08
8	No.of pods/plant	0.40	-0.27	-0.18	0.19	-0.05
9	no of seeds/pod	0.25	-0.17	-0.10	-0.66	0.30
10	100 seed weight (g)	-0.20	-0.32	0.16	0.49	0.43
11	Seed yield /plant (g)	0.26	-0.40	-0.10	0.15	0.53

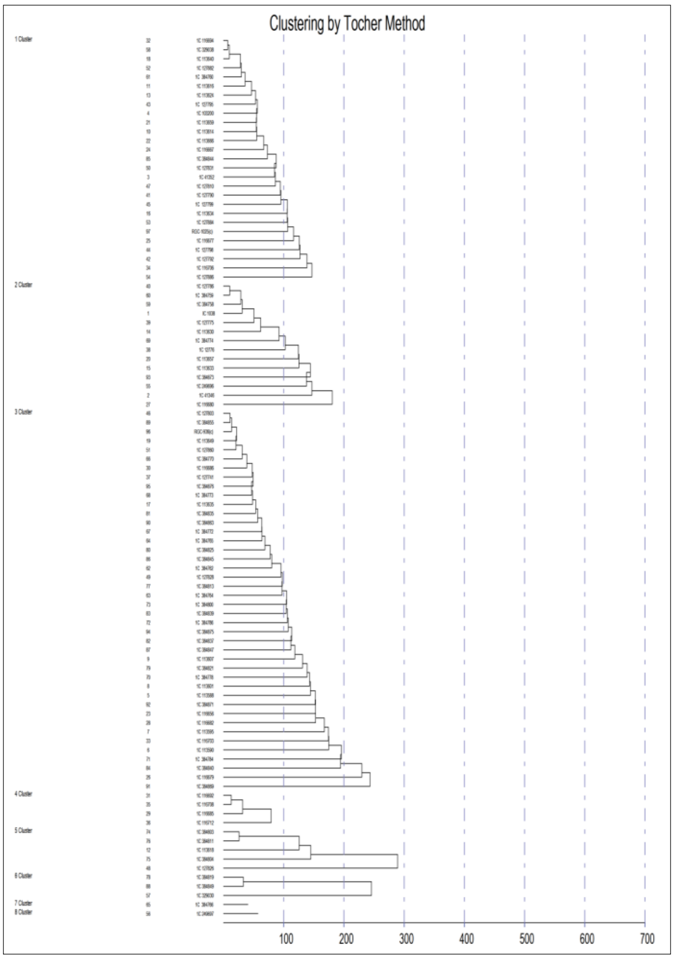

Fig 1: Diagram illustrating the clustering pattern by Tocher's method in guar (*Cyamopsis tetragonoloba* (L.) Taub.)

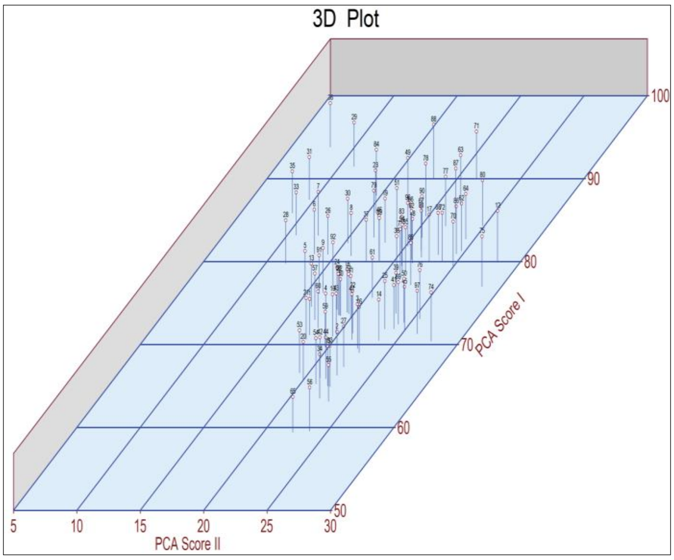

Fig 2: Three Dimensional graph showing relative position of genotypes (serial no.) of guar (*Cyamopsis tetragonoloba* (L.) Taub.) based on PCA scores.

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