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GENETIC DIVERGENCE IN UPLAND COTTON (*Gossypium hirsutum* L.)

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ABSTRACT

Genetic diversity in a population of forty genotypes of cotton (*Gossypium hirsutum* L.) assessed using Mahalanobis D^2 statistic, indicated considerable diversity in the material studied. Five characters were studied and utilized for multivariate analysis. The genotypes were grouped into six clusters. Boll weight, number of bolls per plant and 2.5% span length contributed maximum towards genetic divergence. The genotype 153 E and the genotypes in cluster III could be utilized in the breeding programme for the improvement of boll weight, ginning outturn and yield in cotton.

Cotton(*Gossypium hirsutum* L.) has been under cultivation as an important source of fibre. In formulating a breeding programme for the improvement of any crop, the first problem that often concerns a breeder is the presence or absence of variation present in the germplasm. Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for heterosis breeding programmes. Therefore, the present investigation was taken up to estimate the nature and magnitude of genetic diversity in 40 genotypes of cotton.

MATERIALS AND METHODS

Forty genotypes of cotton (*Gossypium hirsutum* L.) were raised in a randomised block design with three replications during February, 1989 at Cotton Research Station, Srivilliputhur, Tamil Nadu. Each plot consisted of 2 rows of 6m length with 60 x 30cm spacing. Data were recorded on ten plants chosen at random in each genotype for five economic traits namely, number of bolls per plant, boll weight, ginning outturn, 2.5% span length, and seed cotton yield per plant. The mean of ten plants per replication was used for the statistical analysis. The analysis of genetic divergence using Mahalanobis D^2 statistic was carried out as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the 40 genotypes for all the characters studied, indicating the existence of considerable amount of diversity among the genotypes. Hence, further analysis was done to estimate D^2 values and on the basis of relative magnitude of D^2 values. all the 40 genotypes were grouped into six clusters (Table 1). The maximum number of genotypes (20) were included in Cluster I. The clusters II, III and IV had five, nine and four respectively.

The remaining clusters V and VI had only one genotype each. The pattern of distribution of genotypes into different culsters was at random. This tendency of genotypes occurring in clusters cutting across geographical boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity (Nagarajan and Prasad, 1980). Acclimatization of genotypes of different geographical backgrounds under single environment through their domestication by human efforts would have also resulted in helping diversification. Due to the application of selection pressure, lot of variability would have been created in the genotypes under a single environment. Therefore, genotypes originating at the same place might have developed to form different architecture. Likewise, genotypes at different places may possess similar characteristics. Thus, genetic diversity was the outcome of several factors along with a factor of geographical diversity. Therefore, the selection of varieties for hybridization should be based on genetic diversity rather than geographical diversity.

The group constellations also indicated clustering of genotypes from different eco-geographic locations into one cluster. This was attributed to the free exchange of breeding materials from one place to another (Verma and Mehta, 1976). In contrast, many genotypes originated in one place were scattered in various clusters. This kind of genetic diversity among the genotypes from the same geographic origin would be possible due to the factors like heterogeneity, genetic architecture of the populations, past history

Table 1. Composition of clusters and their origin

Cluster	No. of genotypes	Genotypes	Origin
I	20	Deltapine	U.S.A
		Sachz-M 58	Pakistan
		Coker 201	U.S.A.
		Krishna (F)	India
		Atlas 59-7-302	U.S.A.
		MCU.7	India
		Alabar (57) 12	Pakistan
		Uganda 8-9	Uganda
		Mex Acala	U.S.A.
		JR 48	India
		JR 52	India
		CB 2489	Pakistan
		Acala 2-6-1	U.S.A.
		1 3 7 F	U.S.S.R.
		Dixiking 1 I	U.S.A.
		Sindis Wild	Pakistan
		Express Sind (W)	Pakistan
		Stardel	U.S.A.
		Miller 45-9	Australia
		Fergusson	U.S.A.
II	5	Krishna (N)	India
		Glandless Acala	U.S.A.
		NP 52 NC 63	Uganda
		Half and Half 8-2	U.S.A.
		Saudi Arabia	Saudi Arabia
III	9	Alagodenlas brenas	Argentina
		MCU 9	India
		EL 405	India
		DS 28	India
		MCU 5	India
		Pied Mont Cleveland	U.S.A.
		MCU 8	India
		PK 688	India
		Rex Smooth leaf	U.S.A.
IV	4	Coker 413	U.S.A.
		108F	U.S.S.R.
		43/3W	India
		Rowden 2083	U.S.A.
V	1	153 E	U.S.S.R.
VI	1	McNamara wine sap	U.S.A.

of selection, developmental traits and degree of general combining ability.

The average intra and inter cluster D values are presented in Table 2. The highest inter cluster divergence was observed between genotypes of culster III and VI (23.31), while the closest

Table 2. The intra and inter cluster distances among six clusters.

Cluster	I	II	III	IV	V	VI
I	9.16	8.77	11.75	10.80	12.55	17.22
II		7.92	11.72	10.42	10.90	18.89
III			10.59	13.55	15.59	23.31
IV				13.58	11.56	19.65
V					0.00	5.69
VI						0.00

Table 3. Cluster means for different characters.

Cluster	No. of bolls per plant	Boll weight (g)	Ginning outturn (%)	2.5% span length (mm)	Kapas yield per plant (g)
I	10.41	4.27	34.35	26.76	40.28
II	11.30	4.38	35.58	26.14	44.88
III	12.72	4.39	35.41	29.96	50.62
IV	9.55	4.45	35.33	26.55	34.63
V	8.70	5.10	38.20	25.30	27.80
VI	7.90	3.00	25.40	22.10	17.00

proximity was noticed between genotypes of culsters V and VI (5.69). The intra cluster divergence varied from 0.00 to 13.58, the maximum being in cluster IV which comprised four genotypes of diverse origin. The clustering pattern indicated that the genotypes 153 E and McNamara wine sap were genetically distant among themselves and from the rest of the genotypes and formed most divergent single genotypic clusters namely V and VI. The characteristic features of the genotype 153 E contributing towards diversity were more boll weight and higher ginning outturn (Table 3). McNamara wine sap had lower values for all the economic characters studied.

Table 4. Contribution of different characters to diversity.

Character	Number of first ranks	Percentage of contribution
Number of bolls/plant	284	34.63
Boll weight	339	41.34
Ginning cutturn	50	6.10
2.5% span length	101	12.32
Seed cotton yield	46	5.61

The result of the contribution of various characters towards the expression of genetic divergence (Table 4) indicated that boll weight (41.34%) followed by number of bolls per plant (34.64%) and 2.5 span length (12.32%) contributed more to the total genetic divergence in the 40 genotypes of cotton. From the present study, it was clear that these are the three basic attributes of plant architecture which need greater attention.

The higher inter cluster distances were recorded between III and VI (23.31), IV and VI (19.65), II and VI (18.89) and I and VI (17.22). This indicated that the clusters I, II, III and IV had higher inter cluster distances with cluster VI. But the most diverse genotype of cluster VI (McNamara wine sap) had lower mean values for all the economic characters studied. Hence, all these inter cluster distances from 17.22 to 23.31 need not be considered. The next higher inter cluster distance was recorded between clusters III and V(15.59). Thus, hybridization of the genotypes between these clusters would result in maximum hybrid vigour and throw useful recombinants.

The genetically diverse genotype of cluster V (153 E) could be utilized for the improvement of ginning outturn which recorded a maxium of 38.2 per cent and boll weight which recorded a maxium of 5.10 g. The genotypes included in cluster III had maximum number of bolls per plant (12.72) and seed cotton yield (50.62g). Thus, it could be possible to generate a gene pool possessing immense variability by appropriate intercrossing.

REFERENCES

NAGARAJAN, K. and PRASAD, M.N. 1980. Studies on genetic diversity in fox tail millet (*Setaria italica* B.). **Madras Agric. J., 67**: 28-38

RAO, C.R. 1952. **Advanced Statistical Methods in Biometrical Research.** John Wiley and Sons, New York.

VERMA, V.S. and MEHTA, R.K. 1976. Genetic divergence in lucerne. **J. Maharastra Agric. Univ., 1**: 23-28.

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EFFECT OF FERTILIZER APPLICATION ON GROUNDNUT

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ABSTRACT

In order to study the effect of fertilizer nutrients on groundnut (*Arachis hypogaea L.*), field trials were conducted during *kharif* with five, treatments i.e. control, 50, 75, 100 and 150 per cent of recommended doses of fertilizers in randomised block design. Application of 20:80:20 NP_2O_5, K_2O kg/ha (100 % of recomended dose) resulted in 21, 10, 23 and 98 per cent increase in pod yield over 150,75, 50% of recommended dose and control respectively. The haulm, oil yield kg/ha, shelling per cent, 100 kernel weight (g) and SMK % were also higher with this dose. In higher dose of NPK (150% of recommendation) a decline in pod, haulm, oil yield and in all studied characters was observed.

From 1930-31 to 1980-81 the area under groundnut in India has increased by 134% (from 2.9 to 7.6 million hactare) which resulted in increase in the production by 72 per cent (from 2.9 million tonnes to 5.0 million tonnes). The productivity during this period has, however declined by 27 per cent i.e. from 1003 kg/ha to 736 kg/ha The present productivity of 953 kg/ha is less than the world average (978 kg/ha). The scope for further increase in area is limited, the only alternative left for meeting the domestic demand is by increasing productivity. Therefore, it is very essential to find out the suitable dose of fertilizers for maximitation the yield of *kharif* groundnut.

MATERIALS AND METHODS

A field trial was conducted at Zonal Agricultural Research Station, Khargone, (M.P.) during *kharif* seasons of 1988, 1989 and 1990. The soil was medium black in texture having available N, P_2O_5, and K_2O content of 143, 25.32 and 62 kg/ha respectively. The soil pH was 8.0. The five treatments (Table 1 and 2) were replicated four times in a randomised block design. Test variety was Jyoti. The net plot size and spacing were 2.4 x 4.8 m. and 30 x 30 cm. respectively. Nitrogen, phosphorus and potash were applied in the form of Urea, SSP and MOP below the seed row. The