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MULTIVARIATE ANALYSIS IN SUGARCANE

P. S. VERMA

U. P. Council of Sugarcane Research
Shahjahanpur 242001

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ABSTRACT

The genetic divergence in sugarcane populations comprising 11 morphologically different varieties (eight lines and three testers) and their 24 F_1 hybrids has been assessed through Mahalanobis D^2 analysis. The analysis revealed considerable genetic diversity among parents and their effects on the hybrids. The genotypes under study fell into 14 clusters. The clustering pattern indicated no relationship among the parents or their hybrids, and most parents and hybrids are grouped in separate clusters due to more diverse parents and high heterotic effects. Hybrids without substantial heterosis between parents from different cluster may resemble in their genealogy. Thus, the study indicated that selection of parents should be based on genetic divergence along with knowledge of their genealogy for hybridization.

Key words: Multivariate analysis, heterosis, sugarcane.

Joshi and Dhawan [1] and Anand and Murty [2] have emphasized the importance of genetic diversity for parents in hybridization programmes. In sugarcane, genetic divergence has been studied [3, 4], but the effects of the desired parents on their F_1 hybrids have not been analysed. Therefore, the relationship between genetic diversity of parents and yield potential of their hybrids in sugarcane have been investigated.

MATERIALS AND METHODS

Eight sugarcane genotypes were crossed with three male parents to produce 24 F_1 hybrid populations. Thus, the population comprising eight female and three male lines, and 24 F_1 hybrids was grown in randomised block design with four replications at the U.P. Council of Sugarcane Research, Shahjahanpur, in 1979. Each entry was represented by three rows of 6.0 m length, with 90 × 60 cm spacing. Observations were recorded on 20 random seedlings in each plot for millable canes/clump, internodes/cane, stalk weight, stalk girth, kg-brix, sucrose content in juice purity coefficient, invert sugar, c.c.s. in cane, and fibre content.

The data were subjected to analysis of variance as well as multivariate analysis as suggested by Mahalanobis [5], and the entire population was divided on the basis of minimum generalised distances using the Tocher's method (cf. [6]).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences for all characters except purity coefficient (Table 1).

Table 1. ANOVA for parents and hybrids in sugarcane

Source	d.f.	Millable canes/ clump	Inter-nodes/ cane	Stalk weight	Stalk girth	Kg-brix	Sucrose % in juice	Purity coeffi-cient	Invert sugar	C.C.S. in cane	Fibre content
Replications	3	4.22	27.4	0.021	0.043	0.290	0.32	3.3	0.080	0.001	4.80
Parents	10	14.09**	228.0**	0.320**	0.353**	0.970**	6.02**	25.9**	0.811**	0.005**	5.69**
Females	7	10.44**	268.7**	0.388**	0.455**	0.832**	4.16**	20.3**	0.116*	0.006**	7.84**
Males	2	33.31**	151.4**	0.217**	0.127**	1.938**	7.97**	16.9**	0.454**	0.002*	0.42
Females vs males	1	1.18	96.7**	0.039	0.096	0.001	15.19**	82.6**	0.086	0.001**	1.14
Hybrids	23	6.51**	32.1**	0.113**	0.104**	0.345**	5.20**	10.3**	0.094*	0.002**	3.93*
Parents vs hybrids	1	310.31**	2067.7**	2.974**	0.170**	18.686**	15.24**	1.9	2.106**	0.023**	34.79**
Error	102	2.03	8.9	0.030	0.028	0.109	1.25	3.7	0.051	0.001	1.76

*,**Significant at 5% and 1% levels, respectively.

The entire population including parents and F_1 progenies has been grouped into 14 clusters (Table 2). The maximum number of 16 genotypes are grouped in cluster I (Table 3) this cluster also includes two parents, Co 1148 and BO 70, from Coimbatore and Bihar respectively. The next largest cluster II comprises four genotypes, three of which were F_1 progenies and one parent (Co 7314). Clusters III, IV, and V have two hybrid progenies each. The remaining nine clusters (VI, VII, VIII, IX, X, XI, XII, XIII and XIV) comprised only one genotype each. Most parents are included in these clusters, except cluster VII, which has a hybrid progeny. Thus, more than half of the hybrid populations were included in clusters I and II. The clustering pattern indicated no relationship of parents with their hybrids. Clusters I–V and VII include hybrids of all the parents, but none of the parents, except Co 1148, BO 70 (cluster I), and Co 7314 (cluster II). Clusters III, IV, V and VII had only hybrids and no parent. Usually the parents and their hybrids are included in the same cluster or in clusters having minimum distance between them because of the close affinity between them. However, in the present study, the parents and hybrids are mostly grouped in different clusters. This may be due to more diverse parents and high heterotic effects. Chaudhary and Singh [6] also found similar distribution of parents and their hybrids in different groups.

Genetic diversity is generally associated with geographic diversity [1, 7], but the former is not necessarily directly related with geographic distribution [3, 8, 9]. The present findings also support this conclusion. Moreover, few parents of different origin fell in the same cluster, while the parents from same place were placed in different clusters. Keeping this in view, selection of parents for hybridization should

Table 2. Intra- and intercluster D and D^2 (in parentheses) values

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**13.8** **(3.7)**	20.6 (4.5)	28.2 (5.3)	22.4 (4.7)	19.7 (4.4)	26.4 (5.1)	18.5 (4.3)	49.0 (7.0)	55.3 (7.4)	81.8 (9.1)	66.8 (8.2)	146.6 (12.0)	87.4 (9.4)	105.6 (10.3)
II		**19.0** **(4.4)**	34.4 (5.9)	35.3 (5.9)	20.3 (4.5)	22.3 (4.7)	32.1 (5.7)	38.4 (6.2)	48.9 (7.0)	69.7 (8.4)	68.1 (8.3)	133.7 (11.6)	82.4 (9.1)	85.0 (9.2)
III			**19.0** **(4.4)**	40.2 (6.4)	34.0 (5.8)	22.6 (4.8)	24.3 (4.9)	71.8 (8.5)	77.7 (8.8)	99.4 (10.0)	91.5 (9.6)	183.1 (13.5)	93.4 (9.7)	121.2 (11.1)
IV				**18.5** **(4.3)**	53.1 (7.3)	52.2 (7.2)	23.9 (4.9)	82.8 (9.1)	77.3 (8.8)	126.7 (11.3)	101.7 (10.1)	209.1 (14.5)	124.1 (11.1)	156.2 (12.5)
V					**16.6** **(4.1)**	23.7 (4.9)	32.8 (5.7)	55.9 (7.5)	56.3 (7.5)	84.3 (9.2)	69.2 (8.3)	148.1 (12.2)	102.9 (10.4)	98.2 (9.9)
VI						**0.0** **(0.0)**	23.0 (4.8)	44.4 (6.7)	57.4 (7.6)	51.0 (7.1)	53.6 (7.3)	112.9 (10.6)	91.4 (9.6)	71.9 (8.5)
VII							**0.0** **(0.0)**	70.7 (8.4)	79.2 (8.9)	91.8 (9.6)	75.5 (8.7)	146.1 (12.1)	116.8 (10.8)	115.4 (10.7)
VIII								**0.0** **(0.0)**	61.9 (7.9)	88.3 (9.4)	53.0 (7.3)	143.8 (12.0)	87.9 (9.4)	114.3 (10.7)
IX									**0.0** **(0.0)**	52.4 (7.2)	59.4 (7.7)	99.4 (10.0)	117.6 (10.8)	64.7 (8.0)
X										**0.0** **(0.0)**	35.1 (5.9)	52.8 (7.3)	94.1 (9.6)	30.8 (5.6)
XI											**0.0** **(0.0)**	59.3 (7.7)	99.1 (10.0)	41.1 (6.4)
XII												**0.0** **(0.0)**	184.6 (13.6)	40.3 (6.4)
XIII													**0.0** **(0.0)**	101.8 (10.1)
XIV														**0.0** **(0.0)**

Note. Intracluster values are in bold numbers.

not be based on geographic diversity alone. Genetic diversity must be given greater importance in the selection of parents. The D^2 value ranged from 0 to 209.1. The intracluster D^2 value is maximum in clusters II and III, and minimum (0) in clusters VI, VII, VIII, IX, X, XI, XII, XIII and XIV, as they had only one genotype each. The lowest intercluster distance (4.3) between clusters I and VII suggests close relationship between them. Many clusters showed close relationship due to similar intercluster distance, i.e., IV–V, VI–XI, VIII–XI, X–XIII (7.3); XI–XIII, IX–XIII, III–X (10.0); X–XIII, XIII–VII, I–VIII (6.4); III–XI, VI–XIII, VII–X (9.6); III–II, IV–II, X–XI, (5.9); IV–II, VI–III, (4.7); I–VIII, II–IX (7.0); VII–V, IX–V (7.5); VII–XIV, VIII–XIV (10.7); XI–XIV, XII–XIV,III–IV (6.4); I–II, II–V (4.5); IV–VI, IX–X (7.2); V–X, II–XIV (9.2); IV–XI, XIII–XIV (10.1); II–XI, I–XI (8.3); II–X, VII–VIII (8.4) and V–VI, IV–VII (4.9). The maximum intercluster distance was 14.5 between clusters IV and XII.

Table 3. Varieties and hybrids in different clusters

Cluster No.	No. of populations	Varieties/hybrids
I	16	Co 7717 × Co 775, Co 7717 × Co 1148, Co 7004 × Co 775, Co 7004 × Co 1148, Co 7004 × Co 6904, Co 7314 × Co 775, Co 7314 × Co 1148, POJ 2878 × Co 775, POJ 2878 × Co 1148, Q 68 × Co 775, Q 68 × Co 1148, CoS 659 × Co 1148, CoS 659 × Co 6904, CP 44/101 × Co 775, Co 1148, BO 70
II	4	Co 7314 × Co 6904, BO 70 × Co 6904, Q 68 × Co 6904, Co 7314
III	2	Co 7717 × Co 6904, CP 44/101 × Co 6904
IV	2	POJ 2878 × Co 6904, CP 44/101 × Co 1148
V	2	CoS 659 × Co 775, BO 70 × Co 775
VI	1	CoS 659
VII	1	BO 70 × Co 1148
VIII	1	Co 6904
IX	1	Co 775
X	1	Co 7004
XI	1	Co 7717
XII	1	CP 44/101
XIII	1	POJ 2878
XIV	1	Q 68

Origin: Co (Coimbatore), CoS (Coimbatore–Shahjahanpur), BO (Bihar–Orissa), CP (Cannal Point), POJ (Java), and Q (Queensland).

Table 4. Intercluster distances between parent varieties and heterosis in different crosses

Cross	Genetic distance	Heterosis over better parent for yield, %
BO 70 × Co 1148	0	−0.362
Co 7314 × Co 1148	4.54	19.180
CoS 659 × Co 1148	5.14	−0.933
Co 7314 × Co 6904	6.20	7.011
CoS 659 × Co 6904	6.66	−21.279
Co 7314 × Co 775	6.99	18.915
Bo 70 × 6904	7.00	2.703
Co 7004 × Co 775	7.24	61.369
Co 7717 × Co 6904	7.28	46.811
Bo 70 × Co 775	7.43	3.762
CoS 659 × Co 775	7.58	−10.484
Co 7717 × Co 775	7.71	7.011
Co 7004 × Co 6904	7.87	49.930
Q 68 × Co 775	8.04	69.562
Co 7717 × Co 1148	8.17	−1.771
Co 7004 × Co 1148	9.05	11.082
POJ 2878 × Co 1148	9.35	−2.304
POJ 2878 × Co 6904	9.37	15.941
CP 44/101 × Co 775	9.97	57.900
Q 68 × Co 1148	10.28	−1.980
Q 68 × Co 6904	10.69	44.463
POJ 2878 × Co 775	10.84	65.457
CP 44/101 × Co 6904	11.99	37.790
CP 44/101 × Co 1148	12.02	−11.900

Normally genetically diverse parents show high heterotic effects in their hybrids, but this was not so in crosses CP 44/101 × Co 1148, POJ 2878 × Co 1148, Q 68 × Co 1148, CoS 659 × Co 1148, CoS 659 × Co 6904, and CoS 659 × Co 775 (Table 4). Heterosis over better parents in these crosses was negative, which showed very small or zero genetic distance. Two crosses, i.e., CoS 659 × Co 775 and CP 44/101 × Co 1148 were exceptions. This may be either due to similar genealogy or absence of relationship between the varieties and their hybrids in the crosses CoS 659 × Co 775 and CP 44/101 × Co 1148. This indicates that the extent of heterosis varies according to the degree of genetic diversity. The present study, thus, indicates that the genotypes having relatively larger statistical genetic distances or falling in different clusters are likely to produce high heterotic hybrids. In other words, selection of parents should be based on genetic divergence along with knowledge of their genealogy.

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REFERENCES

1. A. B. Joshi and N. L. Dhawan. 1960. Genetic improvement in yield with special reference to self fertilizing crops. Indian J. Genet., **20:** 101–113.

2. I. J. Anand and B. R. Murty. 1968. Genetic divergence and hybrid performance in linseed. Indian J. Genet., **28:** 178–183.

3. H. N. Singh and S. B. Singh. 1979. Genetic divergence in sugarcane, I. S. S. C. T., **17**(2): 1198–1202.

4. M. S. Punia, B. S. Chaudhary and R. S. Hooda. 1983. Genetic divergence in sugarcane. Indian J. agric. Sci., **53**(6): 434–436.

5. P. C. Mahalanobis. 1936. On the generalized distance in statistics. Proc. Nat. Ins. Sci. India, **2:** 49–55.

6. B. D. Chaudhary and V. P. Singh. 1975 Genetic divergence in some Indian and exotic barley varieties and their hybrids. Indian J. Genet., **35:** 409–413.

7. J. Ram and D. V. S. Panwar. 1970. Interspecific divergence in rice. Indian J. Genet., **30:** 1–10.

8. B. R. Murty and V. Arunachalam. 1966. The nature of genetic divergence in relation to breeding system in crop plants. Indian J. Genet., **26:** 188–198.

9. R. B. Singh and M. P. Gupta. 1968. Multivariate analysis in divergence in upland cotton. Indian J. Genet., **28:** 151–167.