Indian J. Genet., 52 (1): 85–93 (1992)

MAHALANOBIS GENERALIZED DISTANCE AND GENETIC DIVERSITY IN SORGHUM

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(Received: August 3, 1990; accepted: August 8, 1991)

ABSTRACT

Eighty nine sorghum genotypes including 70 hybrids resulting from line (5) x tester (14) mating and their 19 parents were classified using D^2 statistic into nine clusters. A comparison of the culturing pattern of parents vis-a-vis their hybrids, the magnitude of heterosis in crosses involving parents in the same cluster with those in different clusters and the D^2 values between parents with heterosis exhibited in their cross combinations revealed absence of any relationship between topological distance and genetic diversity. D^2 statistic might be useful in discriminating materials having high divergence for the factors important for fitness. However, under intense human selection the situation is too complex for being handled by multivariate analysis alone.

Key words: Sorghum, multivariate analysis, genetic diversity, heterosis, D^2 statistic.

Hybridization involving genetically diverse parents is known to provide an opportunity for bringing together gene constellations yielding desirable transgressive segregants in advanced generations. However, postulation of a rational criteria for identification of such parents is still a live problem in plant breeding. To consider geographic diversity among the parents as an index of genetic diversity has been aclaimed and equally disclaimed in numerous published reports. On the other hand, Murty and his co-workers hypothesised that Mahalanobis generalized distance, a measure of metric distance between population centroids, could be a useful multivariate statistical tool for effective discrimination among parents on the basis of genetic diversity [1–5]. But whether topological distances, as determined by D^2 statistic, also reflect genetic distance or genetic divergence has not been fully tested [6]. Keeping this in view, an attempt has been made in the present investigation to findout the relationship between topological distance and genetic diversity.

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MATERIALS AND METHODS

The experimental material consisted of 89 sorghum entries including 5 male sterile lines, 14 restorers and their 70 crosses made in line x tester design. These materials were grown in randomized block design comprising three replications [7]. Individual plot was of three rows for each parent and two rows per single cross. Row length was 4.5 meter, row to row and plant to plant distance being 45 cm and 15 cm, respectively. Observations were recorded on ten randomly selected plants in respect of plant height, days to flowering, panicle length, number of whorls per panicle, number of primaries per whorl, number of grains per primary, number of grains per panicle, 1000-grain weight, protein content in grain, reproductive phase duration (difference between date of anthesis and date of maturity), stover yield, harvest index, and grain yield per plant. Multivariate analysis using Mahalanobis D^2 statistic was used for assessing the divergence and grouping the parents and hybrids according to Tocher's method [1].

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the entries for all the 13 characters, indicating considerable amount of variability in the materials under study. The D^2 values computed for 3916 combinations among 89 genotypes ranged from 16.6 between the crosses 2219 A x SPV 312 and 2219 A x SPV 319 to 2647.5 between line 2219 A and cross 296 A x SPV 345. On the basis of relative magnitude of D^2 values, the parents and hybrids were grouped in nine clusters so that the genotypes within a cluster had smaller D^2 values among themselves than those belonging to different clusters (Table 1). The most distant among them were clusters IV and VI (1817.0), followed by clusters IV and VIII (1707.9). Spatial relationship between clusters, as determined by D values (square root of D^2 values), revealed closeness of the clusters I, III, IV and IX. Similarly, the magnitude of inter-cluster D values between clusters II, V and VI indicated affinity between the populations involved therein. On the other hand, the clusters IX, V and VIII occupied a triangular position in the figure, indicating maximum divergence amongst them.

As regards the composition, the parental lines were classified in three closely placed clusters: I, III and IV. While exotics and exotic x exotic derivatives, viz., 2077 A, 2219 A, 3660 A, IS 84 and SPV 35 were grouped together in cluster IV, the derivatives of exotic x Indian crosses were distributed in clusters I and III (Table 2). Among the male sterile lines, 296 A and 323 A were unique in their diversity from the other female parents and were differentiated in clusters III and I, respectively.

The distribution of hybrids in all the nine clusters revealed greater diversity in hybrids than in their parents. The clustering pattern indicates that there was no relationship between the parental divergence and their hybrid performance (Table 2). Line 323 A and 10 male parents were grouped together in cluster I. However, 7 of the 10 hybrids between them were placed in cluster II. On the other hand, out of the 42 crosses with lines 2077 A, 2219 A and 3660 A, 34 hybrids were classified in cluster I rather than in cluster IV, which included these three female lines. Four out of six crosses of these lines with IS 84 and SPV 35 (also included in the same cluster IV) were also not grouped in cluster IV. Similarly, the crosses involving line 296 A were distributed in cluster I (five), cluster II (three), cluster III (one), cluster V (two), cluster VI (one), cluster VIII (one), and cluster IX (one). Clusters II and V to IX had only hybrids. In contrast, clusters III and IV included eight parents but only three hybrids involving parents in these clusters.

Table 1. Average intra- (in bold) and intercluster D^2 values in sorghum

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**202.6**	535.6	320.1	355.7	688.7	966.1	380.1	1235.7	323.0
II		**203.1**	762.3	1070.0	355.4	355.5	353.4	612.6	1095.8
III			**238.4**	371.2	726.5	1279.9	512.3	1183.9	485.9
IV				**150.8**	1426.4	1817.0	955.5	1707.9	291.7
V					**54.5**	398.6	843.5	1277.1	1313.3
VI						**200.9**	716.9	767.1	1634.3
VII							**00.0**	501.5	719.3
VIII								**00.0**	1885.6
IX									**00.0**

Considering the variable distribution of parents and hybrids, a comparison of topological distance between the parents and heterosis exhibited by their cross combination for grain yield was made. Among the 12 heterotic crosses, also depicting superiority over the released hybrid CSH 5 (2077 A x CS 3541) and CSH 6 (2219 A x CS 3541), 2077 A x SPV 345, 296 A x SPV 345, and 296 A x SPV 245 exhibited wide variation in the magnitude of heterosis as well as in mean grain yield in spite of similar topological distance between their parents (Table 3). On the other hand, though the hybrids 323 A x SPV 245, 323 A x SPV 312 and 323 A x SPV 319 were at par in grain yield and heterosis, the D values among their parents varied widely. The coefficient of correlation worked out between genetic distance between the 27 pairs of parents and heterosis exhibited by their cross combinations for grain yield was also found nonsignificant.

Attempts have been made to find a method for conceiving the limits of topological distance between the parents within which the chances for the occurrence of high frequency of heterotic crosses would be more [9–11]. However, Behl et al. [12] reported that such grouping on the basis of generalized distance is arbitrary and subjective because the parental

Table 2. Number of populations and name of parents and hybrids of sorghum included in each cluster

Cluster	No. of genotypes	Parents	Crosses with different females				
			2077 A	2219 A	3660 A	296 A	323 A
I	55	323 A	SPV 130	SPV 130	SPV 130		
		SPV 312	SPV 312	SPV 312	SPV 312	SPV 312	SPV 130
		SPV 319	SPV 319	SPV 319	SPV 319	SPV 319	
		370 Dwarf	370 dwarf	370 dwarf		370 dwarf	370 dwarf
		SPV 245	SPV 245	SPV 245	SPV 245		
		CSV 5	CSV 5	CSV 5	CSV 5		
		CS 3541	CS 3541	CS 3541	CS 3541		CS 3541
		SPV 170		SPV 170	SPV 170		SPV 170
		SPV 345		SPV 345	SPV 345		
		SPV 187	SPV 187	SPV 187			
		SPV 106	SPV 106		SPV 106		
			SPV 35		SPV 35	SPV 35	SPV 35
			IS 84		IS 84	IS 84	
				SPV 122	SPV 122		
II	15			SPV 106		SPV 106	SPV 106
					SPV 187	CSV 5	SPV 187
							SPV 122
							IS 84
							SPV 345
							SPV 312
							SPV 312
							SPV 319
							SPV 245
						SPV 130	
			SPV 170				
III	5	296 A					
		SPV 130					
		SPV 122	SPV 122			SPV 122	
IV	7	2077 A					
		2219 A					
		3660 A					
		IS 84		IS 84			
		SPV 35		SPV 35			
V	2					SPV 245	
						SPV 187	
VI	2		SPV 345			SPV 345	
VII	1				370 dwarf		
VIII	1					SPV 170	
IX	1					CS 3541	

combinations with low, medium as well as high level of divergence were grouped together and that too irrespective of spatial relation of one cluster with another. Earlier and the present studies confirm that such arbitrary methods of grouping would serve little purpose in increasing efficiency for selection of diverse parents [13, 14].

Table 3. **Topological distance between the parents and heterosis for grain yield in twelve economic heterotic crosses in sorghum**

Cross	Topological distance between parents*	Heterosis (%)	Mean grain yield
2077 A x SPV 106	17.6	52.7	94.5
2077 A x SPV 345	15.5	81.6	99.6
2077 A x SPV 319	7.8	120.7	106.3
2219 A x 370 dwarf	13.9	98.2	105.0
3660 A x SPV 245	13.6	50.6	93.3
296 A x SPV 130	14.9	62.6	104.1
296 A x SPV 245	15.6	104.2	131.1
296 A x SPV 345	15.8	63.3	104.8
296 A x SPV 187	12.9	105.1	136.0
323 A x SPV 245	9.4	72.3	106.7
323 A x SPV 312	11.1	77.8	104.3
323 A x SPV 319	14.6	77.8	104.4
2077 A x CS 3541 (CSH 5)	17.9	18.9	72.8
2219 A x CS 3541 (CSH 6)	24.3	17.5	71.9

*Square root of D^2 value among the parents involved in a particular cross.

Joshi [6] pointed out that a study of crosses between the parents grouped in the same and in different clusters would throw more light on the relationship between topological distance among parents as determined by D^2 statistic and the genetic diversity expressed as heterosis over better parent. A perusal of Table 4 revealed that mean heterosis for grain yield between 10 males in cluster I and line 323 A grouped in the same cluster was 42.70%. Mean heterosis in the crosses between females 296 A in cluster III, 2077 A, 2219 A and 3660 A in cluster IV, and the above 10 male parents was 29.9, 60.0, 49.6 and 30.2%, respectively. Similarly, the crosses between SPV 130 and SPV 122 included in cluster III and female 296 A (also grouped in the same cluster) showed 37.8% mean heterosis. However, when these two male parents were crossed with 323 A (cluster I), 2077 A, 2219 A, 3660 A (all in cluster IV), the heterosis for grain yield was 27.3, 37.7, 19.6 and 27.5%, respectively. Similar trend was observed with the parents included in cluster IV. The data on other attributes, viz. grain/panicle, harvest index, and stover yield further confirmed the absence of any relationship between topological distance of the parents and heterosis recorded in their crosses.

The process of evolution under natural selection is slow, selection advantage being dependant on fitness. In a particular niche, the fitness of individuals is positive. Therefore, multivariate statistical approach enables to know the niche dimensionality with known contributors by each dimension to the separation of races/species in the ecological space. Hence there is greater probability of obtaining high heterosis in the crosses between

Table 4. Inter- and intracluster magnitude of mean heterosis (%) for different characters in sorghum

Female parent	Grain yield per plant	Harvest index	Stover yield per plant	Grains per panicle	Grains per primary
		Males included in cluster I (10 parents)			
323 A (I)	42.70	2.17	27.54	13.79	2.95
296 A (III)	29.92	-5.13	31.76	-1.12	11.77
2077 A (IV)	60.02	21.88	20.29	53.00	33.51
2219 A (IV)	49.60	24.40	8.84	32.61	27.37
3660 A (IV)	30.16	3.06	13.61	12.63	18.49
		Males included in cluster III (2 parents)			
323 A (I)	27.30	-4.25	11.65	0.60	9.50
296 A (III)	37.80	-4.05	29.15	13.55	12.95
2077 A (IV)	37.70	36.85	1.80	43.30	52.45
2219 A (IV)	19.65	2.45	13.85	7.10	35.00
3660 (IV)	27.50	9.20	-4.70	27.00	40.55
		Males included in cluster IV (2 parents)			
323 A (I)	21.90	-16.65	22.15	-1.20	0.35
296 A (III)	-9.45	-13.35	-9.55	-21.10	-2.00
2077 A (IV)	12.90	-15.30	24.70	-2.15	-4.15
2219 A (IV)	0.75	-11.90	19.30	-24.55	-32.85
3660 A (IV)	-1.40	-32.25	37.25	8.20	-1.05

interniche crosses than for the intraniche crosses. However, such generalization could not be made for the materials developed under human selection. There are several instances where human and natural selection operate in opposite directions. Murty and Arunachalam [2] and Arùnachalam and Ram [3] analysed D^2 statistic for two sets of sorghum materials that provided an opportunity to compare casual influences under natural and human selection. Their results confirmed that the pattern of divergence under natural selection was quite distinct from that under human selection in genus *Sorghum*.

Murty and Arunachalam [2] after examining D^2 statistic in a number of crops including sorghum concluded that the most potent factors for divergence, viz., plant height, flowering time, and number of tillers, are also important for fitness under natural conditions, while those selected by man have only limited influence on discriminating genotypes. However, the opposite was true in the present study. Coefficient of variation for stover yield/plant showed maximum variation among cluster means (40.9), followed by grain yield (39.5), grains/panicle (38.0), grains/primary (30.8). However, the coefficient of variation for days

Table 5. Cluster means for thirteen

Cluster	No. of genotypes	Plant height (cm)	Days to 50% flowering	Panicle length (cm)	Whorls per panicle	Primaries per whorl	Grains per primary
I	55	199.3	63.8	27.9	11.18	5.96	45.7
II	15	177.8	67.7	27.8	11.38	6.91	40.9
III	5	127.4	68.6	28.7	12.57	7.89	34.8
IV	7	129.9	56.8	26.2	9.93	6.02	32.3
V	2	159.6	70.1	33.4	13.80	7.28	50.4
VI	2	152.4	70.5	31.4	12.32	6.45	59.1
VII	1	127.8	65.3	21.1	8.07	7.81	28.8
VIII	1	156.0	75.5	32.2	11.93	8.04	24.4
IX	1	121.8	66.8	25.4	10.93	4.06	59.7
Mean		150.2	67.2	28.2	11.35	6.70	41.8
SE		8.8	2.1	1.2	0.55	0.42	4.3
CV (%)		17.5	7.6	13.5	14.53	14.58	38.8

to 50% flowering and plant height was of lower order (Table 5). This was expected as syncronization in flowering and plant height between female and male parents is a prerequisite for commercial hybrid seed production and as such human selection acted against variation in these attributes.

Grain yield is a complex character of polygenic nature. With such a system, similar genotypes could be produced by different combinations of genes/gene blocks. For example, D^2 statistic revealed least variation among ms 323 A and the 10 male parents (all grouped in cluster I). However, 7 out of 10 crosses involving 323 A and these males were grouped in a separate cluster II. A comparison of means of cluster I and II revealed significant differences in stover yield and other characters, which could not be attributed to the major height genes (Table 5). Line 323 A was initially developed from the cross Shallu x GM 2-3-1. The male parent, a local improved variety grown around Dharwar (Karnataka, India) since long, is not high yielding for grain, though it gives good stover yield (R. Parmeswarappa, personal communication). It might have contributed gene complexes to 323 A, which were quite distinct from other male parents. Complementation of different gene complexes in 323 A and the males could, therefore, be the major cause for the observed divergence between parents and their cross combinations. Similar inferences could be drawn for other derivatives of exotic x Indian crosses.

characters in sorghum

Grains per panicle	1000-grain wt. (g)	Protein (%)	Reproductive phase (days)	Stover yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
2884	24.5	10.7	28.1	98.8	43.5	71.7
3096	28.3	10.3	27.7	158.8	37.1	88.5
3211	20.9	9.2	27.3	80.5	45.7	62.8
1847	25.2	11.8	29.5	71.1	41.4	47.1
4767	29.0	8.8	27.7	134.7	55.4	133.5
4560	22.4	11.1	25.4	189.1	35.6	102.2
1852	23.3	12.3	25.9	147.8	25.4	48.1
1710	26.7	12.1	35.0	209.6	20.5	49.4
2622	22.5	12.6	29.7	65.4	50.3	62.0
2950	24.8	11.0	28.5	128.4	39.4	73.9
373.7	1.0	0.4	10.9	17.5	3.7	9.7
811.92	11.9	12.3	9.9	40.9	28.5	39.5

In the sorghum materials advanced through cycles of rigorous human selection of optimizing height and maturity genes in a narrow range, the likelihood of obtaining nearly phenotypically similar parents in spite of accumulation of diverse gene complexes would be quite high. As topological distance is based on phenotypic observations, the limited utility of this tool for revealing the potential genetic diversity is obvious.

REFERENCES

1. B. R. Murty, J. B. L. Mathur and V. Arunachalam. 1965. Self- incompatibility and genetic divergence in *Brassica campestris* var. brown sarson. Sankhya B, **27**: 271–278.

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

3. V. Arunachalam and J. Ram. 1967. Geographic diversity in relation to genetic divergence in cultivated sorghum. Indian J. Genet., **27**: 369–380.

4. S. S. Chandrasekariah, B. R. Murty and V. Arunachalam. 1969. Multivariate analysis of genetic divergence in Eusorghums. Proc. Nat. Inst. Sci. (India), **35**: 172–195.

5. J. N. Govil and B. R. Murty. 1973. Genetic divergence and nature of heterosis in grain sorghum. Indian J. Genet., **33**: 252–260.

6. A. B. Joshi. 1979. Breeding methodology for autogamous crops. Indian J. Genet., **39**: 567–578.

7. V. Arunachalam. 1974. The fallacy behind the use of modified line x tester design. Indian J. Genet., **34**: 280–287.

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

9. P. S. L. Srivastava and V. Arunachalam. 1977. Heterosis as a function of genetic divergence in triticale. Z. Pflanzenzuchtg., **78**: 269–275.

10. V. Arunachalam, A. Bandhopadhyay, S. N. Nigam and R. W. Gibbons. 1984. Heterosis in relation to genetic divergence and specific combining ability in groundnut (*Arachis hypogaea* L.). Euphytica, **33**: 33–39.

11. V. Arunachalam and A. Bandhopadhyay. 1984. Limits of genetic divergence for occurrence of heterosis—experimental evidence from crop plants. Indian J. Genet., **44** : 548–554.

12. R. K. Behl, V. P. Singh and R. S. Paroda. 1985. Genetic divergence in relation to heterosis and specific combining ability in triticale. Indian J. Genet., **45**: 368–375.

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

14. Y. R. Singh, A. Kumar and B. P. S. Chauhan. 1981. Genetic divergence in pearl millet. Indian J. Genet., **41**: 186–190.