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GENETIC DIVERGENCE AMONG A NON-RESTORER COLLECTION OF SORGHUM (*SORGHUM BICOLOR* (L.) MOENCH) AND ITS RELATIONSHIP WITH HETEROSIS*

BHOLA NATH, ABBAS O. OMRAN and L. R. HOUSE

International Crops Research Institute for the Semi-Arid Tropics, (ICRISAT), Patancheru, Andhra Pradesh, India and the University of Peradeniya, Peradeniya, Sri Lanka

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SUMMARY

A genetic diversity analysis in a collection of 171 non-restorer lines of sorghum (*Sorghum bicolor* (L.) MOENCH) using D^2 technique and canonical variate analysis indicated that considerable variation in grain yield has been added to the collection by the addition of lines derived from random mating populations. The efficiency of D^2 and canonical variate techniques in distinguishing extremely diverse genotypes was confirmed. However, the two techniques showed weak correspondence in their clusters. The F_1 hybrids of 15 diverse lines exhibited no relationship between heterosis or per se performance of crosses and diversity in their parents. Therefore, traditional plant breeding methods are being advocated.

INTRODUCTION

The importance of genetic divergence to yield improvement and heterosis in sorghum has been emphasized by several workers (NIEHAUS & PICKETT, 1966; MALM, 1968; RAO, 1962; SUBBA RAO et al., 1975, 1976).

It is reasonable to expect genetic divergence to be associated with geographic diversity. This may be true for landraces but in applied plant breeding, where the origin of lines is not always known, selection of parents based on geographic diversity alone is not always relevant. Statistical techniques such as Mahalonobis D^2 and canonical variate analyses, which quantify the differences among several quantitative traits are efficient methods of evaluating genetic diversity.

The present study was carried out using D^2 and canonical variate analyses to 1) study the diversity among the working collection of non-restorer sorghums that included a large number of maintainers of newly-developed male sterile lines (A-lines), derived from the populations under recurrent selection at ICRISAT and 2) establish the value of these techniques in hybrid breeding programmes.

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MATERIALS AND METHODS

One hundred and seventy one B-lines of potential and commercially used seed parents of sorghum hybrids were grown in a randomized complete block design (RCBD) with three replications during the 1981 rainy season on the research farm of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) at Patancheru in India. The plots were single rows, 2.25 m long and 75 cm apart. Days to 50% flowering and plant height were recorded on five competitive random plants from each plot. Grain yield was recorded on a whole plot basis. Plot means were subjected to D^2 analysis according to MURTY & ARUNACHALAM (1967) and canonical variate analysis adopted from ARUNACHALAM (1967). Clustering of genotypes in D^2 analysis was accomplished by Tocher's method, as described by RAO (1952). Fifteen lines - SPL 34B (1), SPL 76B (2), SPL 85B (3), SPL 118B (4), SPL 160B (5), SPL 199B (6), CK 60B (7), 2219B (8), 2077B (9), 296B (10), 36B (11), SB 323B (12), Kaffinum B (13) Wheatland (14), BT × 623 (15) representing six of the ten D^2 clusters (Table 2) obtained from the D^2 analysis of 171 lines were crossed in a half-diallel series. The lines in the other clusters were not used for the diallel due to agronomic considerations.

The F_1 s and parents were grown in the 1982 rainy season with the same plot size, location and experimental design as in 1981. Days to flowering, plant height (cm), grain yield (t/ha), head length (cm), 100-grain weight (g), and grain number per plant were recorded. All the characters were recorded on five random plants except for grain yield which was taken on a whole plot basis. Parental data were again subjected to D^2 and canonical variate analyses. Simple correlation coefficients between intra - and inter-cluster distances, their mean yield and mid - parent heterosis for grain yield in crosses within and between clusters were calculated.

RESULTS

In 1981, highly significant differences were recorded among the 171 B-lines for all the three characters (Table 1). The coefficients of genotypic variation were largest for grain yield, followed by plant height and days to 50% flowering. The coefficients of variation due to environment also followed a similar trend but were less than the genotypic coefficients. The lines derived from random mating populations showed greater variation in yield than the other lines of the collection. Population derivatives, however, had lower variation in terms of height and days to flowering.

The 171 lines formed 10 clusters in the D^2 analysis (Table 2). The highest number of lines fell into cluster A. These lines were of medium flowering duration, plant height and grain yield. Cluster B comprised lines of similar duration to those in Cluster A but were taller and produced larger grain yield. Lines in Cluster C were shorter in height, lower in yield but of similar duration to those of A and B. The earliest duration lines fell in cluster D. The lines of later duration in different combinations of height and grain yield formed clusters G to J.

As expected, the intra-cluster distances were always smaller than the corresponding inter-cluster distances. The lines in cluster C and F were the closest related, followed by those in A with C and A with B. The widest cluster distances were J with H, F, D and C and E with H. Further, most of the sister selections of the lines included

Table 1. Analysis of variance for the non-restorer lines.

Source of variation	Degrees of freedom	Mean squares		
		days to flower	plant height (cm)	grain yield (t/ha)
Replications	2	3.64	64.67	0.54
Genotypes	170	74.42**	2320.66**	1.87**
Error	340	4.13	72.22	0.35
Environmental CV%				
Overall		3.1	5.9	23.9
PD		2.8	5.9	24.2
Others		3.9	5.7	21.7
Genotypic CV%				
Overall		7.3	18.9	28.8
PD		5.8	17.7	27.9
Others		8.7	18.6	24.5
Phenotypic CV%				
Overall		8.0	19.8	37.4
PD		6.5	18.7	36.9
Others		9.5	19.4	32.8

**Significant at 0.01 level of probability.
PD = Population derivatives.

in the study tended to group together either in the same cluster or in closely related clusters (Table 3).

The canonical distribution of the 171 lines showed weak correspondence with D^2 analysis despite the contribution of the first two canonical roots exceeding 92 percent of the variation. Clusters D, H and J were identical in the two analyses, while E, F, G and I had minor differences and A, B and C had disagreements.

A more detailed genetic diversity analysis of the 15 selected lines based on the six characters in 1982 is shown in Figure 1. The first two canonical roots in this analysis accounted for 85 percent of the variation. Superimposition of D^2 clusters on canonical variate distribution in the figure again indicated weak correspondence between the two techniques even though extremely distant lines such as Wheatland (14) and 36B (11) were clearly distinguished in both cases. The intra- and inter-cluster distances (D-statistics), grain yield and percent heterosis of parents and their F_1s within and between the clusters are presented in Table 4. The cluster distances were neither related to grain yield of the crosses nor their heterosis percent ($r = -0.18$ and -0.063, respectively). On the other hand, the correlation coefficient between the mean cluster yield and heterosis percent was highly significant ($r = 0.667^{**}$). Similar relationships were observed for all the other five characters included in the study.

DISCUSSION

A lack of genetic diversity in the seed parents is recognised as a major bottleneck in developing better sorghum hybrids. The narrow diversity is a consequence of the

Table 2. Number of lines, character means and ranges and genetic distances (D-statistic) among 10 clusters of non-restorer sorghum lines.

Cluster	Number of lines		Character means and ranges			Cluster distances									
	within cluster	selected for diallel	days to flower	plant height (cm)	grain yield (t/ha)	A	B	C	D	E	F	G	H	I	J
A	75	7	66 (60–73)	140 (122–173)	2.49 (1.19–3.64)	3.49	4.84	4.67	6.74	7.69	6.53	6.00	7.90	6.42	12.20
B	37	3	67 (61–71)	169 (140–193)	3.04 (1.54–4.47)		3.78	7.43	8.10	5.09	9.39	7.24	10.74	5.61	9.76
C	22	2	64 (60–70)	113 (103–122)	2.11 (1.27–2.69)			2.78	6.12	10.70	3.79	7.00	5.87	8.80	15.30
D	12	1	55 (55–59)	124 (98–158)	2.07 (1.88–3.25)				3.62	10.02	6.73	10.86	10.96	9.93	15.57
E	8	–	66 (62–69)	199 (183–213)	3.29 (2.21–4.21)					3.07	12.65	9.95	14.34	6.33	7.41
F	4	1	62 (57–67)	97 (83–113)	1.73 (1.24–2.48)						4.20	8.53	6.02	10.56	17.20
G	6	–	76 (72–79)	105 (130–163)	0.96 (0.34–1.74)							3.11	6.70	6.28	11.62
H	3	–	72 (72–72)	93 (82–105)	1.50 (1.17–2.07)								2.24	11.22	17.59
I	3	1	72 (68–78)	178 (162–193)	0.71 (0.44–1.08)									4.25	7.57
J	1	–	78 –	238 –	0.86 –										0.00
$\bar{x}$			66 (52–79)	145 (82–238)	2.47 (0.34–4.47)										

Values in parentheses are ranges.

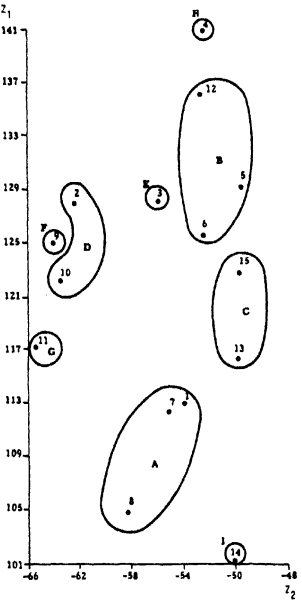

Fig. 1. Genetic diversity in the 15 selected non-restorer lines (Canonical distribution superimposed by D^2 clusters).

relatively lower proportion of maintainers of male sterility than that of the restorers in the milo-kafir system. A large proportion (133 out of 171) of the non-restorers used in this study originated from random mating populations being improved at ICRISAT. The collection exhibited wide genetic variation for all the three characters, especially for grain yield, despite the exclusion of vary tall lines from the study. The new lines from random mating populations appear to have considerably increased the variation in the non-restorer collection for grain yield. Hybrids of the 15 lines among which crosses were made exhibited high mid-parent heterosis for grain yield, especially the population derivatives, SPL 118B and SPL 199B. The use of these lines in the hybrid development program should greatly increase the probability of obtaining improved hybrid combinations.

The grouping of lines in different combinations of flowering duration, height and

Table 3. Distribution of sister lines among D^2 clusters, 1981.

Sister group	Number of lines	% lines in clusters					
		A	B	C	D	E	F
FLB 141 × CSV 4	10	60	30	10			
Rs/R 20	8	75	12				
Diallel 346	7	86				14	
Ind-Syn 89	6	33	66				
US/B 37	6	67		16			
US/B 398	5	80	20				
FLB 274 × CSV 4	5	80		20			
E 35-1 × FLR 204	5	20					
Diallel 465	4	50	50				
Ind-Syn 422	4	25	75				
Serere 21	4	25	75				
Nigerian 7	3	100					
WAE 3	3	100					
US/R 50	2			100			
FLB 266	2	100					
Rs/B 162	2			100			

yield in different clusters and the fact that the majority of the sister lines fell in the same cluster confirm the effectiveness of D^2 technique in classificatory analysis as reported by ARUNACHALAM & JAWAHAR RAM (1967). In the studies of ARUNACHALAM & JAWAHAR RAM (1967) and CHANDRASEKHARIAH et al., (1969) canonical variate and D^2 analyses have given similar results. However, the two techniques in our study showed weak correspondence in their clusters despite the large contributions of days to flowering and plant height to the total variation. Since the D^2 analysis takes a better account of all the characters of genotypes, greater reliance was placed on this technique in our study.

Although D^2 analysis appeared effective in clustering distant groups, the heterosis expressed by hybrids between parents from distant groups was no greater than those of parents from closely - related-clusters. Thus, genetic divergence based on statistical differences of the characters has little relevance in the expression of heterosis in sorghum. The study illustrates the limitations in the use of these techniques in selecting parents for making hybrids. The traditional approach of making a large number of crosses among the parents selected for the traits of value and evaluating their hybrids for yield and other agronomic characters thus remains the most effective approach to the development of sorghum hybrids.

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Table 4. Intra and inter cluster D-statistics (upper), corresponding mean grain yields (t/ha) (middle) and percent heterosis (lower) for crosses among 15 selected sorghum lines.

Number of lines	Cluster	A	B	C	D	E	F	G	H	I	Average inter-cluster
3	A	6.92	16.28	10.97	13.57	13.98	16.18	11.80	22.57	9.74	14.39
		4.58	6.41	4.77	5.83	5.34	4.45	3.95	6.28	4.14	5.15
		28.77	36.63	17.27	36.10	7.21	36.55	4.42	24.62	10.11	21.61
3	B		6.56	10.77	11.76	8.58	15.39	15.85	9.97	21.42	13.75
			6.89	7.18	7.42	7.11	7.23	8.16	8.01	5.88	7.17
			16.39	36.64	34.52	14.70	61.74	3.83	29.39	28.73	38.27
2	C			5.21	13.20	11.23	13.92	16.34	15.74	13.98	13.27
				4.71	6.94	8.46	6.44	4.98	8.47	4.04	6.41
				2.64	43.15	52.76	68.09	16.30	52.78	3.92	36.36
2	D				5.66	8.75	8.70	8.65	14.84	20.78	12.53
					6.86	8.15	5.47	6.26	7.75	5.78	6.70
					33.20	39.62	35.79	37.34	33.94	38.45	37.36
1	E					-	13.10	13.58	10.57	21.06	12.61
						-	6.90	6.25	9.12	4.82	70.20
						-	44.75	18.37	40.47	-0.58	27.16
1	F						-	14.06	16.24	22.32	14.99
							-	5.03	7.34	3.32	5.77
							-	42.55	55.94	7.32	44.09
1	G							-	21.61	18.24	15.02
								-	8.61	3.82	5.88
									63.91	5.96	31.58
1	H								-	28.67	17.52
									-	4.55	7.52
										-5.67	36.92
1	I									-	19.53
										-	4.54
										-	11.03

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