Theor Appl Genet (1998) 96 : 397–405

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Pattern analysis of international sorghum multi-environment trials for grain-yield adaptation

Received: 4 April 1997 / Accepted: 6 October 1997

Abstract Pattern analysis, which consists of joint and complementary use of classification and ordination techniques, was applied to grain-yield data of 12 sorghum genotypes in 25 environments to identify the grouping of genotypes and environments. The 12 genotypes represented a wide geographical origin, different genetic diversity, and three photoperiod-sensitive classes. The 25 environments represented a super population of widely different environments covering latitudes from 20°S to 45°N. The knowledge of environmental and genotype grouping helped reveal several patterns of genotype × environment (GE) interaction. The existence of two mega-environments – African and Asian – was indicated. Within these mega-environments, several subgroups were further discernible. The Asian-type subgroups of environments tended to be closer to one another, suggesting that they discriminated genotypes similarly. By contrast, the African-type sub-groups of environments were more divergent. Differential genotype adaptation patterns existed in the two mega-environments. The repeatability of the GE patterns seen in this multi-environmental trial, however, needs to be established over time.

Key words Pattern analysis · Yield adaptation · Sorghum · Genotype × environment interaction

Approved as journal article No. 2047 by ICRISAT

Communicated by H. C. Becker

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Introduction

Sorghum is an important crop providing food and fodder in the semi-arid tropics (SAT). The sorghum improvement program of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), has been developing and disseminating high-yielding cultivars (for grain and forage/fodder) aimed at the needs of farmers in major sorghum-growing areas in the SAT. Large-scale cooperative international multi-environment trials (IMETs) are conducted to disseminate improved cultivars and to gain insight into their adaptation patterns across widely different SAT climatic conditions. Effictive genotype dissemination, and understanding of adaptation patterns, are complicated by the ubiquitous and inevitable presence of genotype × environment (GE) interactions in the IMETs.

Invariably in the IMETs the relative differences among genotypes (G) across environments (E) are inconsistent due to GE interactions. These differences manifest themselves either qualitatively by altering the relative ranking of genotypes among environments, which reflects a lack of genetic correlations among environments; or quantitatively by changing absolute differences between genotypes without changing ranks, which reflects heterogeneity of variance. In crop-improvement programs, qualitative GE interactions make cultivar selection difficult as they change the genotype composition of selected or rejected groups in a given environment. The quantitative GE interactions, indicating the magnitude of differences among genotypes over environments, become important when disseminating improved germplasm.

A wide variety of statistical approaches exist to analyze GE interactions. The joint-linear-regression method and its different variants (Finlay and Wilkinson 1963; Eberhart and Russell 1966; Perkins and Jinks 1968) have been predominantly used until recently.

These methods require an *a priori* assumption of linearity and of normality of yield response across environments. These assumptions severely limit the application and utility of linear-regression methods to deal with practical situations in most of which, *a priori*, the data are rarely known to fulfil their underlying assumptions. In particular, the linearity of response has been convincingly shown not to hold in many IMETs (Byth et al. 1976), including even for IMETs with carefully managed environments (Chapman et al. 1996). The linear-regression-based methods, and also the recently developed additive main effects and multiplicative lineraction (AMMI) method (Gauch 1992), do not have an in-built mechanism like pattern analysis (PA) to classify the environments and/or the genotypes required to help identify the underlying patterns of GE structure in the environmental and/or the genetic population. The PA is based on the joint and complementary use of classification and ordination, a feature that is absent in AMMI which is basically an ordination technique.

A knowledge of environment classification is an important pre-requisite for effective targeting of the IMETs to representative environment-groups, and thus to bring down the cost of conducting them. This has assumed increasing significance in view of the recent global shrinking of funds for agricultural research. Another practical necessity for environmental classification is to characterize the pattern of adaptation (specific/broad) among genotypes. Pattern analysis applied to many IMETs to analyze GE interactions, has been shown to be very effective for these purposes (Byth et al. 1976; Abdalla et al. 1996; Cooper et al. 1996 a). This, accompanied by the fact that PA does not suffer from the limitations inherent in other methods, prompted the authors to use PA to study grain-yield adaptation in sorghum IMETs.

Materials and methods

Genotypes and test environments

Twelve sorghum genotypes representing genetic diversity (hybrids, breeding lines, and germplasm lines), geographic diversity (originating in Asia, Africa, and Central America), and different response to photoperiod (insensitive to weakly sensitive, moderately sensitive, and highly sensitive) were evaluated in 25 environments during 1991.

The details of the genotypes, their origin, and their photoperiod sensitivity classification are given in Table 1. The IMET was conducted in 25 trans-continentally distributed environments (12 in Asia, 11 in Africa, and two in Central America) situated in latitudes ranging from 20°S to 45°N. One of the 25 was a managed environment in which the day length was artificially modified to 16 h. In one environment irrigation supply was non-limiting, and in eight environments the rainfall was supplemented by irrigation to avoid drought. The geographical location, agroclimatic and agronomic data of these 25 environments are presented in Table 2. Among the environments the maximum temperature during the growing season varied from 24.1 to 37.2°C and the minimum temperature ranged from 14.1 to 25.6°C. The precipitation during the growing season varied from 116 to 661 mm. The mean day length during the first 30 days from seedling emergence varied from 12.1 to 15.7 h. The planting dates of sorghum among the 25 environments varied from 22 March 1991 to 14 February 1992. These data emphasize the diversity of the environments where the IMET was conducted.

Experimental design and data analysis

At each of the $n_l = 25$ environments, a randomized complete block design with $n_r = 4$ replications was used to test the $n_g = 12$ genotypes. Uniform plot size (4 rows × 4 m) and inter-row spacing (75 cm) were used. Data on days to 50% flowering, plant height, and grain yield were recorded, the latter two at harvest, from the central two rows (6-m^2 area) of each plot. This study considers data on grain yield. The grains were sun-dried (duration varying from 5 to 10 days).

The genotype mean-grain-yield values y_{ij}, computed from the four replications for genotype i ($i = 1, \ldots, n_g$) at environment j ($j = 1, \ldots, n_l$) were used as basic data for analysis. Since this study tries to classify environments and genotypes in order to generate, rather than test, hypotheses, we have used data analytical methods that are relatively free of distributional assumptions.

The deterministic linear additive model of Eisemann (1982; see also DeLacy et al. 1990), was adopted to compute a two-way analysis of variance of the genotype-environment matrix $Y = \{y_{ij}\}$ in order to assess the nature and extent of differences among genotypes (G), among environments (E), and the GE interactions. The ratio [(sum of squares due to GE)/(sum of squares due to G)] was computed to measure the relative importance of GE interaction effects in comparison of genotype effects.

Pattern analysis (Williams 1976), which consists of the combined and complementary use of classification and ordination techniques, was applied to the environment-standardized (Fox and Rosielle 1982) data matrix Y in order to: (1) classify the environments into relevant homogeneous groups, and (2) assess the relations among genotypes, among environments, and the interrelations among genotypes and environments. The environment-standardization of grain-yield data as recommended by Fox and Rosielle (1982) removed the location main effects, each location having a mean of zero, and a phenotypic standard deviation of one. This made the clustering to be largely determined by the relative performance of genotypes within location. For the purpose of classification, an agglomerative hierarchical classification procedure (Williams 1976) with an incremental sum of squares grouping-strategy, known as Ward's method (Ward 1963), was employed as recommended by Eisemann (1982) and Milligan (1989). The squared Euclidean distance was used as the required dissimilarity measure for Ward's method (Belbin 1984). The profile plot of performance of different genotype groups across different environment groups was used to assess the specific and broad adaptation of genotypes. A biplot was used to further assess the patterns of relations among genotypes, among environments, and the interrelations among genotypes and environments. The GEBEI package (Watson et al. 1996) was used to generate these analyses.

Results and discussion

The mean grain-yield of genotypes across environments varied from 1.53 t ha^{-1} (genotype IS 2284) to 3.65 t ha^{-1} (genotype CSH 11) as shown in Table 1. The environment mean grain-yield across genotypes varied from 0.28 t ha^{-1} in Tara to 6.23 t ha^{-1} in Shandaweel (Table 2). The mean grain-yield in the GE data matrix ranged from zero at Alupe (due to a severe midge pest attack) to 9.31 t ha^{-1} in Shandaweel. The

Table 1 Name, genetic diversity, origin, agronomic characters, and genotype grouping details of the genotypes evaluated in the IMET

Genotype	Genetic diversity	Origin	Days to 50% flowering	Grain yield (t ha^{-1})	Genotype grouping[a]
A: Insensitive/weakly photoperiod-sensitive					
CSH 1	F_1 hybrid	Asia	59.4	2.82	G1
CSH 11	F_1 hybrid	Asia	65.7	3.65	G3
ICSV 112	Breeding line	Asia	68.6	3.31	G4
IRAT 204	Breeding line	West Africa	59.0	2.58	G7
IS 3693	Breeding line	Southern Africa	70.0	2.30	G7
Dorado	Breeding line	Central America	70.0	2.78	G7
B: Moderately photoperiod-sensitive					
E35-1	Germplasm	Ethiopia	75.7	2.13	G5
S35	Breeding line	Cameroon	66.7	3.20	G4
C: Highly photoperiod-sensitive					
Framida	Germplasm	Southern Africa	72.8	1.91	G5
Naga White	Germplasm	West Africa	66.8	2.64	G2
Seredo	Breeding line	East Africa	75.6	2.02	G5
IS 2284	Breeding line	East Africa	66.6	1.53	G6

[a] Genotype grouping based on genotype dendrogram given in Fig. 1

grain-yield data also indicate that genotypes fail to retain their relative yield ranking (data not shown) across 25 environments.

The partitioning of total sums of squares (SS) of the original GE data matrix, following Eisemann's (1982) deterministic model, indicated that 12%, 61%, and 27% of the total variation was accounted for respectively by differences among genotypes, environments, and GE interactions. The fact that environments accounted for maximum variation, followed by GE interaction and genotypes, in that order, agrees with similar findings in other GE studies (DeLacy et al. 1990; Cooper et al. 1996 b). The GE sums of squares was 2.4-times that of genotypes indicating the presence of sizable GE interactions. This is supported by the fact that the GE mean grain-yield varied from zero to 9.3 t ha^{-1}, in comparison to the genotype mean grain-yield which varied from 1.53 to 3.65 t ha^{-1} (Table 3).

The results of classification analysis are presented in dendrograms for genotypes (Fig. 1) and environments (Fig. 2). The numbers of genotype and environment groups were decided on the basis of the SS retained in the reduced GE matrix. Following this criterion, genotypes were classified into seven groups, and environments into seven groups which retained 56% of the GE sums of squares. The increase in SS beyond this grouping level was minimal. The genotype dendrogram clearly indicated the existence of two major groups at point G of maximum dissimilarity in the dendrogram (Fig. 1). The presence of two major genotype groups confirmed the selectional origin (Asia and Africa) of genotypes in these groups. For the purpose of further analysis, we truncated the hierarchy at the seven-group level. Even though genotype classification was based on grain yield, this grouping reflected the genotype classification based on their response to photoperiod with certain minor exceptions (Fig. 1). The genotypes Framida, and Seredo are the first to separate in the dendrogram. These genotypes were highly sensitive to photoperiod and the average yield of the two ranged from 1.9 to 2.0 t ha^{-1} (Table 3). Genotypes ICSV 112 and S 35 were next to be separated with their mean yields being 3.3 and 3.2 t ha^{-1} respectively. The third group consisted of Dorado, IRAT 204 and IS 3693, their mean yields ranging from 2.3 to 2.8 t ha^{-1}. Genotypes CSH 1 and Naga White comprised the fourth group. The highest-yielding genotype, CSH 11 (3.7 t ha^{-1}), and the lowest-yielding, IS 2284 (1.5 t ha^{-1}), fell into two single-member groups which were separated at a much higher level of hierarchy in the genotype dendrogram.

The environment classification at point E of maximum dissimilarity (Fig. 2) indicated two broad groups, namely African- and Asian-type environments. The African-type environment was represented by environments in Cameroon, Egypt, Kenya, Mali, Niger, Nigeria and Zimbabwe, but also included environments (MH, YE, and MY) in Myanmar, Asia. The Asian-type environment was represented by environments in India, Pakistan, Syria, and Thailand, but also included environments PO in Mexico, and MG in Nicaragua. In general, the mean grain-yield, 2.12 t ha^{-1}, among the African-type of environment was low (excluding the fully irrigated environment in Egypt) compared to 3.01 t ha^{-1} among Asian-type environments (Table 2). The mean time to 50% flowering among African environments was 66 days compared to 68 days in the Asian-type environment. The mean plant height in the African-type environment was 162 cm, while in the Asian-type environments it was 200 cm. The biotic stress (plant diseases) among the two mega-environment groups was different. In the African-type environments foliar diseases like anthracnose, gray leaf spot, and oval leaf spot were the major yield-reducing

Table 2 Grouping of locations, environmental, and agronomic details and group means for the 25 sorghum testing locations

Location group[a]	Location name, country[b]	Latitude (degrees)	Temperature (°C)		Precipitation (mm)	Mean day length[c] (h)	Days to 50% flowering	Plant height (cm)	Grain yield t ha^{-1}
			Max	Min					
Group-E1 African-type environment									
E1-1	AL-Alupe-KEN	0:30 S	27.7	16.6	514	12.8	61	143	1.65
E1-1	KA-Katumani-KEN	1:40 S	24.1	14.1	270	12.2	72	139	1.69
	E1-1 means						*67*	*141*	*1.67*
E1-2	BA-Bagauda-NGA	11:40 N	30.3	21.8	568	13.3	69	206	4.26
E1-2	GU-Guiring-CMR	10:30 N	N.A	N.A	557	13.4	62	187	2.99
E1-2	SH-Shandaweel-EGY	26:00 N	36.9	22.9	IR[d]	14.1	71	225	6.23
	E1-2 means						*67*	*206*	*4.49 (3.62)*[e]
E1-3	KI-Kiboko-KEN	1:30 S	30.4	18.0	116 + IR	12.1	61	130	1.26
E1-4	LU-Lucydale-ZWE	20:50 S	30.2	16.2	216	12.8	80	92	0.53
E1-4	SA-Samanko-MLI	12:50 N	31.5	21.4	661	13.3	72	182	1.95
E1-4	SI-Sikasso-MLI	11:21 N	29.5	21.7	551	13.4	66	187	2.37
E1-4	TA-Tara-NER	11:59 N	31.8	22.7	366	13.3	71	156	0.28
	E1-4 means						*72*	*154*	*1.28*
E1-5	MH-Mahlaing-MYN	21:50 N	32.1	16.4	325	13.0	68	188	2.39
E1-5	YE-Yezin-MYN	19:51 N	30.8	23.1	430	13.4	62	218	2.88
E1-5	MY-Myiangyan-MYN	21:28 N	33.7	25.6	343	12.6	58	138	0.52
	E1-5 means						*63*	*181*	*1.93 (2.64)*[f]
	E1 means						*66*	*162*	*2.12 (2.18)*[f]
Group-E2 Asian-type environment									
E2-1	BH-Bhavanisagar-IND	11:00 N	32.9	19.0	66 + IR	13.2	61	184	3.42
E2-1	HO-Homes-SYR	45:00 N	30.9	19.9	IR	15.7	79	184	1.90
E2-1	MG-Managua-NIC	12:80 N	N.A	N.A	N.A	12.8	61	157	2.72
E2-1	SU-Suphanpuri-THA	14:18 N	32.0	23.9	572	12.8	57	224	4.71
	E2-1 means						*65*	*187*	*3.19*
E2-2	DI-DIKhan-PAK	31:50 N	31.2	25.0	162 + IR	13.2	78	167	1.64
E2-2	YO-Yousafwala-PAK	37:20 N	37.2	25.0	33 + IR	13.5	88	208	2.60
E2-2	LD-Patancheru-IND[g]	17:30 N	29.7	22.3	388 + IR	16.6	66	230	3.30
E2-2	ND-Patancheru-IND	17:30 N	29.7	22.3	388 + IR	13.6	63	230	3.92
E2-2	PO-Pozarica-MEX	20:30 N	N.A	N.A	N.A	13.5	68	234	3.68
E2-2	HF-Patancheru-IND	17:30 N	29.7	22.3	419 + IR	13.6	68	230	3.30
E2-2	LF-Patancheru-IND	17:30 N	29.7	22.3	419 + IR	13.6	71	230	2.94
E2-2	MR-Maradi-NER	13:30 N	N.A	N.A	362	13.3	73	175	1.21
	E2-2 means						*72*	*213*	*2.82*
	E2 means						*68*	*200*	*3.01*

[a] Groups are numbered from two- and seven-group levels e.g., subgroup E1.1 is the first subgroup in environment group E1. (see Fig. 2 for details)
[b] Code numbers identifying the locations in Fig. 2. Country names abbreviated as given in International Standards Organization (ISO:3166.1981)
[c] Mean day length in the first 30 days after germination
[d] IR = irrigated or + IR = supplemental irrigation given
[e] Means in parenthesis exclude value from Shandaweel
[f] Means in parenthesis exclude value from Myiangyan
[g] Managed environment. N.A., data not available

factors. Yield losses of 55–67% in susceptible sorghum cultivars due to anthracnose were recorded (Thomas et al. 1996). In contrast to African-type environments, the leaf diseases are not a major yield-reducing factor in Asian-type environments. In many of the Asian-type environments there is not enough leaf disease pressure to influence grain yield in sorghum.

The response plot of the yield of seven genotype groups across seven environment groups (E1-1 to E2-2) indicated certain patterns (Fig. 3). Genotype groups G4 and G7 expressed nearly no interaction with environment and therefore may be considered to have a stable yield across all E groups. However, G4 had a higher yield compared to G7. G1 showed a relatively higher yield in environment groups E1-3, while G2 showed a relatively high yield in E1-4. Both groups gave a poor yield in E1-5 indicating their poor adaptation to these E groups. G6 (IS 2284) showed a consistently lower yield for all E groups indicating its uniformly poor performance in all environments (Fig. 3). This genotype, IS 2284, is severely affected by anthracnose, both in the foliage and in the panicle. Anthracnose in the panicles and in the grains are known to severely reduce the grain yield in sorghum in West Africa (Thomas et al. 1996). G3 contained only one genotype, a high-yielding sorghum F_1 hybrid, CSH 11.

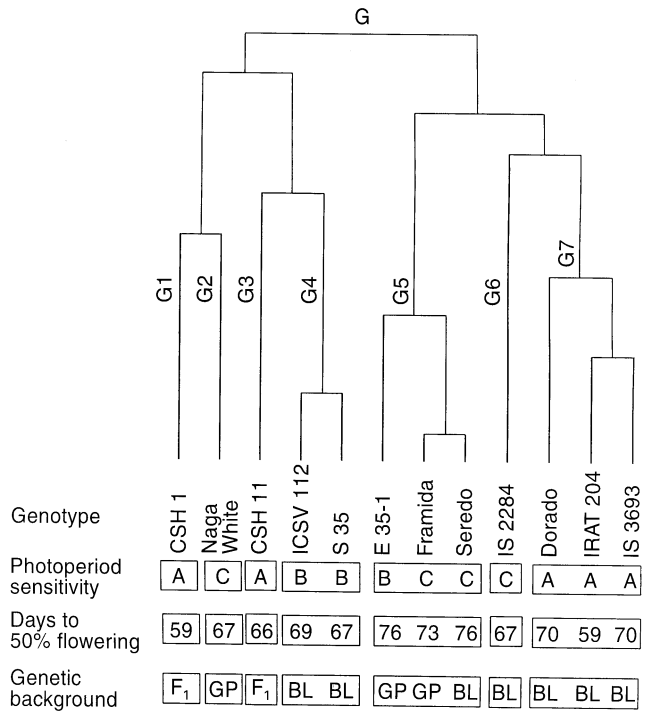

Fig. 1 Genotype dendrogram showing hierarchial classification of 12 genotypes using environment standardized grain-yield data from 25 locations. Photoperiod sensitivity: *A* = insensitive/weakly sensitive; *B* = moderately sensitive; *C* = highly sensitive. Genetic background: F_1 = hybrid; *GP* = germplasm; *BL* = breeding line

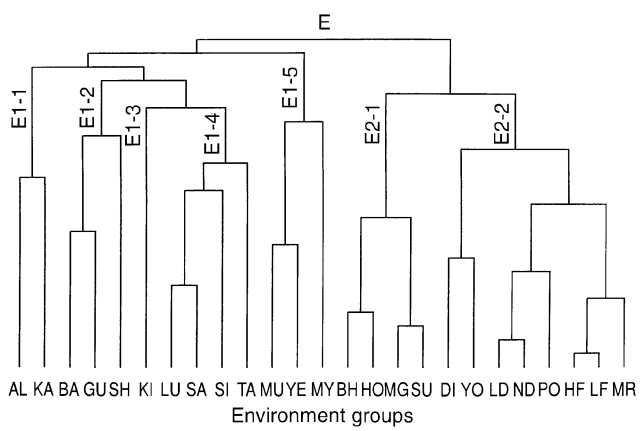

Fig. 2 Dendrogram showing hierarchical classification of 25 environments using standardized grain-yield data from 12 genotypes grown in them. Environmental names are: *AL* = Alupe, *KA* = Katumani, *BA* = Bagauda, *GU* = Guiring, *SH* = Shandaweel, *KI* = Kiboko, *LU* = Lucydale, *SA* = Samanko, *SI* = Sikasso, *TA* = Tara, *MH* = Mahlaing, *YE* = Yezin, *MY* = Myiangian, *BH* = Bhavanisagar, *HO* = Homes, *MG* = Managua, *SU* = Suphanpuri, *DI* = DIKhan, *YO* = Yousafwala, *LD* = long day in Patancheru, *ND* = normal day in Patancheru, *PO* = Pozarica, *HF* = high-fertility Patancheru, *LF* = low-fertility Patancheru, *MR* = Maradi

Among the 12 genotypes in this IMET, CSH 11 is the only one that showed a high yield in Asian-type environments, indicating its specific adaptation to these environments (Fig. 3). Its yield was intermediate in the African-type E groups E1-2, E1-3, E1-4 and E1-5. Strikingly, it showed the poorest yield in African-type environment E1-1 demonstrating its lack of specific adaptation to that environment. G5 showed the lowest yield in E2-1 and E2-2 (Fig. 3), an yield response opposite to that of G3. The genotype group is not well adapted to the Asian-type environment group.

Environmental classification reflected a strong correlation among environments within a group. For example, Samanko in Mali and Lucydale in Zimbabwe were grouped together ($r = 0.79$, $P < 0.001$), but they had no correlation with another environment group containing Bhavanisagar in India and Holmes in Syria. Similarly in Alupe and Katumani in Kenya, the African-type environments were grouped together ($r = 0.32$, $P < 0.05$) but had a strong negative correlation with the Asian-type environment group that contained Patancheru in India ($r = -0.38$, $P < 0.01$).

The results of ordination analysis of this IMET are presented in the biplot (Fig. 4) as suggested by Gabriel (1971) and Kempton (1984). The first two vectors in the biplot explained 59% of total SS of the GE. The environment vectors covered a wide range of Euclidean space indicating that the 25 environments represent a super-population of widely different environments, which agrees with the fact that they cover a wide range of latitudes from 20°S to 45°N.

The angles between vectors in a biplot are useful measures in interpreting similarities between environments (Basford et al. 1996). The more acute the angle between any two vectors, the more strongly they indicate a strong positive correlation of genotypic yield among environments. These environments would then discriminate genotypes in a similar fashion. The environment vectors making an angle of 180° demonstrate exactly the opposite type of discrimination among genotypes, whereas environment vectors at 90° indicate that there is no correspondence between the discrimination among genotypes in these environments. The following results and discussion are based on these interpretations of the biplot.

The maximum angle among the vectors of Asian-type environments is well below 90° corresponding to environments SU and MR in Fig. 4. This suggests that these environments tend to discriminate genotypes in a similar manner. The genotype CSH 11 was the top-yielding genotype in 9 out of 12 Asian-type locations, while Seredo was the lowest-yielding genotype in 10 out of 12 of the Asian-type environments. The African-type environments did not show the same degree of closeness as the Asian types, with TA and KA making an angle of more than 90°. If we consider African-type environments without Katumani, the remaining environments tend to discriminate among genotypes in similar fashion. Genotype CSH 11 was the lowest-yielding and Seredo was the highest-yielding genotype in Alupe and Katumani. The high-altitude Katumani environment behaves quite distinctly.

Table 3 Genotype × environment data on mean grain-yield (t ha^{-1}) of 12 sorghum genotypes tested in 25 locations

Genotype	Location[a]												
	AL	KA	KI	SA	SI	TA	LU	BA	GU	SH	YE	MY	MH
CSH1	2.76	1.60	1.82	2.74	2.75	0.25	0.92	4.86	3.41	7.64	0.48	0.31	0.57
CSH 11	0.81	0.59	1.11	2.09	2.18	0.32	0.56	3.93	3.91	5.79	4.64	0.32	2.98
E 35-1	2.26	1.82	1.11	1.64	1.49	0.02	0.45	5.09	3.33	7.67	4.44	0.39	2.69
ICSV 112	1.90	1.12	1.58	1.83	2.19	0.29	0.60	4.80	3.61	6.85	4.63	0.55	4.50
Framida	1.78	1.80	1.28	1.83	2.66	0.36	0.14	4.32	3.13	4.31	4.13	0.78	1.78
IS 2284	1.13	1.77	0.95	1.09	1.08	0.12	0.50	3.30	2.31	5.78	1.28	0.15	0.74
Seredo	2.81	2.47	1.46	1.82	3.46	0.10	0.31	3.81	2.54	4.62	4.05	0.75	3.66
Dorado	1.88	2.22	0.72	1.69	2.22	0.32	0.31	3.83	2.30	7.43	1.87	0.07	2.21
IRAT 204	0.83	1.49	1.67	2.05	2.24	0.22	0.50	4.12	3.12	5.67	1.69	0.75	2.76
N White	1.68	2.33	1.31	3.11	4.44	0.55	1.21	4.66	3.17	5.49	1.57	0.32	1.50
S 35	1.92	1.46	1.06	1.97	1.64	0.54	0.76	4.81	3.35	9.31	3.50	1.09	3.90
IS 3693	0.00	1.42	1.06	1.53	2.12	0.19	0.17	3.58	1.76	4.19	2.26	0.60	1.41
Mean	1.646	1.70	1.26	1.95	2.37	0.28	0.53	4.26	2.99	6.23	2.88	0.52	2.39
$LSD_{5\%}$	0.638	1.097	0.477	0.530	1.030	0.29	0.50	1.51	1.16	0.99	1.27	0.46	0.86

[a] Details of location and country are given in Table 2

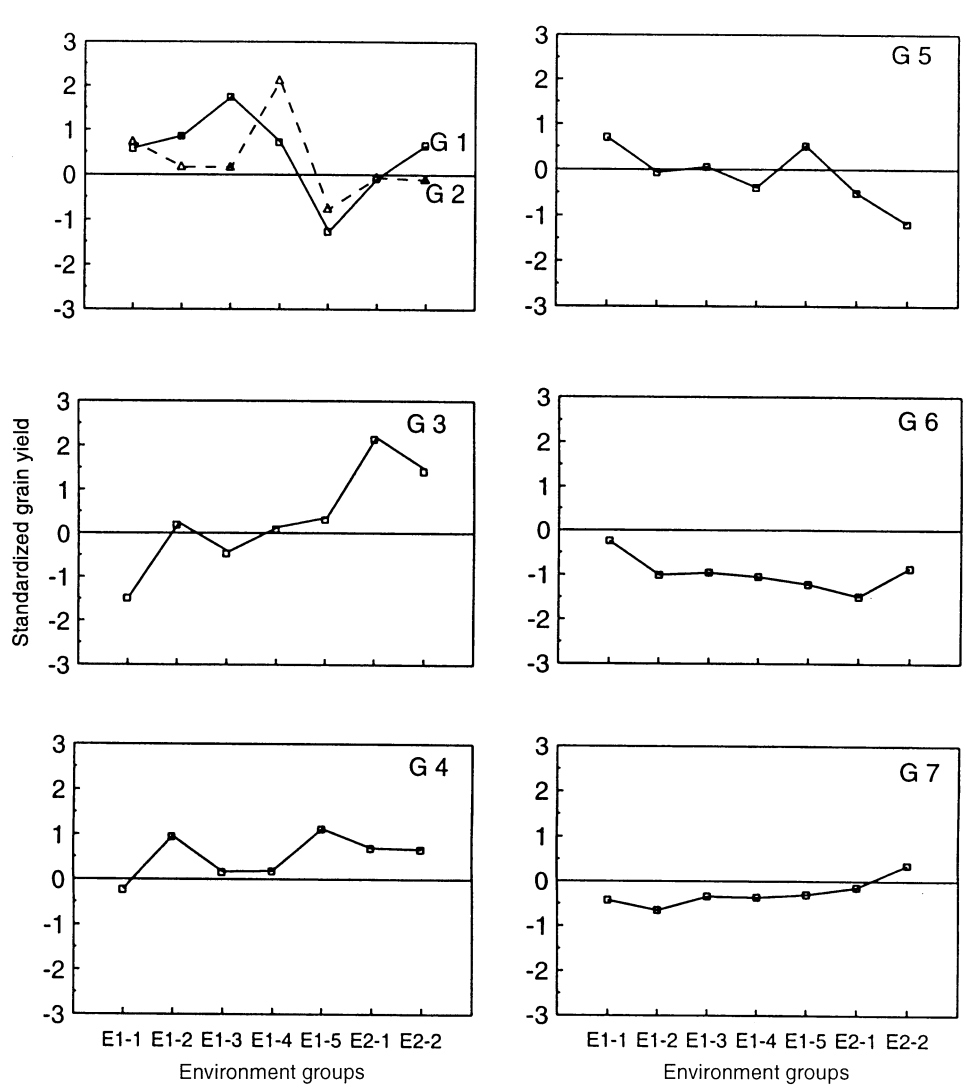

Fig. 3 Response plot of seven genotype groups over seven environment groups. Details of genotype and environment groups are given in Tables 1 and 2 respectively. Grain yield was standardized as suggested by Fox and Rosielle (1982)

Table 3 Continued

Genotype	Location[a]												Mean
	MR	DI	YO	PO	ND	LD	HF	LF	MG	SU	BH	HD	
CSH1	2.04	2.29	4.29	3.52	4.50	4.10	4.32	3.80	3.29	4.72	1.81	1.89	2.82
CSH 11	1.70	3.13	3.74	5.33	6.51	6.69	6.80	4.86	3.97	7.49	6.80	4.26	3.65
E 35-1	0.14	1.40	0.76	2.68	2.28	1.28	1.07	1.52	2.23	3.47	2.76	1.19	2.13
ICSV 112	1.18	2.00	4.75	4.36	5.66	5.62	4.14	3.34	3.63	5.95	4.43	3.00	3.31
Framida	0.34	0.77	0.58	2.12	1.80	1.17	0.77	1.16	2.32	4.68	2.53	1.30	1.91
IS 2284	0.88	1.11	1.11	2.58	2.63	0.58	1.00	1.95	1.45	2.06	1.85	0.81	1.53
Seredo	0.37	1.29	1.69	1.84	0.93	0.16	0.33	0.66	2.38	4.66	3.27	1.09	2.02
Dorado	1.35	1.33	2.43	3.54	4.82	5.13	4.99	3.62	2.80	5.22	4.82	2.17	2.78
IRAT 204	1.81	2.25	3.69	3.66	3.09	2.78	4.21	3.86	2.45	4.57	2.95	1.85	2.58
N White	0.61	1.08	2.33	4.60	4.73	3.44	2.53	2.91	2.84	5.53	2.91	1.28	2.64
S 35	1.74	1.48	2.48	6.20	5.39	3.96	5.16	3.91	3.06	5.00	4.18	2.28	3.20
IS 3693	1.45	1.50	3.40	3.80	4.68	4.74	4.36	3.65	2.04	3.21	2.78	1.69	2.30
Mean	1.21	1.64	2.60	3.68	3.92	3.30	3.30	2.94	2.72	4.71	3.42	1.90	
$LSD_{5\%}$	0.90	0.58	1.15	0.73	0.81	0.87	0.52	0.71	0.68	0.99	1.30	0.16	

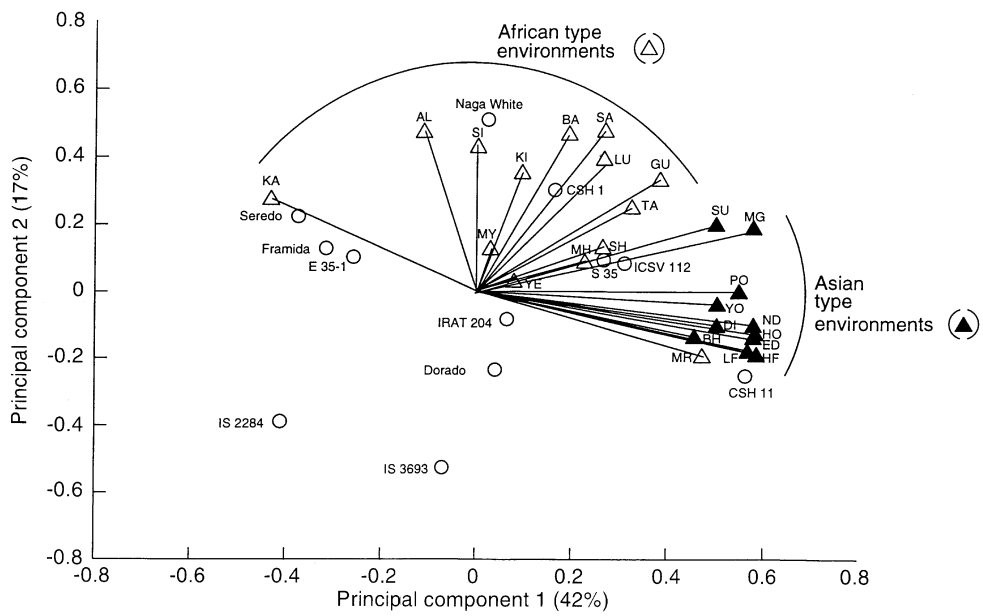

Fig. 4 Biplot for principal components 1 and 2 obtained from the ordination of environment standardized grain-yield data of 12 sorghum genotypes in 25 environments. The 25 environments are indicated as vectors drawn from the origin. Abbreviations of environment names are expanded in Table 2 and genotypes are indicated by their names

On average, the angle between Asian- and African-types of environments tends towards 90°, which suggests that these tend to be two distinctly independent groups of environments in discriminating among genotypes. It will be interesting to see whether this mega-grouping is repeatable over years.

The environment vector for Katumani (KA) in Africa, made an angle of nearly 180° with the majority of Asian environments. The genotype discrimination at this environment was therefore expected to be almost opposite in direction to that of Asian-type environments. For example at Katumani, the top-yielding entry was Seredo and lowest genotype was CSH 11 (Table 3), whereas the ranking of these genotypes at many Asian-type environments was reversed.

The genotypes ICSV 112 and S 35 that are closer to the origin in the biplot are average in their performance across environments. ICSV 112 is known for its wide adaptation.

The position and perpendicular projection of genotype points onto an environmental vector (Kempton 1984) can be used to identify a genotype(s) having specific adaptation in that environment. The genotypes that are farther along the positive direction of the

vector tend to give higher yields, and are better adapted in that environment. Thus the genotype CSH 11 is well adapted to Asian-types of environments and the genotype CSH 1 to certain African environments (AL, KI, SA, and SK). The G5 group, comprising Framida, Seredo and E 35-1, is well adapted to Katumani but poorly adapted to Asian-types of environments.

Conclusion

Pattern analysis permitted a sensible and useful summarization of this GE data set and assisted in examining the natural relationships and variations in genotype performance among various environmental groups. It has also assisted in the structuring the sorghum testing environments leading to the identification of the existence of two mega-environment groups – Asian- and African-types. Within these mega-environment groups, several sub-environment groups were also identified. The environments within the Asian mega-environment tended to be closer in the biplot indicating that they discriminate among these sorghum genotypes similarly. This suggests that it may be possible to reduce the number of sorghum testing environments and thereby economize on the conduct of IMETs. In contrast, the environments within the African mega-environment were widely separated, suggesting the need to use more testing environments to evaluate genotype adaptation.

In the majority of IMETs, there is a ubiquitous presence of GE interaction. Eisemann et al. (1990) and Cooper et al. (1996 b) argued that there could be three ways to handle the GE interactions: to ignore, avoid, or to exploit them. In most of the IMETs, ignoring the GE interaction is not a practical strategy, and therefore there is a need to accommodate it. If the GE interaction is to be managed by avoiding it, there is a need to classify the testing environments into sub-environments in which the genotype discrimination is similar. Exploiting the GE interaction depends on its nature, especially its repeatability within the target population of environments (Baker 1988; Cooper et al. 1993). With repeatable GE interaction, it is possible to economically structure the IMETs. The results of the present study suggest the existence of two-mega environments in this IMET. PA is applied to this sorghum IMET as a research and methodological tool and the results presented here are preliminary in nature. The repeatability of the pattern revealed in this IMET needs to be established over a number of years before this information can be used with confidence to structure the sorghum IMETs.

Acknowledgments Several national program scientists conducted the IMET at various locations and we gratefully acknowledge their valuable cooperation in generating data for this analysis.

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