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Open Access Journal of Agricultural Research
ISSN: 2474-8846

Stability in Advanced Gezira Population of Sorghum (*Sorghum Bicolor (L.) Moench*) at Drought Porne Environments in Sudan

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Research Article
Volume 7 Issue 2
Received Date: June 27, 2022
Published Date: July 19, 2022
DOI: 10.23880/oajar-16000288

Abstract

In Sudan, grain sorghum (*Sorghum bicolor (L.)* Moench), is the most important cereal crop, in terms of total acreage, production and consumption. One hundred and twenty S1 families were taken at random from an advanced random mating Gezira sorghum population (G S P^{-1}) developed and improved for six cycles using S1 family selection, at Rain-fed Crop Research Centre for Arid and Semi-Arid areas (RCRCASA) in the University of Gezira, Wad Medani Sudan. The study was conducted during two seasons (2004-2005) to study genetic variability in the population (GSP^{-1}) at four rain-fed areas in Sudan namely; Gedarif University farm at northern Gedarif environment (2004), Gedarif Research Station at northern Gedarif environment (2005), Rahad Scheme rain-fed at marginal Gedarif environment (2004) and Kasamoor North east Gedarif (2005). The design used was a modified Randomized Complete Block Design (RCBD) with two replications nested within six blocks. Stability was estimated for the 120 families yield (Kgh^{-1}). The combined analysis over environments revealed significant differences between environments, which indicated that four environments are contrasting for evaluating the genotypes. In average over environments the genotypes have shown G×E interaction was not significant for yield, indicating relative ranking of the genotypes remained constant and yield was stable over all environments. The mean was1448Kgh^{-1}. The Additive Main Effect and Multiplicative Interaction (AMMI) stability analysis with the first principal components (PCA1) axes for grain yield identified stable families as the families with a lower absolute PCA1 score which were 101, 95, 93, 96, 94, 103, 97, 102, 99, 100, 104, 98 respectively, would produce a lower absolute GE interaction effect and would have a less variable yield across the four Gedarf studied environments. These could provide a good source for sorghum improvement in Gedarif rain-fed area.

Keywords: Drought Porne Environments; Grain Sorghum; Genotype x Environment

Abbreviations: AMMI: Additive Main Effect and Multiplicative Interaction; PCA: Principal Components Analysis; GSP: Gezira Sorghum Population; RCRCASA: Rain-fed Crop Research Centre for Arid and Semi-Arid; SAS: Statistical Analysis System; GE: Genotype x Environment; GEI: Genotypes x Environment Interaction.

Introduction

Ninety percent of the world's area cultivated to sorghum is in the developing countries, it is cultivated in the dry and hot lowlands [1]. Low soil fertility, poor stand establishment, and a highly unpredictable drought stress pattern are major

production constraints in these areas. The local farmers usually do not have access to irrigation facilities or fertilizer stocks and are totally reliant on the adaptability and yield stability of their rain-fed crop varieties.

Adaptedness to extreme and variable stress environments may be improved by growing hybrids and/or population genotype mixtures, thereby strengthening individual and/or population buffering mechanisms [2,3]. However, only limited knowledge is available about the effects of population buffering, and their interaction on the performance of sorghum grown under severe, unpredictable stress conditions. The present study was, therefore, designed to study: The stability from G×E interactions on advanced Gezira random mating sorghum population (G S P-1) under rain-fed conditions of Sudan.

Materials & Methods

Experimental Material

One hundred and twenty S1 families were taken at random from an advanced random mating Gezira sorghum population(G S P-1) developed and improved for six cycles using S1family selection, at Rain-fed Crop Research Centre for Arid and Semi-Arid areas (RCRCASA) in the University of Gezira, Wad Medani Sudan. The experiments were conducted during two seasons (2004-2005) at four rain- fed environments namely; Gedarif University farm at Gedarif northern marginal environment (200-300 mm) in 2004, Rahad rain-fed area (300-400mm) in 2004, Gedarif Research Station at northern Gedarif in 2005 and Kasamor at Gedarif middle environment (500-600mm) in 2005. One hundred and twenty S1 families were taken at random from an advanced random mating Gezira sorghum population (G S P-1); each family was grown in one row 5.0 m long, 0.6 m between rows and 0.2 m within row spacing. After 3 weeks from sowing, plants were thinned to 2 plants/hole. Weeds were controlled manually when necessary. No fertilizer or other inputs were added. At harvest, a 3.0 m length in the middle of each row was marked as experimental unit and all data were then based on 3.0 m of row length. Harvesting and threshing were done manually.

Experimental Layout

The design used in this study was a modified randomized complete block (replications-in-block) design; the hundred and twenty S_1 families were divided into 6 sets of 20 families each. Each block contained two replications of the same set from the population. Blocks were assigned at random, and replications were assigned at random within each block. The 20 families, representing a group from the population, were assigned at random to each replication. A modified randomized complete block (replications-in-block) design has been used because it was more efficient than a blocks-in-replication design for controlling the experimental error and it allows loss of whole blocks only, if necessary, rather than the loss of whole or an entire replication.

Parameters Studied

i. Days to 50% flowering (Bloom): The number of days from planting to the date when approximately 50% of the plants in the row were at half-bloom (had their flowers open).

ii. Grain yield (kgh^{-1}): Panicles were harvested by hand from a three-meter section in the center of each row, where total panicle weight and total grains weight were measured and used to estimate grain yield and threshing percent Weight of actual grain yield was taken to estimate total grain yield in kgh^{-1}. Harvested area = 3.0 x 0.6 =1.8 m^2.

$$\text{Estimated grain yield } (kgh^{-1}) = \frac{\text{Yield from harvested area} \times 10000}{1.8 \times 1000}$$

iii. Plant height (cm): The average of heights, taken at random from each family was measured from the soil surface base of the plant to the tip of the panicle for representative plants in each plot.

Statistical Approaches

The least squares method was used in genetic variability analyses, utilizing the Statistical Analysis System (SAS) as outlined by Jane T Helwig, et al. [4], while the IRRISTAT software was used to conduct the AMMI analysis [5] for stability or G×E interaction. According to Gauch, et al. [6] and Nichit, et al. [7] as in the following:

Analysis of variance of data for each trait combined over different environments: A combined analysis for each trait in each environment was performed. The additive linear model assumed was: $Y_{ijkl} = u + L_i + b_j + Lb_{ij} + r_{ijk} + f_{il} + Lf_{ijl} + e_{ijkl}$. Where:

Yijkl: the observation on the l^{th} family at the k^{th} replication within the i^{th} block in the i^{th} location (environment).

U: the overall mean of all families.

L_i: the random effect associated with the i^{th} environment; I = 1, 2,…4.

b_j: the random effect associated with the j^{th} block; I = 1,2,…,6.

Lb_{ij}: the random effect of the interaction between the i^{th} environment and j^{th} block.

r_{ijk}: the random effect of the k^{th} replication within the j^{th} block in the ith environment.

f_{il}: the random effect associated with the l^{th} family in the j^{th} block .

L_{fijl}: the random effect resulting from the interaction of the l^{th} family in j^{th} block with the i^{th} environment.

e_{ijkl}: the random error effect associated with the plot containing the l^{th} family in the k^{th} replication within the j^{th} block in the i^{th} environment.

As mentioned, the various effects in the model were computed as deviations about the mean within which they were nested, so that the sum of the deviations about the mean adds to zero. The form of the analysis of variance pertinent to the assumed model is given in Table 1.

Sources of Variation	Symbol df	df	Days to flowering	Yield Kgh^{-1}	Plant height cm^{-1}
Environ.(E)	e-1	3	44951***	149372712***	3077***
Block(B)	b -1	5	60.7***	1270447***	4127***
EXB	(e-1) (b-1)	15	22.2***	3180420***	296.5**
Replic./B	e b	24	16.9***	506770***	837.1***
Families (F)/B	b(f-1)	114	11.7***	51671***	343.3***
G(EXB)	b(f-1)(e-1)	342	5.7 *	25837 n.s	164.2**
Residual	(r-1)(f-1)be	456	4.83	23595	131.6

*, **, *** are the levels of significance 0.05, 0.01, and 0.001 respectively.

Table 1: Mean squares for the combined analysis of variance for three traits in120 families sorghum population evaluated at four low input areas in Sudan.

The coefficient of variation (CV) was calculated as: C.V = (Me ^{½})/overall mean x 100.

Since the design had nested features, the effects of the parameters in the model were computed as deviations about the next mean up in the hierarchy, i.e., the block effect was computed as the deviation of the individual block from the grand mean, replication effect as the deviation of the replicate value from the block mean in which the replicate was located, and the family effect was calculated as the deviation of the observed family value from the block mean in which it is nested.

Genetic differences among families nested with blocks were tested by the null hypothesis: Ho: $\sigma^2_{f/b} = 0$.

The interaction between the families and environments:

It was computed using the F-test as:

F: $M_{sf/b}/M_e$ with b (s-1) (f-1), s b (f-1) (r-1) degrees of freedom.

Where: s is for site (environment).

The various parameters and their SE's for the combined environments data from each of the populations were estimated as follows:

Familles X Environment Interactions Variance

$$\sigma'^2_{sf/b} = (M_{sf/b} - M_e)/r, \text{ and its SE}$$

$$SE(\sigma'_{sf/b}) = \left[\left(\frac{1}{s^2r^2}\right)\left(\frac{2M^2_{sf/b}}{b(f-1)(s-1)+2} + \frac{2M^2_e}{s\,b(f-1)(r-1)+2}\right)\right]^{1/2}$$

Stability Analysis

Combined analysis of data generated from four production environments (Combination of location and years) was carried out for estimation of stability parameters for grain yield.

The Additive Main Effect and Multiplicative Interaction (AMMI) Analysis

It was carried out to show the stability and pattern of adaptation sorghum families to the four environments. AMMI analysis fits additive effects due to genotypes (G) and environments (E) and by usual additive analysis of variance procedure and then fits multiplicative effects for genotype × environment interactions (GE) by principal components analysis (PCA). The IRRISTAT software was used to conduct the AMMI analysis [5] as in the following; Equation of AMMI model:

$$Y_{ij} = \mu + g_i + e_i + \sum \lambda_n \alpha_{in} \gamma_{jn} + R_{ij}$$

Where:

Y_{ij}: is the grain yield of the ith genotype in the jth environment.

μ: is the grand mean.

g_i: is the deviation of the genotype mean from the grand mean .

e_i: is the deviation of the environment mean from the grand mean.

λ_n: is the eigenvalue of the nth PCA.

α_{in} and γ_{jn}: are the genotype and environmental interaction principal components eigenvectors(PCA_g and PCA_e, respectively) for axis n .

N: is the number of IPCA retained in the model.

R_{ij}: is the residual.

Environmental and genotype PCA scores are expressed as unit vector time the square root of λn. The multiplicative part of the model is obtained by PCA (α_{in} and γ_{jn}). The principal advantage of the AMMI is that the interaction can be modeled by only one or two PCA-axes.

To analyze genotype-environmental interaction and adaptation graphically, AMMI –bi-plot with the PCA1 scores was plotted against the mean yield (main effect). Genotypes or environments that appear almost on a perpendicular line have similar means and those that fall almost on a horizontal line have similar interaction patterns. Genotype (or environments) with large PCA1 scores (either positive or negative) have high interactions, whereas Genotypes (or environments) with PCA1 scores near zero have small interactions. To further explain the GE and adaptation a biplot between the PCA1 scores and PCA2 scores was drawn. The AMMI expected yield of any genotype and environmental combination can be calculated from the biplot as indicated by Zobel, et al. [8]. The interaction part is simply the genotype PCA1 score times the environmental PCA1 score. Genotype and environments with PC1 scores of the same sign produce positive interaction effects, whereas combinations of PC1 scores of opposite signs have negative interactions.

Results and Discussion

Stability is the measurement of phenotype-environmental interactions [9]. A large phenotype x environmental interaction (GEI) variation usually impairs the accuracy of the yield estimation and reduces the relationship between genotypic and phenotypic values. However, the predictive accuracy of yield estimate is achieved by improving experimental field technique, and/or better statistical analysis for GE partition and interpretation as reported by Nachit, et al. [7]. Hence, the AMMI analysis with its merits is used for stability. For example partitioning and interpretation of GE interaction are generally based on linear regression techniques or multivariate analysis .Because linear regression techniques show several deficiencies, multivariate analysis techniques such as the additive main effect and multivariate interaction (AMMI) procedure with prediction assessment can be powerful in analyzing multi-location trials and explaining GE interactions than linear regression models. AMMI models is more effective in Partitioning interaction SS than the linear regression techniques resulting in increased precision equivalent to the number of replications by a factor of two to five. Such gain may be used to reduce cost by reducing the number of replications, to include more treatments in the experiment or to improve efficiency in selecting the best genotypes [7,10].

The Additive Main Effect and Multiplicative Interaction (AMMI) Analysis

The parametric approach such as mean yield over-environments, genotypic coefficient of variability, genotype variance, the ecovalence, Shukla's [11] stability variance (interaction variance) and Eberhart and Russell [12] stability parameters(regression coefficient or slope and deviation from regression) give only the individual aspect of stability but cannot provide an overall picture of the responses. So it is difficult to reconcile all of these assessments into a unified conclusion because genotype response to environments is multivariate. Consequently, nonparametric approach (multivariate) has been proposed to overcome univariate problems associated with parametric approach [13]. Multivariate analysis such as AMMI analysis groups genotypes or environments in a qualitative manner according to their similarity of performance rather than quantitative manner of the stability parameters. In AMMI analysis the genotype response to environment is multivariate, AMMI analysis involves the clustering analysis to classify genotypes under the most adapted sites for them depending on the AMMI principal components scores similar signs in genotypes and sites (genotypes having PCA scores < 0 responded positively to environments, Those having PCA scores < 0 and the reverse is true for families that had PCA scores > 0). Also AMMI models integrate the usual additive analysis of variance (ANOVA) for the additive effect with the principal component analysis (PCA) for the multivariate effects [6,7].

AMMI analysis of variance model: In this study, AMMI analysis of variance indicated that grain yield was significantly affected by environment (E), genotype (G) and genotype x environment interaction (GE), which explained 86.7%, 2.4% and 10.9% of the total variation (E + G + GE), respectively (Table 2). This result indicated that environment component represented the largest amount of total variation, while variations due to genetic component and GE interaction were considerably low. The partitioning of GE interaction through AMMI model analysis revealed that the four multiplicative terms first (PCA_1), second (PCA_2) and third (PCA_3) principal components, were significant factors that captured 81.3%, 9.8 % and 8.9 % of variation due to GE interaction sum of squares, respectively. Together they accounted for 100% of GE interaction sum of squares (i.e. PCA_1 represented 8.9 % out of 10.9% of total sum of squares). Hence, most of the variation was explained by the first principal component (PCA_1) and it was the most informative as shown in Table 3.

Source of variation	Df	SS	MS	Efficiency (%)
Genotypes (G)	119	6121360	51440	2.4
Environment (E)	3	224059000	74686400	86.7
Families×environment interaction (GEI)	357	28271200	79191 N.s	10.9(sst)=100(GEI)
Families × environment Regression	119	6469400	54365**	22.9
Deviations	238	21801800	91604 N.s	77.1

*, **, ***are the levels of significance 0.05, 0.01 and 0.001 respectively.

Table2: AMMI analysis of variances of environment (E), genotypes(G) and genotypes x environment interaction(GEI) on grain yield (kgh^{-1}).

Source of variation	Df	SS	MS	Efficiency (%)
Genotypes (G)	119	6121360	51440	2.4
environment (E)	3	224059000	74686400	86.7
environment interaction (GEI)	357	28271200	79191	100
1st AMMI principal component (PCA1)	121	22974800	189875***	81.3
2nd AMMI principal component (PCA2)	119	2782530	23383	9.8
3rd AMMI principal component (PCA3)	117	2513890	21486	8.9
Total	479	258452000	539566	

Df, degree of freedom; SS: sum of square; MS: mean square, Efficiency%, percentage of GEI sum of squares, and *** significance at 0.001 probability level, N.s, not significant.

Table3: AMMI analysis of variances of environment (E), genotypes (G) and genotypes x environment interaction (GEI) on grain yield (kgh^{-1}) and the partitioning of GEI into AMMI scores.

Non-significant differences among families x environments interaction indicating the stability of population as a whole over the four targeted environments, whereas the G x E interaction partitioning into AMM1 principle-components has shown highly significant differences ($p \leq 0.01$) due to APC_1 that is 81.3% out of GEI, (which is equal 8.9% SStot) as in Table 3.

A large variation among the studied genotypes for grain yield and their interaction to the environment was determined. According to the highest average grain yield (yield potentialities) the best environment was KAS (2180.4) that ranked 1st followed by Rahad environment (1967.2), GRS environment (1194.8) and the lowest environment in yield was UG that obtained 449.47 kg h^{-1}. Based on AMMI biplot G and E having PCA values close to zero have small interaction effects, whereas those having large positive or negative PCA absolute values largely contribute to GE interaction [14,15]. Hence UG was the least interactive among the four environments, while Rahad was the most interactive, because environment in Rahad exhibited the largest absolute value of PCA score (+0.9082460), whereas the smallest score was shown by UG (-0.3451480) as shown in Table 5.

This indicated the relative ranking of genotypes were more stable at UG than at Rahad, making it too difficult to recommend a genotype for Rahad. This may be due to the fact that Rahad area was more marginal. Also a large variation among the studied families for grain yield kg ha^{-1} was explained in Table 4. Where family MD90 (99), obtained 1604.9 as highest yield (it ranked 1st in order of the total 120 families in the population) and SB191(116) has got 977.4 as lowest yield (among selected families) and it ranked number 120 in order (of the total 120 families in the population) Tables 4-6.

Family serial. No.	Family Code no.	Predicted Mean	Duancan LSD test	Ranked Order	SE±
99	MD90	1604.9	1	1st	141
98	MD395	1603.1	11	2nd	141
97	MD68	1595.2	111	3rd	141
94	MD106	1592.9	1111	4th	141
107	SB112	1585.4	11111	5th	141
96	MD415	1581.5	111111	6th	141
93	MD122	1576.4	1111111	7th	141
100	MD 412	1573.6	11111111	8th	141
108	SB33-A	1571.5	111111111	9th	141
109	SB50	1567.1	11111111111	eleven	141
95	MD7	1564.5	1.10E+15	16th	141
110	SB196	1549.8	1.10E+25	26th	141
106	SB161	1543.9	1.10E+35	35th	141
104	SB186	1519.6	1.10E+44	45th	141
103	SB176	1489.4	1.10E+46	47th	141
101	SB74	1482.5	1.10E+47	48th	141
102	Ed133	1481.6	1.10E+48	49th	141
111	SB4	1438.4	1.10E+62	63th	141
105	SB146	1427.9	1.10E+69	70th	141
113	SB45	1424.4	1.10E+72	73th	141
112	SB22	1421.5	1.10E+74	75th	141
114	SB180	1338	1.10E+102	103th	141
115	SB78	1327.4	1.10E+113	114th	141
116	SB191	977.4	1.10E+119	120th	141
Environments	Kas	2180.4	1	1si	25.7
	Rahad	1967.2	11	2nd	25.7
	GRS	1194.8	111	3rd	25.7
	UG	449.47	1111	4th	25.7

Table 4: Predicted mean and multiple comparisons for the high yielding families combined over four environments.

fam.serial No.	Fam.Code	mean	Fam.order	Cp1
101	SB74	1482	1st	-5.837
95	MD7	1564	2nd	-6.286
93	MD122	1576	3rd	-6.544
96	MD415	1582	4th	-6.934
94	MD106	1593	5th	-6.955
103	SB179	1489	6th	-6.98
97	MD68	1595	7th	-7.036
102	Ed133	1482	8th	-7.11
99	MD90	1605	9th	-7.644
100	MD412	1574	10th	-7.7
104	SB186	1520	11th	-7.804
98	MD395	1603	12th	-7.827
105	SB146	1428	13th	-9.13

112	SB22	1422	14th	-12.49
109	SB50	1567	15th	-13.27
106	SB161	1544	16th	-13.43
111	SB4	1438	17th	-13.69
108	SB33-A	1572	18th	-13.82
114	SB180	1338	19th	-14.57
113	SB45	1424	20th	-14.79
107	SB112	1585	21st	-15.27
110	SB196	1550	22nd	-15.55
115	SB78	1327	23rd	-17.15
116	SB191	977.4	24th	-44.76
	Envir.code			
	UG	2180.4	1st	-0.345148
	GRS	1194.8	2nd	0.45533
	KAS	2180.4	3rd	-0.512043
	Rahad	1967.2	4th	0.908246

Table 5: Stability ranking of the selected families and the four environments according to 1st AMMI principal component (Cp1).

Fam.Code	mean	Slope	SE±	MS-TXL	MS-Reg	MS-dev	R**2 (%)	Cp1	Cp2	Cp3
Ed378	1576	1.253	0.174	77644	119560	56686	51	-6.544	3.25	-2.52
Ed52	1593	1.279	0.182	89726	145654	61761	54	-6.955	3.46	-3.31
Ed150	1564	1.25	0.165	72845	116396	51070	53	-6.286	3.01	-2.98
Ed313	1582	1.277	0.182	89054	143229	61968	54	-6.934	3.23	-3.49
Ed179	1595	1.297	0.181	95694	165147	60967	58	-7.036	3.4	-4.39
Ed105	1603	1.326	0.201	119212	197860	75388	57	-7.827	4.18	-4.04
Ed346	1605	1.327	0.194	113491	199405	70534	59	-7.644	3.97	-4.64
Ed95	1574	1.317	0.199	111815	187794	73825	56	-7.7	4.69	-3.02
Ed63	1482	1.152	0.21	69474	43407	82507	21	-5.837	-2.45	-4.71
Ed41	1489	1.235	0.238	104930	102747	106021	33	-6.98	-1.5	-6.99
Ed86	1520	1.261	0.261	127120	127278	127041	33	-7.804	-1.4	-7.37
Ed147	1428	1.16	0.309	134431	47625	177835	12	-9.13	-1.06	1.09
Ed186	1544	1.332	0.423	291028	205699	333692	24	-13.43	2.26	0.6
Ed180	1585	1.418	0.466	379115	325656	405845	29	-15.27	3.32	-0.79
Ed56	1572	1.373	0.424	309892	259476	335100	28	-13.82	1.25	-2.69
Ed214	1567	1.374	0.411	297245	261750	314992	29	-13.27	-2.65	-5.51
Ed355	1550	1.334	0.505	387312	208588	476673	18	-15.55	6.05	1.17
ED388	1438	1.161	0.493	318381	48557	453293	5	-13.69	-2.33	5.49
Ed418	1422	1.332	0.455	268392	32337	386420	4	-12.49	-5.74	1.25

Slope: slopes of Regression of families means on environmental index .Indicated slopes significantly different from the slope for overall regression, which is -20.48. **Ms-tx:** contribution of each family to interaction Means Squares. **Ms-Reg**: contribution of each family to Regression components of the families' x environment interaction. Interaction Components of **Ms-Dev**: Deviations from Regression**. R2**** (%): Squared correlation between residuals from the main effects model and the environmental index**. cp1, cp2, cp3**: 1st ,2nd and 3rd AMMI principal components respectively.

Table 6: Scores best families stability, regression and AMMI principal component.

The families from 93 to 116 were selected as superior from the total of 120 families population based on yield potential, because they ranked at the top and/or they have specific adaptability to certain environment over the others (Not adapted to other). Also some satisfied all the basis of stability measurements in comparison. Among the selected families family SB74 (101) revealed the smallest absolute PCA_1score (5.837), indicating its least variability in interaction, while SB196 (110) showed the largest score (15.55), pointing out its highest variability in interaction (Table 5). Hence, depending on high yield potentiality the high yielding families were MD90(99), MD395(98), MD68(97) and MD106(94) those ranked as the 1st four families, while the lowest yield was obtained by SB191(116) family that ranked 120th (Table 4). On the other hand depending on the AMMI residuals, additive effects and multivariate scores the families order for stability as flowing; SB74(101) -5.837, MD7 (95) -6.286, MD122 (93) -6.544, MD415 (96) -6.934, MD106 (94) -6.955, SB179 (103) -6.98, MD68 (97) -7.036, Ed133 (102) -7.11, MD90 (99) -7.644, MD412 (100) -7.7, 104(SB186) 7.804 and MD395 (98) -7.827 respectively (Table 5).

The AMMI cross site analysis: The AMMI cross site analysis of main and PCA1 effect of both G and E on yield explained that sorghum families having PCA scores < 0 responded positively (adapted) to environments, Those having PCA scores < 0, and the reverse is true for families those having PCA scores > 0 [16] in wheat. Hence the families with the lower PCA scores are the SB74 (101) -5.837, MD7 (95) -6.286, MD122 (93) -6.544, MD415 (96) -6.934, MD106 (94) -6.955, SB179 (103) -6.98, MD68 (97) -7.036, Ed133 (102) -7.11, MD90 (99) -7.644, MD412 (100) -7.7, SB186 (104) -7.804 and MD395 (98) -7.827 (Table 5). This indicates their least variability contribution in the GEI and therefore, they would have less variability across environments. These best families all responded positively or adapted to UG (-0.34518), Kas(-0.51204300), and negatively to Rahad (+0.9082460) and G.R.S (+0.4553300) as in Table 5.

AMMI biplot analysis: AMMI model is found to be the best predicting model, a graphical display of the GE interaction. PCA1 and their main effects should be useful for revealing favorable pattern in genotype response across environments [10]. The AMMI biplot of the main and PCA1 effects of both G and E on grain yield explained 98 % of the treatment sum of squares, with 2.4%, 86.7% and 8.9% due to genotype, environment and PCAI sum of squares, respectively (Table 3 and Figure 1). Wheat genotypes that had PCAI scoring > 0 responded positively (adapted) to environments, that had PCAI scoring > 0 (i.e., their interaction is positive) but responded negatively to environments that had PCAI scoring < 0 and the reverse applied for genotypes that had PCAI scores < 0 [16]. Consequently all the families from 93-116 responded negatively therefore, they are adapted to environments UG obtained -0.345 and environments KAS that got -0.512, (Their GE interaction with negative sign), but they responded negatively to environment Rahad that obtained + 0.908 and GRS which obtained + 0.456 Table 5.

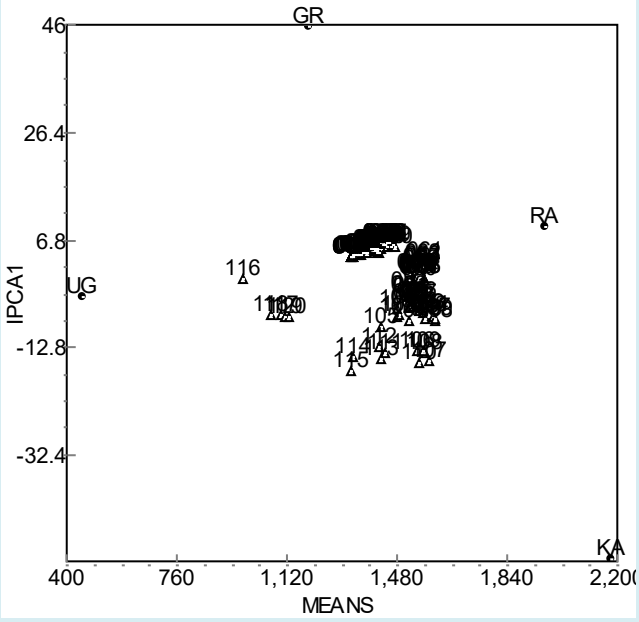

Figure 1: AMMI biplot of main and PCA1 effects of both families and environments on yield of 120 families sorghum population grown at four low input areas in Sudan.

Families are represented by values from 1-120, Environments are represented by letters.

The families with a lower absolute PCA_1 score such as 101, 95, 93, 96, 94, 103, 97, 102, 99, 100, 104 and 98 would produce a lower absolute GE interaction effect and would have a less variable yield across sites than families with a higher absolute PCA_1 score such as 116, 115 and 110 Table 5.

AMMI biplot of the first two principal component axes is a powerful way of detecting important sources of GE effects [8]. This analysis represents stability of the cultivars across environments in terms of principal component analysis. It is used to identify broadly adapted cultivars that offer stable performance across sites, as well as cultivars that perform well under specific conditions. In this study, the first two principal component axes (PCA1 and PCA2) in the ordination (biplot) analysis explained a large proportion of the variation 91.1% of the total GE sum of squares (Figure 2). The AMMI biplot displays similar genotypes or environments near to each other (have small vectors angles) and dissimilar items are farther apart (have large vectors angles). Accordingly, the environments UG with Rahad and Kas with GRS, as an example, were similar to each other in the way they

discriminate among genotypes (Figure 2). Environment UG and Rahad showed relative similarity (appeared near to each other) in the way they discriminate among genotypes. UG had the widest vector angles (appeared at far distant) from Kas and GRS, indicating its extreme dissimilarity from them. UG was noticed as a unique and the lowest yielding environment. On the other hand, family SB191 (116) appeared at a far distance from the other families and environments, reflecting the different characteristics of this family in that it had poor performance and consistently lower yielding than the average at all environments. In contrast the families SB4 (111), SB180 (114), SB45 (113) and SB22 (112), for example, showed similar performance across the production environments or appeared near to each other (Figure 2).

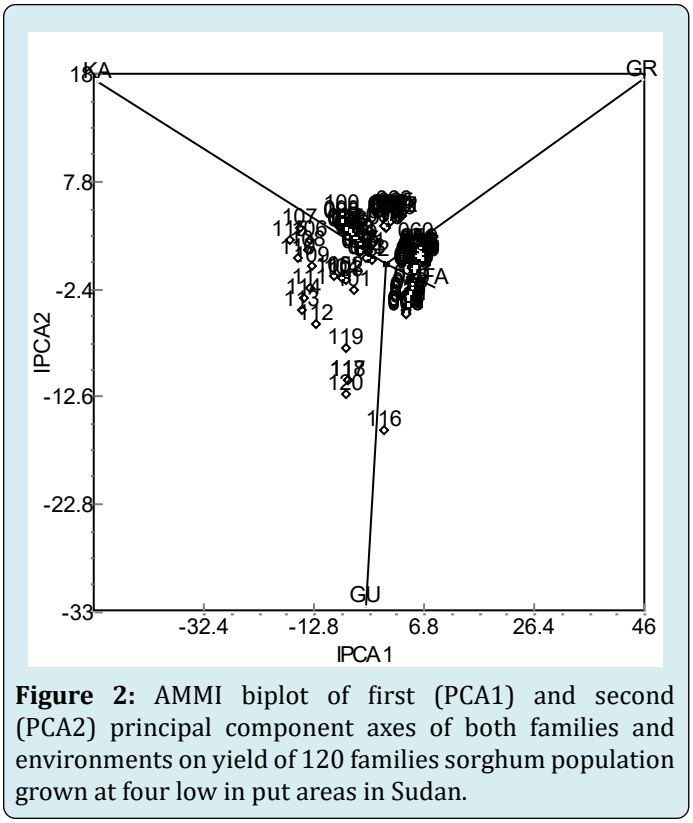

Figure 2: AMMI biplot of first (PCA1) and second (PCA2) principal component axes of both families and environments on yield of 120 families sorghum population grown at four low in put areas in Sudan.

Families are represented by values from 1-120, Environments are represented by letters.

The analysis of the genotype and environment parameters resulting from AMMI helps to describe the interaction effects of the genotypes and environments. On AMMI biplot, genotypes and environments having PCA values close to zero (near the origin) have small interaction effects, whereas those having large positive or negative PCA values (distant from zero) largely contribute to GE interaction [14,15]. Hence, the families SB4 (111), SB180 (114), SB45 (113) and SB22 (112) were the most interactive, while SB191 (116) was the least interactive. Entries yield relatively better in sites having PCA values of the same sign, but not in sites with opposite sign. Genotypes that are farther along in the positive direction of the environment vector are higher yielding and vice-versa [17]. Hence the family 119 was higher yielder than the family 116 (Figure 2). Acute angles between any two vectors indicate positive associations (i.e. they influence the genotypic relative performance in similar manner), 90˚ indicates negative associations [17]. Hence Rahad has positive associations with UG and GRS (due to acute angles between Rahad and each of them), whereas negative associations were detected between Rahad and Kas (angle > 90˚) as shown in figure 2. On the other hand, environment UG, KAS and GRS appeared at a far distance from the origin (large PCAI score); hence, they had large interaction effect, whereas Rahad had small interaction effects (Figure 2 and Table 5). Hence in this investigation, visual observations of AMMI biplot analysis enable to identify genotypes and testing environments that exhibited major sources of GE interaction as well as those that were stable. Similar results were reported in wheat by Thomason and Phillips [18].

Comparing the effectiveness of regression and AMMI analysis for analyzing GE interaction, it was found that PCAI in AMMI accounted for the GE sum of squares by 81.3%, while regression analysis accounted for GE by 22.9 % (Table 2). Hence, AMMI analysis was superior to the regression techniques in accounting more effectively partitioning of the interaction sum of square. The same results were reported in wheat [7,15,19]. Cornelius [20] showed that regression analysis and AMMI analysis with one PCA have the same model form, differing only in fitting procedure.

Conclusion

1. The breeding method followed in generating the current populations (recurrent selection) presenting cyclic improvement of population, has led to concentration of favorable alleles that increased the probability of extracting elite lines for variety development or parents for hybrids.
2. The statistical procedures used in this study (AMMI analysis) showed an effective GE analysis and provided agronomical meaningful interpretation of the data that were useful for performing mega-environment analysis. Therefore, such wide rain-fed areas could be subdivided into homogenous sub-regions that have similar interaction patterns and cultivar rankings, simplifying recommendations cultivar particularly in widely extending regions alike in Sudan rain–fed sector.
3. The results of AMMI analysis are useful in supporting the future breeding program decisions such as breeding for specific adaptations to target and selection of environments or test sites. Therefore the four targeted

environments area can be treated as one mega environment, and the best families can be used as foundation for released varieties for rain-fed areas and/or as superior genotypes for farther recombination.

4. The low magnitude of the genotype x environment interaction variance for yield observed during this study could be an indication of the adaptation of the population to targeted environments. This suggests that, although the populations were tested at areas which are classified as sub- marginal to marginal rainfall zone (of unpredictable stressed weathers), out of this population some genotypes would be expected to be adapted to many similar environments in Sudan.

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