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Stability Analysis in Dual Purpose Sorghum [*Sorghum bicolor* (L.) Moench]

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A B S T R A C T

The present investigation was under taken for 10 lines and 3 tester using line x tester mating design consisted of 46 entries including 10 lines, 3 testers, 30 hybrids and three checks *viz.*, CSV 23, CSV 27 and CSH25. These were evaluated in RBD with three replications during *kharif* 2015 in four environments created by using different spacing *viz.*, 22.5 x 5 cm (E_1), 30 x 10 cm (E_2), 45 x 10 cm (E_3) and 60 x 10 cm (E_4). The analysis of variance for L x T mating design in individual environment revealed significant differences between genotypes for most of the characters in most of the environments. The Bartllet test revealed homogenous error variance for plant height and ear head length. The pooled analysis revealed significant differences between the environments, genotypes, parents and crosses for both the characters. This indicates presence of significant variability for these characters. In 22 stable genotypes for plant height line L_4 and crosses L_2 x T_1 and L_4 x T_2 having b_i = 1 for rest of the 19 genotypes b_i neither deviating from zero nor from unity. Similarly, for ear

Introduction

Sorghum is predominantly self-pollinated crop endowed with a wide range of genetic variability due to its wide range of adaption and free gene exchange among various races. Careful selection of parents for hybridization is a key of success in any breeding programme. Some idea about the usefulness of parents may be obtained from their *per se* performance, breeding for wide adaption is important aspect in genetic improvement of crop plants. It is well known that a specific genotype may not exhibit the same performance in all the environments nor all the genotypes respond alike to a specific environment.

Such differential response of genotypes to varying environmental conditions reduces the agricultural production. Therefore, knowledge about behavior of genotypes in different

environment is essential for their recommendation and their further use in breeding programme. For this, it is desirable to see the impact of various environments on the sorghum genotypes in order to identify the parents and /or crosses for further utilization in breeding programme. *Sorghum bicolor* (L.) Moench (2n = 20), family poaceae is one of the most important crops in the world because of its adaptation to a wide range of ecological conditions, suitability for low input cultivation and diverse uses (Doggett, 1988).

Sorghum occupies fifth position after wheat, rice, maize and barley at world level, both in area and production. The crop is widely grown for food, feed, fodder, forage and fuel in the semi-arid tropics (SAT) of Asia, Africa, America and Australia. It occupies 58.20 m ha area in the world with an annual grain production of 68.87 m tones and productivity of 1535 kg/ha (FAO, 2015). In India, it covers about 5.82 m ha with an annual grain production of 5.39 m tonnes and productivity of 926 kg/ha (FAO, 2015).

The stability in the production is on account of availability of high yielding varieties and inputs. Maintenance of plant population in per unit area is very difficult. Buffering ability of the genotypes is the only way to cope up with the available space. Therefore, breeding for buffering ability is important aspect in genetic improvement of crop plants. Development of such a hybrid/variety, which gives a constant and desirable performance over wide range of spacing (Meena *et al*., 2018), is needed.

For this, it is desirable to see the impact of various spacing on the yield of sorghum genotypes and identification of genotypes having buffering ability. In view of the above facts, present investigation entitled **"**Stability Analysis in Dual Purpose Sorghum [*Sorghum bicolor* (L.) Moench]" has been planned and genotypes were evaluated during kharif, 2014 and *kharif*, 2015 at Instructional Farm, Rajasthan college of Agriculture, Udaipur to estimate stability of genotypes.V

Materials and Methods

The present investigation entitled Stability Analysis in Dual Purpose Sorghum [*Sorghum bicolor* (L.) Moench] was conducted at Instructional farm, Rajasthan College of Agriculture, Udaipur during kharif 2014 and *kharif* 2015.

Experimental site and condition

Geographically Instructional Farm is situated at 24° - 35' North latitude and 73° - 42' East longitude. The elevation of institution farm is 582.17 meters above mean sea level. The climatic conditions of the area represent subtropical condition with humid climate. The soil of experimental fields was clay loam, deep, well drained, alluvial in origin and having fairly good moisture holding capacity (Table 3.3).

Experimental material

On the basis of days to flowering and suitability for dual purpose 36 lines were received from ICRISAT. After evaluation at this station 10 lines were identified on the basis of nicking of flowering. Three testers were identified on the basis of availability of restorer gene and past performance. Checks CSV 23, CSV 27 and CSH 25 were national checks in coordinated trials. The experimental material comprised of 10 male sterile lines *viz.*, ICSA 29003(L_1), ICSA 29004 (L_2), ICSA 29006 (L_3), ICSA 29010 (L_4), ICSA 29011(L_5), ICSA 29012 (L_6), ICSA 29013 (L_7), ICSA 29014 (L_8), ICSA 29015 (L_9) and ICSA 29016 (L_{10}), three restorer testers viz., SPV 245 (T_1), SPV 1430 (T_2) and SPV 1822 (T_3) and three checks *viz.* CSV 23, CSV 27, and CSH 25. These 10 lines and three testers

were crossed in factorial fashion to obtain the 30 hybrids. The crossing programme was attempted at Udaipur during kharif 2014 and at Warangal during rabi 2014-15.

Experimental design

In Line x Tester mating design experiment total 46 genotypes (10 lines, 3 testers, 30 crosses and 3 checks) were grown in a randomized block design with three replications in four different environments during *kharif* 2015 at Instructional farm, Rajasthan College of Agriculture, Udaipur (Rajasthan).

Each genotype was sown in a single row plot of 2-meter length maintaining a separate crop geometry (spacing) for each environment. The row to row and plant to plant spacing was 22.5 cm x 5 cm, 30 cm x 10 cm, 45 cm x 10 cm and 60 cm x 10 cm in E_1, E_2, E_3 and E_4, respectively.

Traits under investigation

Following phenological, fodder and quality traits were measured. Days to 50 % flowering, plant height (cm), ear head lngth, grain yield (q ha^{-1}), green fodder yield (q ha^{-1}), protein content in grain (%), protein content in fodder (%), seed index and harvest index (%),

Statistical analysis

Plot means of all the characters were subjected to various statistical analysis. The statistical analysis followed for Line x Tester mating design experiment was as follows.

The plot means of each character were subjected to analysis of variance for individual environment as well as over the environment where error variance in different environment were homogeneous using least square technique of Fisher (1932).

Analysis of variance for individual environment

ANOVA for individual environment is presented in Table 3.7. In this table looking to the materials used the genotypic variation was further partitioned as mentioned in the table.
The linear model of analysis of variance for individual environment was as under:

$$Y_{ij} = \mu + G_i + R_j + \sigma_{ij}$$

Where,

Yij = Value of ith genotype in jth replication,
μ = Population mean,
Gi = An effect of ith genotype which were further partitioned in Parents, Checks, Crosses, Lines, Testers and Line x Tester
Rj = An effect of jth replication and
σij = An uncontrolled variation associated with ithgenotype and jth replication.

The mean, general mean, standard error, critical difference and coefficient of variation were calculated as:

$$\text{Mean } (\bar{X}_i) = \sum_{i=1}^{r} X_{ij} \text{ /r}$$

$$\text{General Mean } (\bar{X}) = \sum_{i=1}^{g} \sum_{j=1}^{r} X_{ij} \text{ /rg}$$

If mean square due to genotype was significant then CD was calculated as follow:

CD = SE (Diff.) x $T_{[(r-1)\ (g-1)]}$ at 5% or 1% level of significance

$$CV\% = \frac{\sqrt{MSE}}{\bar{X}} \times 100$$

Where,
$\bar{X}_i$ = mean of the i^{th} genotype

$\overline{X}$ = mean over genotypes and replications

$\overline{X}_{ij}$ = value of i^{th} genotypes in j^{th} replication

r, g = number of replications and genotypes, respectively

$$SE(Diff.) = \sqrt{\frac{2MSE}{r}}$$

MSE = Error mean square

Analysis of variance over environments

The statistical model for pooled analysis of variance was as under:

$$Y_{ijk} = \mu + G_i + R_j + E_k + GE_{jk} + \sigma_{ijk}$$

Where,

Yijk = Yield of the ith genotype in jth replication of kth environment,

μ = General mean,

Gi = An effect of ith genotype where genotypes were further partitioned into checks, parents, hybrids, parent v/s checks and parent's vs hybrids.

Parents were further partitioned between testers, lines and testers' v/s lines. Hybrids were partitioned into effects of testers (GCA tester), effects of lines (GCA line) and their interactions line x tester (SCA).

Rj = An effect of jth replication,

Ek = An effect of kth environment,

(GE)ik = An interaction effect of ith genotype with kth environment.

This effect was further partitioned into the interaction of environment with checks, parents (testers, lines and testers v/s lines) parents v/s checks, parents v/s hybrids and hybrids (GCA tester, GCA line and SCA)

□ ijk = An uncontrolled variation associated with ith genotype in jth replication and kth environment.

Bartlett's test

Before doing the pool analysis of variance homogeneity of error variance was tested using the Bartlet test. Pool analysis was performed only when error variance was homogeneous in different environments.

$$Corrected\ \chi^2 = \frac{\chi^2}{CF}$$

Where

$$\chi^2 = (\sum_{i=1}^{l} df_i) \times log_e EMSP - \sum_{i=1}^{l}(df_i . log_e EMS_i)$$

$$CF = 1 + \frac{1}{3(l-1)} \times [\sum_{i=1}^{l} \frac{1}{df_i} - \frac{1}{\sum_{i=1}^{l} df_i}]$$

df_i = Error degrees of freedom in i^{th} environment

l = Number of environments

EMSP = Pool error mean square, and

EMS_i = Error mean square in i^{th} environment.

Genotype x environment interactions and stability parameters

The phenotypic stability of genotype for different characters having homogeneous error variance in different environment was estimated according to model proposed by Eberhart and Russell (1966).

The statistical model of the analysis was as follows:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$$

Where,

Y_{ij}= Mean performance of i^{th} genotype in j^{th} environment

μ_i = Mean of i^{th} genotype over the environments

β_i = The regression coefficient of i^{th} genotype

δ_{ij} = Deviation from regression of the i^{th} genotype in j^{th} environment.

I_j = The environmental index for j^{th} environment.

The analysis of variance for stability parameters the significance of different estimates tested by 'F' test:

Mean difference

F = MS_1/MS_4 (When the pooled deviation is significant)
F = MS_1/MS_5 (When the pooled deviation is non-significant)
G x E interaction
F = MS_2 / MS_5

G x E (linear)

F = MS_3/MS_4 (When the pooled deviation is significant)
F = MS_3/MS_5 (When the pooled deviation is non-significant)

Estimation of stability parameters

Two parameters of stability *viz.* regression coefficient (b_i) and mean square deviation from linear regression (S^2d_i) were calculated. The regression coefficient (b_i) is the regression of the performance of each genotype under different environments on the environmental index. It was estimated as:

$$b_i = \frac{\sum_{j=1}^{s} Y_{ij} \times I_j}{\sum_{j=1}^{s} I_j^2}$$

Hypothesis Regression coefficient assumed zero and unity was tested by using 't' test

H_0: b = 0 $\quad t_{[n-2]} = \frac{b}{SEb}$

H_0: b = 1 $\quad t_{[n-2]} = \frac{b-1}{SEb}$

$$SE_{bi} = \sqrt{\left[\left(\delta_i^2 / \{(s-2)\right) \sum_{j=1}^{s} I_j^2\ )\}\right]}$$

Where,

Estimation deviation from regression (S^2d_i) for each genotype was calculated as follow:

$$S_{di}^2 = \frac{\delta_i^2}{s-2} - \frac{MSE}{r^2}$$

Significance of S^2d_i was tested as follows:

$$F_{[1,s-2]} = \left[\frac{s_i^2}{s-2}\right] / \left[\frac{MSE}{r}\right]$$

Where,

$$\delta_{i=}^2 \left[\sum_{k=1}^{s} \left(\sum_{j=1}^{r} X_{ijk} \right)^2 / r - \left(\sum_{k=1}^{s} \sum_{j=1}^{r} X_{ijk} \right)^2 / sr \right] - \left\{ \sum_{k=1}^{s} \left(\left(\sum_{j=1}^{r} X_{ijk} \right) I_k \right)^2 / r \sum_{k=1}^{s} I_k^2 \right\}$$

I_k = Environmental index for k^{th} environment
i.e.

$$\sum_{i=1}^{g} \sum_{k=1}^{r} X_{ij} / rg - \left(\sum_{k=1}^{s} \sum_{i=1}^{g} \sum_{j=1}^{r} X_{ijk} \right) / sgr$$

X_{ijk} = Value of i^{th} genotypes in j^{th} replication of k^{th} environments.
r and s = Number of replications and environments, respectively
MSE = Pooled error mean square

Results and Discussion

Stability analysis

The stability of the genotypes was estimated using the Eberhart and Russell (1966) model. Analysis of variance for phenotypic stability was carried out only for plant height and ear head length as error variance was homogeneous in different environments for these two traits only. Analysis of variance (Table 1) revealed significant mean square for genotypes, environment linear, G x E linear and pooled deviation for both the characters.

The genotypes had non-significant S^2d_i along with higher mean values were classified on the basis of b_i as b_i <1, bi =1 and bi >1. For plant height a perusal of S^2d_i revealed that out of 46 genotypes, 22 genotypes, (5 lines, 16 crosses and 1 check) exhibited non-

significant deviation from regression (S^2d_i). Out of these only L7 x T3 (242.25) was having plant height more than the best check CSV 23 (224.25). Out of 5 lines L_4 was having b_i =1 (1.97) as it significantly deviating from zero but not deviating from unity. In rest of the four lines b_i neither deviating from zero nor from unity. Among the crosses L_6 x T_1 (1.91) and L_4 x T_2 (1.26) were having $b_{i\ =\ 1}$ as the b_i were deviating from zero but not from unity. In rest of the 14 hybrids b_i neither significantly deviating from zero nor from unity. The similar situation was observed in check CSH 25 also (Table 3). As regards to ear head length **a** perusal of S^2d_i revealed that out of 46 genotypes, 29 genotypes, (10 parents, 16 crosses and 3 checks) exhibited non-significant deviation from regression (S^2d_i). None of these parents and crosses exhibited mean values more than best check CSH 25 (33.75).

The regression coefficient b_i greater than 1 was observed in L_2 (2.98) and L_8 x T_2 (2.10), b_i =1 in T_1 (1.84), L_4 x T_2 (1.64), L_5 x T_1 (1.36) and check CSH 25 (1.01). The b_i for these genotypes were significantly deviating from zero but not from unity. For rest of the genotypes where S^2d_i was non significant b_i neither deviating from zero nor from unity (Table 3).

For judging buffering ability of genotypes under variable plant populations testing of stability is essential. Genotypes having buffering ability for fluctuation of plant population are most desirable, secondly genotype having predictable behaviour may be recommended for that plant population. In present investigation different plant population were maintained by adopting different spacing and Eberhart and Russell (1966) model was used to estimate the stability and genotypes with high per se performance with non-significant S^2di were classified on the basis of regression coefficient (b_i). The genotypes with b_i <1 (significantly less than 1) were identified for adverse environmental conditions, bi > 1 (significantly higher than 1) for favorable environmental conditions and b_i =1 for unknown or unpredictable environmental conditions. The error mean square was homogeneous for plant height and ear head length therefore; stability was worked out for these two characters. For plant height 22 genotypes including five lines, one check and 16 crosses having none significant S^2d_i. In these one line L_4 and two crosses L_2 x T_1 and L_4 x T_2 having b_i = 1. In rest of the genotypes where S^2d_i was non-significant bi neither deviating from zero nor from unity. All the three crosses having economic heterosis for grain yield were having significant S^2d_i. For ear head length the S^2d_i was non-significant in three testers, seven lines, sixteen crosses and three checks.

The regression coefficient b_i >1 observed in L_2 and L_8 x T_2 and b_i = 1 in T_1, L_4 x T_2 and L_5 x T_1 and check CSH 25. For rest of the genotypes where S^2d_i was non-significant, b_i neither deviating neither from zero nor from unity. The cross L_1 x T_3 having economic heterosis for grain yield having non-significant S^2d_i and b_i. For other two crosses L_2 x T_3 and L_6 x T_3 the S^2d_i was significant this indicates instability for plant height and ear head length in crosses L_2 x T_3 and L_6 x T_3 therefore these hybrids may be tested under wider range of environmental condition with more control to reduce the error variance between the environments. Similar results *i.e.*, non significant S^2d_i and identification of genotypes on the basis of b_i for one or more characters were also obtained by Palanisamy and Prasad, (1980), Dangi *et al*., (1980), Desai and Deore (1980, Singh and Nayeem (1980), Meena *et al.,* (2017) Shahane and Bapat (1981) Patil *et al*., (1991) and Prabhakar and Patil (2002).

Table.1 Mean square for plant height and ear head length [Eberhart and Russel, 1966]

S. No.	Characters	Genotype	E+(G x E)	E (L)	G x E (L)	Pool dev.	Pool Err
		[45]	[138]	[1]	[45]	[92]	[360]
1	Plant height	3802.29**	640.00**	4.08	727.65**	604.04**	84.82
2	Ear head length	14.30**	5.20**	0.07	7.19**	4.29**	1.69

*, ** Significant at 5 and 1 percent level of significance

Table.2 Mean square over the environment for plant height and ear head length

S. No.	Source	df	Plant height	Ear head length
1.	Environment	3	8631.70**	148.40**
2.	Rep./Env	8	894.14**	10.80*
3.	Genotype	45	11407.00**	42.91**
	Check	2	7361.40**	160.19**
	P vs Chk	1	69417.00**	72.93**
	Parent	12	5505.50**	51.04**
	Tester	2	13099.00**	136.69**
	Line	9	4037.30**	35.39**
	T v/s L	1	3532.60**	20.53**
	P v/s C	1	127000.00**	144.26**
	Cross	29	9816.50**	28.74**
	Tester	2	98585.00**	60.43**
	Line	9	3819.90**	45.46**
	L x T	18	2951.70**	16.87**
4.	G x E	135	1770.90**	12.66**
	Check x E	6	1880.80**	6.27
	Chk Vs P x E	3	1454.10**	6.79
	P x E	36	1697.10**	11.20**
	T x E	6	574.45*	4.88
	L x E	27	1443.50**	12.75**
	T v/s L x E	3	6225.00**	9.82
	P v/s C x E	3	668.12*	1.27
	Cross x E	87	1855.60**	14.27**
	T x E	6	1047.20**	23.60**
	L x E	27	2067.90**	14.72**
	L x T x E	54	1839.30**	13.01**
5.	Pooled Error	360	254.47	5.07

*, ** Significant at 5 and 1 percent level of significance

Table.3 Stability parameters for plant height and ear head length

S. No.	Genotype	Plant height (cm)			Ear head length (cm)		
		μ_i	b_i	S^2d_i	μ_i	b_i	S^2d_i
1	T1	139.50	-0.97	510.862**	25.67	1.84*	-1.461
2	T2	157.92	0.75	853.106**	32.33	2.81	1.253
3	T3	203.67	0.82	237.840*	28.08	0.78	-1.516
4	L1	145.00	3.24	2553.194**	28.42	1.92	2.847
5	L2	161.50	1.23	24.794	31.67	2.98*+	-1.043
6	L3	143.08	0.61	-34.102	28.08	0.29	-1.009
7	L4	127.67	1.97*	-58.299	25.25	-0.07	7.010**
8	L5	152.17	0.38	272.884*	28.17	2.19	2.388
9	L6	154.17	-0.01	-24.221	28.17	0.56	1.183
10	L7	193.00	2.31	1370.194**	26.00	0.13	0.395
11	L8	177.42	2.93	1813.476**	28.25	1.00	0.502
12	L9	155.17	1.87	252.644*	26.92	0.04	3.570*
13	L10	148.17	1.16	-41.386	27.42	-0.67	4.959*
14	L1 x T1	152.17	-0.64	-38.625	26.08	0.77	0.384
15	L2 x T1	188.58	2.20	2019.305**	30.08	4.12	5.698*
16	L3 x T1	182.08	1.08	1285.494**	26.58	0.88	11.219**
17	L4 x T1	189.42	-1.79	776.279**	29.25	2.58	5.698*
18	L5 x T1	203.83	0.37	144.481	31.42	1.36*	-1.542
19	L6 x T1	187.58	1.91*	-69.062	29.33	1.40	9.275**
20	L7 x T1	180.08	-0.10	-69.694	29.67	1.55	-0.807
21	L8 x T1	168.25	-0.29	-49.598	28.75	0.72	1.176
22	L9 x T1	168.50	1.62	26.777	28.33	1.10	3.130
23	L10 x T1	207.67	1.36	1567.323**	27.67	0.71	0.380
24	L1 x T2	150.50	0.28	17.608	30.17	1.22	-1.385
25	L2 x T2	171.92	1.63	74.839	31.25	1.95	0.561
26	L3 x T2	160.50	3.07	449.861**	30.33	-1.51	7.867**
27	L4 x T2	141.75	1.26**	-81.965	29.08	1.64*	-1.568
28	L5 x T2	200.50	-0.20	376.324**	30.00	2.12	3.870*
29	L6 x T2	179.58	1.66	41.428	29.58	2.03	6.037*
30	L7 x T2	173.50	-0.61	66.230	32.08	-1.74	3.782*
31	L8 x T2	177.42	-0.80	17.294	31.58	2.10**+	-1.558
32	L9 x T2	175.58	-2.13	100.751	27.92	0.44	8.152**
33	L10 x T2	168.08	2.44	29.223	28.00	0.66	7.058**
34	L1 x T3	224.67	-1.41	557.547**	30.08	0.14	-0.571
35	L2 x T3	217.25	3.29	723.488**	29.17	0.74	6.809**
36	L3 x T3	251.00	4.01	217.570*	29.50	0.69	7.033**
37	L4 x T3	223.17	-0.19	1636.850**	28.17	1.22	2.411
38	L5 x T3	222.50	5.56	777.227**	29.42	0.55	-0.352
39	L6 x T3	230.58	1.93	1397.485**	29.33	0.33	-0.426
40	L7 x T3	242.25	3.21	56.159	30.33	1.26	13.427**
41	L8 x T3	229.17	0.03	486.347**	29.42	0.90	0.032
42	L9 x T3	190.17	1.45	-35.793	25.75	0.52	-1.313
43	L10 x T3	216.75	-3.04	1881.016**	27.17	0.97	7.064**
44	CSV 23	224.25	2.27	386.981**	28.25	0.62	-1.276
45	CSV 27	218.25	-0.46	1425.628**	26.83	-0.89	1.638
46	CSH 25	178.67	0.70	-41.740	33.75	1.01*	-1.620

*, ** Significant at 5 and 1 percent level of significance

+ Significant deviation of b from unity at 5 percent level of significance

Two crosses L_2 x T_3 and L_6 x T_3 having economic heterosis more than 15 per cent for grain yield and dry fodder yield, good SCA, involving one good GCA parents, nicking in flowering in normal spacing environment and male parent taller than the female parent are identified to contribute in the coordinated trials for multilocation testing. If perform well these crosses will serve the purpose of dual purpose sorghum. Apart from above, cross L_1 x T_3 is also identified for contribution in coordinated trials for grain purposes as it has very high economic heterosis for grain yield (56.65%) in medium spacing environment *i.e.30 x 10 cm* along with good nicking in flowering and taller male parent. Selection may also be exercised for transgressive segregants in segregating generations of ICSA 29003 B × SPV 1822 as this cross having high heterosis, good SCA and involving both good general combiner parents.

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