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Stability of Ethanol Yield and Related Traits in Sweet Sorghum (*Sorghum bicolor* (L.) Moench) Over Environments

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ABSTRACT

Genotype × environment interaction was studied for ethanol yield and their component characters in eleven parents and their 30 hybrids of sweet sorghum under three environments during *kharif* 2010. The environment + (genotype × environment) was significant for all the characters except brix (%) indicating distinct nature of environments and genotype × environment interactions in phenotypic expression. The genotype × environment (linear) interaction component showed significance for the characters plant height, TSS, TSI, total biomass, juice yield and ethanol yield studied. This indicated significant differences among the genotypes for linear response to environments (b_i) behaviour of the genotypes could be predicted over environments more precisely and G × E interaction was outcome of the linear function of environmental components. Based on stability parameters and over all mean, the hybrid NSS 1007A × CSV 19SS was found stable in performance for total biomass, juice yield and ethanol yield. The male parents SSV 84 and RSSV 120 can be used for developing stable hybrids over the environments.

Key words : Ethanol, Genotype × Environment interaction, Stability, Sweet sorghum.

Sorghum (*Sorghum bicolor* (L.) Moench) (2n = 20) is the fifth major cereal crop in the world and occupies fifth position in acreage after wheat, rice, maize and barley. It is a special type of sorghum that can be grown for food, fuel, fodder and fibre (a crop of 4 FFFF's). Varietal adaptability to environmental fluctuations is important for the stabilization of crop production over both the regions and years. An information on genotype × environment interaction leads to successful evaluation of stable genotypes, which could be used for general cultivation. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations. Hence, the selection for superior genotypes based on yield *per se* at a single location in a year may not be very effective. Thus, evaluation of genotypes for stability of performance under varying environmental conditions for yield has become an essential part of any breeding programme. An understanding of the causes of genotype × environment interaction can help in identifying traits and environments for better cultivar evaluation. Development of sweet sorghum hybrids with high ethanol yield for different environments is one of the exciting research leads to successful evaluation of stable genotype, which could be used for general cultivation. Therefore, the present investigation was carried out for identifying stable genotypes with high yield using Eberhart and Russell (1966) model.

MATERIAL AND METHODS

The experimental material for the present investigation consisted of forty – four genotypes which included 11 parents *viz.,* NSS 8B, NSS 10B, NSS 1007B, NSS 1016B, RS 1220B, SSV 84, M 11, CSV 19SS, SSV 74, RSSV 76 and RSSV 120) and their thirty hybrids along with three checks (CSH 22SS, PAC 52093 and NSSV 13). Crosses were effected between five female (NSS 8B, NSS 10B, NSS 1007B, NSS 1016B and RS 1220B) and six male parents (SSV 84, M 11, CSV 19SS, SSV 74, RSSV 76 and RSSV 120) in Line × Tester fashion to obtain 30 hybrids . All these 44 genotypes were evaluated in randomized block design with three replications at three locations *viz.,* Directorate of Sorghum Research (DSR) farm, Hyderabad (E_1), Sorghum Research Station farm, Mahatma Phule Krishi Vidyapeeth, Rahuri (E_2) and Centre for Plant Breeding and Genetics farm, Tamil Nadu Agricultural University, Coimbatore (E_3) during *kharif* 2010. Each entry was sown in two rows of 4m length with a spacing of 60 cm between rows and 15 cm between plants. Recommended fertilizer doses and cultural practices were adopted. Observations were recorded for the characters *viz.,* days to 50 percent flowering,

Table 1. Pooled analysis of variance for stability in 44 sweet sorghum genotypes.

Source of variation	df	Mean sum of squares						
		DFF	DM	PH (cm)	Brix (%)	TB (t ha^{-1})	JY (l ha^{-1})	EY (l ha^{-1})
Genotypes (G)	43	46.12***	48.14 ***	6371.14 ***	3.26 ***	552.97***	17230730.00 ***	129059.91 ***
Environments (E)	2	1247.92 ***	4810.87 ***	134750.55***	7.72 **	36792.80***	1033019584.00 ***	7206927.00 ***
G × E	86	8.71	11.51	662.55	0.95	322.62 ***	11402291.0 ***	70012.79 **
E + (G × E)	88	36.87***	120.59 ***	3710.01 ***	1.11	1151.49***	34620868.00 ***	232215.39 ***
Environments (linear)	1	2495.85 ***	9621.73 ***	269501.09 ***	15.43 ***	73585.59***	2066039168.00***	14413854.00 ***
G× E (linear)	43	9.62	13.71	891.00 **	0.85	561.27***	18172024.00 ***	104933.39***
Pooled Deviation (non-linear)	44	7.62 ***	9.10 ***	424.23 ***	1.04 ***	82.06***	4527272.50 ***	34294.63***
Pooled Error	258	1.73	2.13	199.24	0.52	6.35	791732.75	8779.36

*Significance at 5% level   ** Significance at 1% level and *** Significance at 0.1% level

DFF - Days to 50% flowering, DM - Days to maturity, PH - Plant height, TB - Total biomass, JY- Juice yield, EY- Ethanol yield

days to maturity, plant height (cm), brix per cent, total biomass (t ha^{-1}), juice yield (l ha^{-1}) and ethanol yield (l ha^{-1}). The analysis was done using Indostat software. The error variances in the trials conducted in three locations were homogeneous, as revealed by Bartlett's test (Bartlett 1937), providing statistical validity to carry out combined ANOVA. Stability parameters and G × E interaction components for all the characters were estimated by Eberhart and Russell (1966) model.

RESULTS AND DISCUSSION

The pooled analysis of variance for stability revealed highly significant differences among genotypes and environments for all the characters except juice extraction per cent with respect to genotypes indicating the presence of variability among genotypes and environments (Table 1). The mean sum of squares for Genotype (G) × Environment (E) interaction effect were significant for total soluble solids (TSS), total sugar index (TSI), total biomass, juice yield, grain yield and ethanol yields. Similar results were also reported by Burli *et al*., (2004) and El-Menshawi (2005) for the traits plant height and total biomass. Similarly, the linear component of variance was higher than the non-linear component for all the characters except brix per cent. Similar results of higher values of non-linear component were reported by Iyanar and Ravikesavan (2005). As linear component is higher for all most all the characters performance prediction of genotypes based on these traits would be more accurate across the environments. The mean squares due to environment (linear) was found significant for all the characters, indicating differences between environments and their influence on genotypes for expression of these characters (Table 1). The environment + (genotype × environment) was significant for all the characters except for brix per cent indicating distinct nature of environments and genotype × environment interactions in phenotypic expression. The genotype × environment (linear) interaction component showed significance for the characters plant height, total soluble solids (TSS), total sugar index (TSI), total biomass, juice yield and ethanol yield studied. This indicated significant differences among the

Table 2. Stability parameters for total biomass and juice yield over three locations in 44 genotypes of sweet sorghum

S.No.	Genotypes	Total biomass (t ha^{-1})			Juice yield (l ha^{-1})		
		μ Mean	βi	σ^2di	μ Mean	βi	σ^2di
Hybrids							
1	NSS 8A × SSV 84	61	0.92	-1.16	10496	1.01	-737970.94
2	NSS 8A × M 11	45	0.23	25.06*	9563	0.53	-365441.38
3	NSS 8A × CSV 19SS	72	1.48	118.69***	12471	1.24	12788473.00
4	NSS 8A × SSV 74	73	1.52*	-4.97	11994	0.91	9590299.00
5	NSS 8A × RSSV 76	68	1.53*	135.53***	8839	0.25	911031.88
6	NSS 8A × RSSV 120	58	0.79	2.62	9800	1.02	-830356.38
7	NSS 10A × SSV 84	55	0.47	192.76***	9428	1.39	2757317.50
8	NSS 10A × M 11	51	0.27	263.97***	8983	1.54	13935478.00
9	NSS 10A × CSV 19SS	83	2.01	167.69***	12649	1.33	2268272.75
10	NSS 10A × SSV 74	67	1.28	11.94	10495	1.16	-470441.25
11	NSS 10A × RSSV 76	41	0.15	34.88*	6737	0.71	10297054.00
12	NSS 10A × RSSV 120	51	0.58	45.15**	9757	0.52	14566051.00
13	NSS 1007A × SSV 84	48	0.56	-6.36	7495	0.86	4116344.00
14	NSS 1007A × M 11	68	1.74	321.02***	7988	0.40	504458.19
15	NSS 1007A × CSV 19SS	73	1.00	-2.71	13438	0.98	-3714298.50
16	NSS 1007A × SSV 74	65	1.37	45.80**	9457	1.11	726692.81
17	NSS 1007A × RSSV 76	49	0.56	16.09	8759	0.86	-72870.22
18	NSS 1007A ×RSSV 120	53	0.48	184.05***	9958	1.51	14921501.00
19	NSS 1016A × SSV 84	80	1.99	243.08***	11076	1.01	5105686.00
20	NSS 1016A × M 11	55	0.86	-6.02	9515	1.01	1169458.25
21	NSS 1016A × CSV 19SS	51	0.55	28.50*	10359	1.05	1379557.88
22	NSS 1016A × SSV 74	62	1.21	26.30*	10740	1.34	-526710.31
23	NSS 1016A × RSSV 76	66	1.53*	127.06***	8325	0.34	3075355.75
24	NSS 1016A ×RSSV 120	60	1.03	-2.40	9283	0.95	-298052.38
25	RS 1220A × SSV 84	62	0.91	73.14***	9460	1.37	3069096.75
26	RS 1220A × M 11	73	1.50	6.37	10843	1.43*	-834018.31
27	RS 1220A × CSV 19SS	64	0.85	218.15***	11807	2.05	16933710.00
28	RS 1220A × SSV 74	67	0.84	699.83***	13307	2.48	971849.31
29	RS 1220A × RSSV 76	82	2.01*	14.05	10843	1.25	2225161.00
30	RS 1220A × RSSV 120	83	2.07*	20.03*	12110	1.59	2649406.50

*Significance at 5% level ** Significance at 1% level; *** Significance at 0.1% level

Table 2 Cont.

S.No.	Genotypes	Total Biomass (t ha^{-1})			Juice Yield (l ha^{-1})		
		μ Mean	βi	σ^2di	μ Mean	βi	σ^2di
Females							
31	NSS 8B	35	0.21	10.74	4367	-0.27	2134656.50
32	NSS 10B	42	0.35*	-3.88	5869	0.20	1986131.25
33	NSS 1007B	29	-0.09	-0.69	3583	-0.36	1018765.81
34	NSS 1016B	34	0.16	5.55	3787	-0.20	2220119.75
35	RS 1220B	40	0.23*	-1.57	6501	0.50	6593085.50
Males							
36	SSV 84	64	1.08	-4.54	10704	1.10	-689526.94
37	M 11	50	0.62	-0.99	6667	0.08	1488719.50
38	CSV 19SS	68	1.26*	-6.83	11787	1.64	-518571.03
39	SSV 74	57	0.78	39.15*	9443	1.33	32762.55
40	RSSV 76	63	1.12	3.14	9542	0.37	2959407.00
41	RSSV 120	65	1.23	109.19***	12011	1.05	3521692.50
Checks							
42	CSH 22SS	81	1.63*	-5.78	12568	1.64*	-778647.88
43	PAC 52093	64	1.05	70.59***	11136	1.52*	-774933.44
44	NSSV 13	74	1.68*	97.16***	11632	0.98	19767482.00
	Mean	60	1.00		9672	1.00	
	S.Em±		6.40		1504.50		
	S.E b_i		0.30		0.30		0.30

genotypes for linear response to environments (b_i) behaviour of the genotypes could be predicted over environments more precisely and G × E interaction was outcome of the linear function of environmental components. Hence, prediction of performance of genotypes based on stability parameters would be feasible and reliable.

Eberhart and Russell (1966) defined a stable genotype as the one which showed high mean yield, regression co-efficient (b_i) around unity and deviation from regression near to zero. Accordingly, the mean and deviation from regression of each genotype were considered for stability and linear regression was used for testing the varietal response.

The simultaneous consideration of three parameters of stability for the individual genotype revealed that one parent (SSV 84) and one hybrid (NSS 1007A × CSV 19SS) for total biomass; none of the parents and six hybrids (NSS 8A×SSV 74, NSS 1007A × CSV 19SS, NSS 8A × SSV 84, NSS 1016A × SSV 84, NSS 8A × RSSV 120 and NSS 1016A × RSSV 9) for juice yield (Table 2) and one parent (SSV 84) and one hybrid (NSS 1007A × CSV 19SS and NSS 8A × SSV 84) for ethanol yield (Table 3) showed nearly unit regression, high mean and non-significant deviation from regression. Hence, these genotypes may be considered as stable genotypes.

Identification of a hybrid with high mean values for total biomass, juice yield and ethanol yield, stability and average response is of immense value. A perusal of stability parameters indicated

Table 3. Stability parameters for ethanol yield for over three locations in 44 genotypes of sweet sorghum.

S. No.	Genotypes	Bioethanol Yields (l ha^{-1})		
		μ Mean	βi	σ^2di
Hybrids				
1	NSS 8A × SSV 84	849	0.92	-4769.46
2	NSS 8A × M 11	747	0.55*	-9259.50
3	NSS 8A × CSV 19SS	1067	1.33	106726.39
4	NSS 8A × SSV 74	950	0.89	43650.88
5	NSS 8A × RSSV 76	741	0.36	31500.79
6	NSS 8A × RSSV 120	789	0.97	-9044.12
7	NSS 10A × SSV 84	776	1.42	36748.13
8	NSS 10A × M 11	729	1.44	108989.81
9	NSS 10A × CSV 19SS	908	0.99	10954.02
10	NSS 10A × SSV 74	793	1.08	-8519.56
11	NSS 10A × RSSV 76	473	0.59	42735.75
12	NSS 10A × RSSV 120	791	0.55	108287.09
13	NSS 1007A × SSV 84	613	0.93	26842.15
14	NSS 1007A × M 11	610	0.43	6638.04
15	NSS 1007A × CSV 19SS	1150	1.01	-16628.38
16	NSS 1007A × SSV 74	785	1.16	51.01
17	NSS 1007A × RSSV 76	740	0.83	-1429.26
18	NSS 1007A × RSSV 120	802	1.42	131389.11
19	NSS 1016A × SSV 84	889	1.01	20633.13
20	NSS 1016A × M 11	740	0.95	1348.56
21	NSS 1016A × CSV 19SS	829	0.99	-2415.96
22	NSS 1016A × SSV 74	822	1.23	-7065.32
23	NSS 1016A × RSSV 76	643	0.38	7286.19
24	NSS 1016A × RSSV 120	633	0.74*	-9260.41
25	RS 1220A × SSV 84	824	1.36	32725.36
26	RS 1220A × M 11	819	1.23	-6920.39
27	RS 1220A × CSV 19SS	883	1.77	93604.53
28	RS 1220A × SSV 74	1071	2.29	3041.53
29	RS 1220A × RSSV 76	897	1.27	-6631.53
30	RS 1220A × RSSV 120	987	1.46	-4591.39

*Significance at 5% level

Table 3 Cont.

S. No.	Genotypes	Bioethanol Yields (l ha^{-1})		
		μ Mean	βi	σ^2di
Females				
31	NSS 8B	320	-0.22	-488.65
32	NSS 10B	418	0.23	-3287.03
33	NSS 1007B	257	-0.25*	-8469.28
34	NSS 1016B	273	-0.14	-789.42
35	RS 1220B	513	0.47	22846.43
Males				
36	SSV 84	909	1.04	-2814.36
37	M 11	861	1.57	114208.48
38	CSV 19SS	1017	1.69	-6083.89
39	SSV 74	762	1.32	-7479.21
40	RSSV 76	741	0.41	40094.20
41	RSSV 120	1002	1.10	42876.09
Checks				
42	CSH 22SS	997	1.55	-5553.90
43	PAC 52093	930	1.55	-862.72
44	NSSV 13	1036	0.96	157036.88
	Mean	782	1.00	
	S.Em±	130.90		
	S.E b_i	0.30		

*Significance at 5% level

that out of eleven parents, the male parent CSV 19SS and hybrids *viz.,* NSS 8A × SSV 74 and RS 1220A × RSSV 76 for total biomass, RS 1220A × M 11 for juice yield registered high mean, significant bi value (bi > 1) and non-significant deviation from regression (Table 2). Therefore, these genotypes perform better under favourable environmental conditions.

Out of the thirty hybrids, four hybrids *viz.*, NSS 10A × SSV 74, NSS 1007A × CSV 19SS, RS 1220A × M 1 and RS 1220A × RSSV 120 for total biomass; nine hybrids *viz.*, NSS 10A × SSV 74, NSS 8A × CSV 19SS, RS 1220A × RSSV 76, NSS 10A × CSV 19SS, NSS 1016A × SSV 74, NSS 1007A × RSSV 120, RS 1220A × RSSV 120, RS 1220A × CSV 19SS and RS 1220A × SSV 74 for juice yield (Table 2) and three hybrids *viz.*, NSS 8A × CSV 19SS, RS 1220A × RSSV 120 and RS 1220A × SSV 74 for ethanol yield expressed high mean, non-significant regression value (bi > 1) and non-significant deviation from regression (Table 3). Hence, these genotypes were found to be suitable for favourable environments. The hybrids *viz.*, NSS 8A× SSV 84 for total biomass, NSS 10A × RSSV 120 and NSS 8A × M 11 for juice yield (Table 2) and NSS 8A × SSV 74 for ethanol yield had high mean, the regression value below one (bi < 1) (Table 3) and were found to be suited for unfavourable environments.

Taking into account all the parameters of stability it can be inferred that overall the experiment has resulted into identification of one parent (SSV 84) and one hybrid (NSS 1007A × CSV 19SS) for total biomass; one parent (RSSV 120) and six hybrids for juice yield (NSS 8A×SSV 74, NSS 1007A × CSV 19SS, NSS 8A × SSV 84, NSS 1016A × SSV 84, NSS 8A × RSSV 120 and NSS 1016A × CSV 19SS) and two parents (SSV 84 and RSSV 120), one check (NSSV 13) and two hybrids (NSS 1007A × CSV 19SS and NSS 8A × SSV 84) for bioethanol yield were stable in performance. Thus the genotypes can be directly introduced as cultivars and also used as parents for stability for total biomass, juice yield and ethanol yield in sweet sorghum improvement.

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