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Research Article

Identification of stable genotypes based on grain yield response over different environments in sorghum (*Sorghum bicolor* L. Moench)

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Abstract

The genotype × environment (G × E) interaction has a significant impact on plant yield performance and is an important focus of researchers in developing stable varieties. This study aims to find stable, high yielding sorghum hybrids suited for a wide range of environmental conditions in Telangana. A total of 64 sorghum genotypes/hybrids were evaluated in three environments during *Rabi* 2020–2021 for adaptability and stability. The regression method of stability analysis was used to study grain yield adaptability and stability. Results revealed that, genotypes, environments, G × E interaction, and G × E (linear) all differed significantly. According to the findings, the highest yielding hybrid was SG-16 (2.78 kg/plot). Based on the regression coefficient (b_i) and deviation from regression (s^2d_i) scores, the high yielding hybrids, *viz*., SG-26, SG-16, SG-3, SG-29, and SG-6, were found to be stable and adapted to a wide range of environments.

Keywords: Adaptability, G × E interaction, *Sorghum bicolor* and Stability.

INTRODUCTION

Yield stability has always been a major concern in plant breeding. But the continued variation in environmental conditions will make this even worse. An individual's phenotype is a combination of genotype (G) and environment (E). Crop varieties may not perform consistently in varied environments as a result of genotype × environment (G × E) interaction. In countries like India, with a diversity of agro-ecologies, the G × E interaction analysis is essential for sorghum crop improvement. Significant G × E interaction occurs as a result of variations in the extent of differences among genotypes in different environments or variations in the genotypes' comparative ranking (Falconer, 1952; Fernandez, 1991 and Peto, 1952).

Before releasing genotypes as cultivars, plant breeders must identify both adapted and stable genotypes to the environment(s), allowing for rapid genetic gain (Showemimo *et al*., 2000; Mustapha *et al*., 2001; Yan and Kang, 2003). Proper biometrical or statistical techniques are required to unravel the G × E interaction. The analysis of variance is helpful in evaluating the existence, significance, and magnitude of the G × E interaction, but it does not explain its relevance or implications. As a result, statistical models were created to describe the number of G × E interactions, their patterns, and their implications in plant breeding.

Joint Regression analysis is one of the most simple and easy methods of stability assessment, introduced by Yates and Cochran (1938), which was later modified by Finlay and Wilkinson (1963) and Eberhart and Russell (1966) and is now a commonly used method. According to this model, stability is measured using the trait mean (M), the slope of the regression line (b_i), and the sum of squares for deviation from regression (s^2d_i). The high mean value is the precondition for stability. The response of a genotype to the environmental index, which is calculated from the average performance of all genotypes in each environment, is indicated by the slope (b_i) of regression. It does not, however, account for stability, crop performance, or the extension of stability (Eberhart and Russell, 1966; Yue *et al*., 1997). If b_i does not differ much from unity, the genotype is adaptable to all environments. A bi greater than unity denotes genotypes that are more sensitive to environmental change (below average stability) and more specific to high yielding environments. A b_i value of less than unity indicates stronger resistance to environmental change (above average stability), increasing adaptation specificity to low yielding conditions. According to the Eberhart and Russell model, genotypes are grouped based on the variance of the regression deviation (s^2d_i) (either equal to zero or not). A genotype with a variance in regression deviation equal to zero has a highly predictable response. In contrast, a genotype with a regression deviation greater than zero has a less predictable response (Scapim *et al*., 2010).

The regression statistical approach should be used with caution when only a few low or high performing environments are included in the analysis (Westcott, 1986 and Crossa, 1990). This study tested genotypes in three diverse environments to determine grain yield adaptability and stability. Earlier, many stability analyses have been carried out on sorghum in India (Patel *et al*., 2019; Rakshit *et al*., 2016) and abroad (Alemu *et al*., 2020, Hamidou *et al*., 2018 and Souza *et al*., 2013). However, there is a scarcity of information on sorghum genotype adaptation and stability. Hence, the objective of the present study is to identify new hybrids in sorghum with high and stable yields across the environments studied.

MATERIALS AND METHODS

Fourteen parental genotypes (obtained from ICRISAT), including six female parental lines *viz*., ICSA 418, ICSA 419, ICSA 427, ICSA 433, ICSA 435, and ICSA 29004 (male sterile, A lines) were crossed with eight male restorers ICSR 13004, ICSR 13009, ICSR 13025, ICSR 13031, ICSR 13042, ICSR 13043, ICSR 13046, and ICSR 29 (R lines and high yielding) developed 48 hybrids during *Kharif,* 2019 at the Regional Agricultural Research Station, Palem, India. All of these parental genotypes and their 48 experimental hybrids, as well as two standard checks, CSV 41 and CSH 16, were included in the evaluation.

The experimental material was evaluated in three environments at PJTSAU research stations in Palem, Tandur and Rajendranagar (**Table 1**) during *Rabi* 2020–2021 using a Randomized Block Design (RBD) with two replications. The experimental plot in each location consisted of two rows of four metres each, with 45 cm inter-row spacing and 10 cm intra-row spacing. The recommended fertilizer doses per acre were 80:40:40 kg N:P:K was used. Split nitrogen application of 25 % at sowing + 50 % at 30 DAS + 15 % at boot leaf stage (BLS) + 10 % at grain filling stage (GFS), which was equivalent to treatment of 25 % at sowing + 45 % at 30 DAS + 5% foliar spray at 45 DAS + 15 % at BLS + 10 % GFS, and treatment with 25 % N at sowing + 50 % at 30 DAS + 25 % at boot-leaf stage (BLS) was followed (Annual Report of IIMR, 2020). Data was recorded on grain yield per plot (kg) in each environment and subjected to data analysis.

All recorded data were statistically analyzed using windostat software (version 9.2, from Indostat services), with environments treated as random effects and genotypes treated as fixed effects. The following linear model was used for combined ANOVA estimation according to Ding *et al*. (2008).

$$Y_{ijr} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + b_j + \varepsilon_{ijr}$$

Where, y_{ijr}, is the value of the dependent variable of genotype i in environment j average over block r, μ is overall mean, α_i is the effect of the ith genotype in the jth environment, β_j is the effect of the jth environment for all genotypes, $\alpha\beta_{ij}$ is the effect of the ith genotype by the jth environment, b_j is the block effect at the jth environment and ε_{ijr} is the residual error term.

Eberhart and Russell's (1966) model was used to performing the stability analysis. The model's detailed statistical formulae are specified in published literature

Table 1. Description of three test locations

Location	Latitude	Longitude	Soil type
Regional Agricultural Research Station (RARS) Palem	16˚ 35' N	78˚ 01' E	Red sandy
Agricultural Research Station (ARS), Tandur	17˚ 17' N	77˚ 30' E	Medium Black
College Farm, Rajendranagar	17˚ 19' N	78˚ 24' E	Sandy loam

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Table 2. ANOVA for grain yield in sorghum

Source of variation	Degrees of freedom	Grain yield per plot
Replications within Environment	3	0.025
Genotypes	63	0.422***
Environment + (G × E)	128	0.151***
Environments	2	5.702***
G × E	126	0.063***
Environments (Linear)	1	11.405***
G × E (Linear)	63	0.095***
Pooled Deviation	64	0.030***
Pooled Error	189	0.020
Total	191	0.240
SE±		0.413
CD @ 5 %		0.28

***significant at $P \leq 0.001$

(Eberhart and Russell, 1966; Lin *et al*., 1986). The stable genotypes in three environments were identified considering a regression coefficient equal to one (b_i =1), deviation from regression equal to zero, (S^2d_i = 0) and the acceptable genotype should yield above the general mean.

RESULTS AND DISCUSSION

The combined analysis of variance representing the mean squares due to different sources of variation for grain yield at three locations is presented in **Table 2**. The joint ANOVA revealed highly significant differences among the genotypes for grain yield when tested against the pooled error and pooled deviation, demonstrating that the observed differences in yield performances had genetic causes and, thereby, offered the possibility of selection and genetic gains for grain yield. The differences among the environments were also found to be highly significant for grain yield. There were significant G × E as well as G × E (linear) interactions for grain yield per plot when tested against pooled error and pooled deviation, indicating that genotypes had distinct yield responses to the environments tested, and there may even be genotypes with specific adaptability. Similar findings were reported for significant effects of genotype × environment (interaction effect) on grain yield by Hassan *et al*. (2015) and Ezzat *et al*. (2010).

The mean grain yield per plot ranged from 2.915 kg to 0.805 kg at RARS, Palem and from 3.045 kg to 1.025 kg at ARS, Tandur. At Rajendranagar, the plot grain yield varied from 2.045 kg to 0.720 kg (**Table 3**). It was observed that hybrid SG-16 recorded the highest grain yield per plot in both environments, RARS, Palem and ARS, Tandur. However, the other hybrid, SG-25, recorded a low grain yield per plot in RRAS, Palem (1.150 kg) and ARS, Tandur (1.305 kg). The mean grain yield per plot for each genotype at the Rajendranagar environment was low compared to the other two environments. The mean grain yield data of an environment makes it easy for breeders to select the best location-specific high-yielding genotypes. Earlier, Hamidou *et al*. (2018) and Al-Naggar *et al*. (2018) documented genotypes based on grain yield performance in each environment studied.

The aim of selection in the present study is to produce a population that has a mean value greater than the average mean value of all 64 genotypes evaluated. This difference should be due to differences in genotype and not to the environment (House, 1985). All the hybrids represented in **Table 4** were considered high yielding hybrids as they recorded a higher mean grain yield than the average grain yield of all the 64 genotypes evaluated. The hybrids, *viz*., SG-26 (b_i = 1.139, s^2d_i = -0.013), SG-16 (b_i = 1.171, s^2d_i = -0.016), SG-3 (b_i = 1.206, s^2d_i = -0.02), SG-29 (b_i = 1.230, s^2d_i = -0.02) and SG-6 (b_i = 1.381, s^2d_i = -0.019) recorded regression coefficient (b_i) values almost equal to unity and deviation from regression (s^2d_i) values of near zero, indicating that they would be adapted to all three environments (b_i = 1) with a high prediction of average stability (s^2d_i = 0) (**Table 4**). Regression coefficients greater than one with a minimum deviation (S^2d_i) value were observed for SG-12 (b_i = 2.037, s^2d_i = 0.028), SG-14 (b_i = 2.035, s^2d_i = -0.015) and SG-35 (b_i = 2.715, s^2d_i = -0.019) with mean grain yields above the grand mean grain yield, indicating that these hybrids were not stable under adverse conditions, but may respond better in favorable environments (**Fig. 1**). However, hybrids found to be above average stable (b_i < 1) with increasing specificity towards low yielding (unfavourable) environments were SG-23 (b_i = 0.084, s^2d_i = 0.038), SG-28 (b_i = 0.006, s^2d_i = -0.02), SG-20 (b_i = -0.129, s^2d_i = 0.045) and SG-9 (b_i = 0.568, s^2d_i = 0.005). The commercial check genotypes SG-63 (CSV-41) and SG-64 (CSH-16) had the least b_i (0.091 and -0.302) and the lowest minimum significant deviation s^2d_i values (-0.005 and -0.02), confirming that

Table 3. Performance of best 20 and least five genotypes out of 64 sorghum genotypes for grain yield per plot

Environment 1 (RARS, Palem)		Environment 2 (ARS, Tandur)		Environment 3 (Rajendranagar)	
Genotypes	Grain yield per plot (kg)	Highest yielding genotypes	Grain yield per plot (kg)	Highest yielding genotypes	Grain yield per plot (kg)
		Highest yielding genotypes			
SG-16	2.915	SG-16	3.045	SG-23	2.405
SG-6	2.515	SG-35	3.030	SG-16	2.380
SG-35	2.485	SG-6	2.810	SG-28	2.365
SG-37	2.475	SG-22	2.755	SG-22	2.245
SG-34	2.415	SG-37	2.675	SG-20	2.115
SG-12	2.385	SG-14	2.580	SG-6	1.995
SG-8	2.380	SG-3	2.565	SG-3	1.860
SG-28	2.380	SG-23	2.525	SG-41	1.755
SG-3	2.340	SG-8	2.520	SG-37	1.750
SG-42	2.250	SG-48	2.520	SG-9	1.730
SG-23	2.185	SG-12	2.465	SG-48	1.705
SG-29	2.160	SG-29	2.395	SG-29	1.675
SG-9	2.125	SG-28	2.365	SG-26	1.670
SG-22	2.120	SG-26	2.360	SG-21	1.560
SG-14	2.105	SG-42	2.320	SG-42	1.545
SG-15	2.075	SG-43	2.255	SG-45	1.480
SG-48	2.075	SG-4	2.245	SG-15	1.470
SG-36	2.065	SG-13	2.230	SG-39	1.460
SG-46	2.055	SG-2	2.210	SG-2	1.455
SG-26	2.035	SG-33	2.210	SG-35	1.435
		Lowest yielding genotypes			
SG-38	1.165	SG-25	1.365	SG-13	0.820
SG-25	1.150	SG-31	1.305	SG-8	0.810
SG-32	1.075	SG-19	1.265	SG-40	0.810
SG-31	1.015	SG-1	1.135	SG-5	0.805
SG-19	0.805	SG-24	1.025	SG-32	0.720
S.E ±	0.287	S.E ±	0.145	S.E ±	0.287
C.D @ 5 %	0.573	C.D @ 5 %	0.290	C.D @ 5 %	0.573

they were only responsive to poor growing conditions. The stability of hybrids, *viz*., SG-22, SG-34 and SG-8 is unpredictable as they recorded significant deviations from regression values (**Table 4**).

When stability parameters suggested by Eberhart and Russell (1966) were investigated for different genotypes, it was found that hybrids SG-26, SG-16, SG-3, SG-29, and SG-6 showed wider adaptability to all three environments with stable performance for high grain yield per plot, while hybrids SG-12, SG-14, and SG-35 were found to be adapted to specific, favourable high yielding environments, while hybrids SG-23, SG-20, and SG-9 adapted to unfavourable environments based on their regression scores. It is suggested that these genotypes could be useful in the breeding programme as sources of stability genes. There is reason to believe that many of the farmers' own varieties have good stability but low yield (Majisu and Doggett, 1972). The challenge of the breeding programme is to obtain a high level of yield while maintaining stability.

In the present study, hybrids SG-26, SG-16, SG-3, SG-29, and SG-6 were found to be higher yielding with more stability than check genotypes CSV-41 and CSH-16, which have been chosen over many years under local climatic conditions. Grain yields in sorghum have previously been reported to be highly stable by Seyoum *et al*. (2020), Hamidou *et al*. (2018), Al-Naggar *et al*. (2018), Sujatha *et al*. (2016) and Hassan *et al*. (2015). High-yielding genotypes that are adaptable and stable in general and specific

Table 4. Regression coefficient (b_i) and deviation from regression (s^2d_i) scores of top 20 genotypes based on their overall mean grain yield from three environments

Genotypes	Pooled mean grain yield per plot (kg)	Regression coefficient (b_i)	Deviation from regression (s^2d_i)
SG-16	2.78	1.171	-0.016
SG-6	2.44	1.381	-0.019
SG-22	2.373	0.683	0.123**
SG-23	2.372	0.084	0.038
SG-28	2.37	0.006*	-0.02
SG-35	2.317	2.715*	-0.019
SG-37	2.3	1.621	-0.015
SG-3	2.255	1.206*	-0.02
SG-48	2.1	1.32	0.002
SG-29	2.077	1.230*	-0.02
SG-12	2.063	2.037	0.028
SG-42	2.038	1.397	-0.001
SG-26	2.022	1.139	-0.013
SG-14	2.018	2.035	-0.015
SG-20	2.008	-0.129	0.045
SG-64	1.995	-0.302**	-0.02
SG-63	1.958	0.091	-0.005
SG-9	1.957	0.568	0.005
SG-34	1.952	1.721	0.161**
SG-8	1.903	3.089	0.082*

*significant at P ≤ 0.05, **significant at P ≤ 0.01

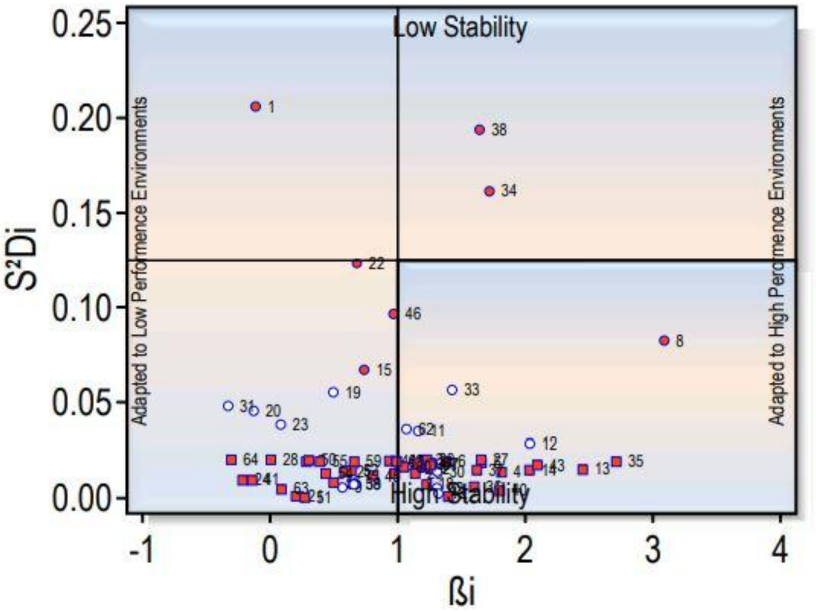

Fig. 1. Stability and adaptability of all 64 sorghum genotypes for grain yield per plot

The X-axis indicates the b_i (Regression coefficient) value of a genotype. The Y-axis indicates the s^2d_i (Deviation from the regression) value of the genotype.

environments have been identified and are considered commercial release candidates (Souza *et al*., 2013). However, new investigations into adaptability and stability in different seasons and conditions are needed to get a more complete picture of genotype × environment interaction.

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