## SHORT RESEARCH ARTICLE



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

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## Abstract

A set of 64 sorghum genotypes was evaluated for adaptability and stability in three environments during *rabi* 2020–2021. 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. Hybrid SG-16 (2.78 kg/plot) was identified as the highest yielding. Based on the regression coefficient (b<sub>i</sub>) and deviation from regression (s<sup>2</sup>d<sub>i</sub>) scores, the high-yielding hybrids, namely, 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, stability

### Introduction

In plant breeding, yield stability has long been a primary concern. This will only get worse due to the ongoing environmental variation. An individual's phenotype is a result of their genetics (G) and environment (E). Because of the interplay between genotype and environment (G  $\times$  E), crop types may not perform consistently in various environments. The G  $\times$  E interaction analysis is crucial for sorghum crop development in nations like India with a variety of agroecologies. Variations in the magnitude of variances between genotypes in various environments or variations in the comparative ranking of the genotypes lead to significant G  $\times$  E interaction (Peto 1982). One of the simplest and most convenient ways of stability evaluation is joint regression analysis, which is now a widely used technique (Eberhart and Russell 1966).

The trait mean (M), the slope of the regression line  $(b_i)$ , and the sum of squares for deviation from the regression are used in this model to quantify stability  $(s^2d_i)$ . Keep in mind that stability is reliant on a high mean value. The slope  $(b_i)$ of regression indicates how a genotype responds to the environmental index, which is derived from the average performance of all genotypes in each environment. However, it does not consider stability, crop performance, or stability extension (Eberhart and Russell 1966). If bi does not deviate significantly from unity, the genotype is environmentDepartment of Genetics and Plant Breeding, College of Agriculture, Professor Jayashankar Telangana State Agricultural University (PJTSAU), Rajendranagar, Hyderabad, Telangana, India <sup>1</sup>Department of Genetics and Plant Breeding, PJTSAU Regional Agricultural Research Station, Palem, Nagarkurnool, Telangana, India

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Table 1.	Genotypic codes with their <b>i</b>	espective names of sorghu	m genotypes evaluated ir	n three environments during	2020-2021 rabi season.

Genotype code	Name	Genotype code	Name
1	ICSA 418 × ICSR 13004	33	ICSA 435 × ICSR 13004
2	ICSA 418 × ICSR 13009	34	ICSA 435 × ICSR 13009
3	ICSA 418 × ICSR 13025	35	ICSA 435 × ICSR 13025
4	ICSA 418 × ICSR 13031	36	ICSA 435 × ICSR 13031
5	ICSA 418 × ICSR 13042	37	ICSA 435 × ICSR 13042
6	ICSA 418 × ICSR 13043	38	ICSA 435 × ICSR 13043
7	ICSA 418 × ICSR 13046	39	ICSA 435 × ICSR 13046
8	ICSA 418 × ICSR 29	40	ICSA 435 × ICSR 29
9	ICSA 419 × ICSR 13004	41	ICSA 29004 × ICSR 13004
10	ICSA 419 × ICSR 13009	42	ICSA 29004 × ICSR 13009
11	ICSA 419 × ICSR 13025	43	ICSA 29004 × ICSR 13025
12	ICSA 419 × ICSR 13031	44	ICSA 29004 × ICSR 13031
13	ICSA 419 × ICSR 13042	45	ICSA 29004 × ICSR 13042
14	ICSA 419 × ICSR 13043	46	ICSA 29004 × ICSR 13043
15	ICSA 419 × ICSR 13046	47	ICSA 29004 × ICSR 13046
16	ICSA 419 $\times$ ICSR 29	48	ICSA 29004 × ICSR 29
17	ICSA 427 × ICSR 13004	49	ICSA 418
18	ICSA 427 × ICSR 13009	50	ICSA 419
19	ICSA 427 × ICSR 13025	51	ICSA 427
20	ICSA 427 × ICSR 13031	52	ICSA 433
21	ICSA 427 × ICSR 13042	53	ICSA 435
22	ICSA 427 × ICSR 13043	54	ICSA 29004
23	ICSA 427 × ICSR 13046	55	ICSR 13004
24	ICSA 427 $\times$ ICSR 29	56	ICSR 13009
25	ICSA 433 × ICSR 13004	57	ICSR 13025
26	ICSA 433 × ICSR 13009	58	ICSR 13031
27	ICSA 433 × ICSR 13025	59	ICSR 13042
28	ICSA 433 × ICSR 13031	60	ICSR 13043
29	ICSA 433 × ICSR 13042	61	ICSR 13046
30	ICSA 433 × ICSR 13043	62	ICSR 29
31	ICSA 433 × ICSR 13046	63	CSV 41 (Check variety)
32	ICSA 433 × ICSR 29	64	CSH 16 (Check hybrid)

adaptive. Genotypes are more specialized to high-yielding environments and more sensitive to environmental change as indicated by genotypes with bi values greater than unity. A b<sub>i</sub> value, smaller than unity, suggests increased adaptive specificity to low-yielding environments and better tolerance to environmental change (above-average stability). The variance of the regression deviation (s<sup>2</sup>d<sub>i</sub>) is used by Eberhart and Russell to classify genotypes (either equal to zero or not). Results from genotypes with a variation in regression deviation of zero are quite predictable. On the other hand, a genotype with a regression deviation larger than zero results in a response that is less predictable (Scapim et al. 2010). The goal of the current study is to find new sorghum hybrids that provide high and consistent yields in all of the environments examined.

Fourteen parental genotypes (obtained from ICRISAT), including six female parental lines namely, ICSA 418, ICSA 419, ICSA 427, ICSA 433, ICSA 435, and ICSA 29004 (male sterile, A lines) were crossed with eight male fertility 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



Fig. 1. Display of stability and adaptability of all 64 sorghum genotypes for grain yield per plot (kg) evaluated in three environments during the 2020-2021 rabi season according to the Eberhart and Russell model (1966).

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

agricultural research station, Palem, India. All the parents and their 48 experimental hybrids as well as two standard

checks, CSV 41 and CSH 16 (Table 1) were evaluated in three environments at Professor Jayashankar Telangana state Agricultural University, regional research stations, Palem, Tandur, and Rajendranagar 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 meters 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 were used. Data was recorded on grain yield per plot (kg) in each environment and subjected to data analysis. The stability analysis was performed using Eberhart and Russell's model (1966).

Results from the stability analysis revealed that, when tested against the pooled error and pooled deviation, the joint ANOVA revealed highly significant differences (data not shown) among the genotypes for grain yield, clearly demonstrating that the observed variations in yield performances had genetic causes and opening the door to selection and genetic gains for grain yield. The variations across the environments were also shown to be quite important for grain yield. When grain yield per plot was assessed against pooled error and pooled deviation, there were significant  $G \times E$  as well as  $G \times E$  (linear) interactions, demonstrating that genotypes exhibited different yield responses to the environments examined and maybe even

Table 2. Regression coefficient (b<sub>i</sub>) and deviation from regression (s<sup>2</sup>d<sub>i</sub>) scores of top 20 genotypes (based on their overall mean grain yield from three environments) out of 64 genotypes evaluated in 2020-2021 *Rabi* season

Genotypic code	Pooled mean grain yield per plot (kg)	Regression coefficient (b <sub>i</sub> )	Deviation from regression (s <sup>2</sup> d <sub>i</sub> )
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  $p \le 0.05$ , \*\*significant at  $p \le 0.01$ .

different levels of adaptability.

In this work, selection is used to create populations whose mean values are higher than the mean values of the 64 genotypes that were considered as a whole. This variation ought to result from different genotypes rather than environmental factors (House 1985). Due to their greater mean grain yields than the mean grain yield of all 64 genotypes evaluated, all of the hybrids shown in table 4 were considered high-yielding hybrids. The hybrids, namely, SG-26 (b<sub>i</sub> = 1.139, s<sup>2</sup>d<sub>i</sub> =-0.013), SG-16 (b<sub>i</sub> = 1.171, s<sup>2</sup>d<sub>i</sub> =-0.016), SG-3 (b<sub>i</sub> = 1.206, s<sup>2</sup>d<sub>i</sub> =-0.02), SG-29 (b<sub>i</sub> = 1.230, s<sup>2</sup>d<sub>i</sub> =-0.02), and SG-6 ( $b_i = 1.381$ ,  $s^2d_i = -0.019$ ), recorded regression coefficient (b<sub>i</sub>) values almost equal to unity and deviation from regression (s<sup>2</sup>d.) values of near zero, indicating that they would be adapted to all three environments  $(b_1 = 1)$ with a high prediction of average stability ( $s^2d_1 = 0$ ) (Table 1). Regression coefficients greater than one with a minimum deviation  $(s^2d)$  value were found for the SG-12 (b = 2.037,  $s^2d_i = 0.028$ ), SG-14 (b<sub>i</sub> = 2.035,  $s^2d_i = -0.015$ ), and SG-35 (b<sub>i</sub> = 2.715,  $s^2d_i = -0.019$ ) hybrids with mean grain yields higher than the grand mean grain yield, indicating that these hybrids were not stable under (Fig. 1). The hybrids 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) were shown to be above average stable (bi 1) with increasing selectivity towards low yielding (unfavorable) environments. Commercial check genotypes SG-63 (CSV-41) and SG-64 (CSH-16) showed the lowest minimum significant deviation s<sup>2</sup>d values (-0.005 and -0.02) and the least b<sub>1</sub> (0.091 and -0.302), indicating that they were solely sensitive to unfavorable growing conditions. Because SG-22, SG-34, and SG-8 record notable departures from regression values, their stability is unclear (Table 1).

When stability parameters recommended by Eberhart and Russell (1966) were examined for various genotypes, it was found that hybrids SG-26, SG-16, SG-3, SG-29, and SG-6 demonstrated wider adaptability to all three environments with stable performance for high grain yield per plot, whereas hybrids SG-12, SG-14, and SG-35 were discovered to be adapted to specific, high-yielding environments, while hybrids SG-23, SG-20, It is proposed that these genotypes could serve as sources of stability genes for the breeding effort. The current investigation observed that the hybrids SG-26, SG-16, SG-3, SG-29, and SG-6 had greater yields and stability than the check genotypes CSV-41 and CSH-16, which had been chosen over a long period of time under local environmental circumstances. Previous studies by Da Silva et al. (2022), Anjaneya et al. (2020), Sandeep et al. (2020), and Seyoum et al. (2020) revealed that grain yields in sorghum were highly stable. High-yielding genotypes that can adapt and remain stable in a variety of environments have been identified and are thought to be possibilities for commercial release (Souza et al. 2013). More studies into adaptation and stability in various seasons and environments are needed to provide a full picture of the relationship between genotype and environment.

## Authors' contribution

Conceptualization of research (CVSK, VS, BVV); Designing of the experiments (VS, CVSK, SR, KS, KVY); Contribution of experimental materials (CVSK); Execution of field/lab experiments and data collection (SM, KS, SR, VS, KVY); Analysis of data and interpretation (VS, CVSK, BVV); Preparation of the manuscript (VS, CVSK, BVV).

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