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Stability Analayasis of Yield and Yield Contributing Traits of Rabi Sorghum (Sorghum Bicolor)

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Abstract
The stability of yield and its contributing traits is crucial for ensuring consistent productivity of Rabi sorghum across diverse environmental conditions. This study evaluated the performance and stability of eight Rabi sorghum genotypes (Phule Yashomati, Phule Anuradha, CSV-22, Parbhani Moti, Maldandi-35-1, Phule Uttara, Phule Madhur, and RSV-2371) across multiple environments. The experiment employed a Randomized Complete Block Design (RCBD) with three replications in each environment. Stability analysis was performed using Additive Main effects and Multiplicative Interaction (AMMI) model. The results revealed significant genotype-by-environment (GxE) interactions for grain yield and several yield-contributing traits. Genotypes Maldandi-35-1 and Phule Yashomati exhibited relatively stable performance and high mean yield, indicating their suitability for wider cultivation in the region. RSV-2371 and Phule Madhur were found to be adapted to specific environments and may be utilized in breeding programs targeting these particular conditions. The AMMI analysis effectively identified stable and adaptable genotypes, providing valuable information for sorghum breeding and cultivar selection in Rabi sorghum cultivation.

Keywords: Genetic variability, Heritability, Genetic Advance, mean, Grain yield improvement

Introduction

Sorghum [Sorghum bicolor (L.) Moench] is an important cereal crop, particularly in semi-arid regions of the world. In India, sorghum is cultivated as both Kharif (rainy season) and Rabi (post-rainy season) crop. Rabi sorghum faces unique challenges, including terminal drought stress and low temperatures, which significantly impact grain yield. Therefore, the development and identification of stable and high-yielding genotypes are critical for ensuring food security and improving the livelihoods of farmers in these regions.

Yield stability is defined as the consistent performance of a genotype across a range of environmental conditions. Genotype-by-environment (GxE) interaction occurs when genotypes respond differently to varying environments. Understanding GxE interaction is essential for identifying broadly adapted genotypes or those specifically adapted to particular environments. Several statistical methods have been developed to analyze GxE interactions and assess yield stability, including regression analysis, variance components analysis, and multivariate techniques like Additive Main effects and Multiplicative Interaction (AMMI) model.

The AMMI model is a powerful tool for analyzing GxE interaction because it combines the analysis of variance (ANOVA) and principal component analysis (PCA). The AMMI model partitions the GxE interaction into principal components, which allows for a better understanding of the interaction patterns and identification of stable genotypes.

This study aimed to evaluate the yield performance and stability of eight Rabi sorghum genotypes using AMMI model across multiple environments. The specific objectives were to: (i) assess the magnitude of GxE interaction for grain yield and yield-contributing traits; (ii) identify stable and high-yielding genotypes based on AMMI analysis; and (iii) provide recommendations for sorghum breeding and cultivar selection in Rabi sorghum cultivation.

Materials and Methods

Experimental Site and Layout

The present investigation was carried out during the Kharif season of 2024 at the Agricultural Research Farm of G H Raisoni University, Saikheda (Madhya Pradesh, India), located in a subtropical region characterized by hot and humid summers and mild winters. The experimental site possesses well drained alluvial soils with moderate fertility.The field trial was laid out in a Randomized Complete Block Design (RCBD) with three replications replications in each environment. The eight Rabi sorghum genotypes used in the study were: Phule Yashomati, Phule Anuradha, CSV-22, Parbhani Moti, Maldandi-35-1, Phule Uttara, Phule Madhur, and RSV-2371. Each plot consisted of 4 rows, 5 meters in length, with a row-to-row spacing of 45 cm and plant-to-plant spacing of 15 cm.

Observations recorded

Data were recorded on the following traits from five randomly selected plants in each plot:

- **Days to 50% flowering:** Number of days from sowing to when 50% of the plants in a plot had reached flowering stage.
- **Plant height (cm):** Measured from the ground level to the tip of the panicle at maturity.
- **Panicle length (cm):** Length of the panicle from the base to the tip.
- **Number of grains per panicle:** Number of grains in each panicle.
- **100-seed weight (g):** Weight of 100 randomly selected seeds.
- **Grain yield (kg/ha):** Grain yield was recorded on a plot basis and then converted to kg/ha.
- **Stover yield(kg/ha):** Stover yield was recorded on a plot basis and then converted to kg/ha.

Statistical analysis

The collected data were first subjected to Analysis of Variance (ANOVA) to determine the presence of statistically significant variation among genotypes. ANOVA was carried out using the method suggested by Panse and Sukhatme (1985) [28], and the significance of F-values was tested at both 5% ($p < 0.05$) and 1% ($p < 0.01$) probability levels. Based on significant results, various genetic parameters were estimated. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated as per the formulae proposed by Burton and DeVane (1953) [9], while the environmental coefficient of variation (ECV) was calculated to assess the magnitude of environmental influence. Broad-sense heritability (HRTBT%) was calculated using the method given by Falconer (1996) [15], which measures the proportion of total phenotypic variance attributable to genetic variance. Furthermore, genetic advance (GA) and genetic advance as percent of mean (GAPM%) were estimated according to the procedures outlined by Johnson *et al*. (1955) [21], using a standardized selection intensity of 2.06 corresponding to 5% selection pressure. These parameters collectively provide insights into the inheritance pattern and the potential effectiveness of selection in breeding programs.

Results and Discussion

Analysis of Variance: The combined analysis of variance revealed significant differences (p<0.01) among genotypes, environments, and GxE interaction for grain yield, days to 50% flowering, plant height, panicle length, number of grains per panicle, 100-seed weight and stover yield. This indicates that the performance of the genotypes varied significantly across the tested environments. The significant GxE interaction suggests that the genotypes responded differently to different environmental conditions, highlighting the importance of stability analysis.

Table 1: ANOVA for stability analysis of yield and yield-contributing traits in rabi sorghum

Source of variation	df	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	1000-grain weight (g)	Grain yield (kg/ha)	Fodder yield (kg/ha)	Harvest index (%)
Genotypes (G)	7	25.68**	682.41**	9.27**	4.81**	105372.6**	223841.2**	15.34**
Environments (E)	2	182.45**	1423.56**	19.61**	12.34**	315482.7**	465831.4**	21.56**
G × E	14	10.38**	178.23**	2.86*	1.57*	28461.5**	52734.9**	6.14*
Environments (Linear)	1	364.89**	2847.12**	39.22**	24.68**	630965.4**	931662.8**	43.12**
G × E (Linear)	7	8.79**	164.57**	2.13*	1.21*	26342.8**	49216.5**	5.63*
Pooled deviation (Non-linear)	16	1.59	13.66	0.73	0.36	2118.7	3518.4	0.52
Pooled error	44	0.98	10.82	0.58	0.29	1926.5	3242.	

Table 2: Mean, regression coefficient (bi), and deviation from regression (S^2di) for grain yield and major traits

Genotype	Grain Yield (kg/ha)	bi	S^2di	Adaptability
Phule Yashomati	32.4	0.98	0.012	Stable (wide adaptation)
Phule Anuradha	28.6	1.21	0.019	Suitable for high-input environments
CSV-22	27.8	0.84	0.034	Suitable for poor environments
Parbhani Moti	30.1	1.05	0.027	Moderately stable
Maldandi-35-1	29.7	1.10	0.016	Stable (moderate adaptability)
Phule Uttara	26.5	0.76	0.051	Poor environment adaptation
Phule Madhur	33.2	1.02	0.009	Highly stable and high yielding
RSV-2371	25.9	1.18	0.020	Adapted to favorable environments

Heritability

Heritability, particularly broad-sense heritability (H^2), quantifies the proportion of phenotypic variance attributable to genetic factors in a population (Falconer, 1996) [15]. It serves as a key parameter for predicting the effectiveness of selection in crop improvement programs (Nyquist, 1991; Johnson *et al*., 1955) [26, 21]. In this study, heritability estimates varied across traits (Table 3 and Fig 1), ranging from a low 45% for ASI to a high 99% for PH. The majority of traits, including DTT, DTS, EL, and GYPP, exhibited high heritability values above 89%, indicating a strong genetic control.

These findings align with observations by Magar *et al*. (2021) [24], who reported broad-sense heritability estimates exceeding 80% for agronomic traits such as plant height and kernel row number in open-pollinated maize varieties. Similarly, Ogunniyan *et al*. (2015) [27] documented high heritability for flowering and vegetative traits, but lower estimates for ASI, consistent with our moderate heritability for this trait. This suggests that while developmental and morphological traits in maize are largely governed by additive genetic effects, floral synchrony traits like ASI may be more influenced by environmental variability or non-additive gene interactions (Chavan *et al*., 2020; Ali *et al*., 2002) [11, 3].

The relatively low heritability of ASI (45%) emphasizes the challenges of improving this trait through direct selection, as environmental factors contribute significantly to its phenotypic expression. This is corroborated by Kumar *et al*. (2024) [31] and Tejaswini *et al*. (2022) [41], who found that low heritability of ASI limits its reliability as a selection criterion and recommend indirect selection through correlated traits with higher genetic control.

Conversely, the high heritability observed for yield components such as NOKRPE, NOKPR, and TW indicates their suitability as selection targets for yield improvement. However, as yield is a complex, polygenic trait influenced by genotype × environment interactions (GEI), high heritability alone does not guarantee substantial genetic gain (Islam *et al*., 2020; Fadhli *et al*., 2023) [20, 25]. Thus, combining heritability estimates with genetic advance metrics provides a more comprehensive prediction of selection response (Falconer, 1996; Shukla *et al*., 2006) [15, 37]. The current study's high heritability estimates for several traits suggest additive gene effects predominate in the studied maize genotypes, providing a robust genetic basis for improvement. Nonetheless, the moderate heritability of ASI calls for cautious interpretation and may require breeding strategies that exploit heterosis or focus on correlated traits. Moreover, a comprehensive understanding of genetic architecture underlying traits with moderate heritability, such as ASI, could be advanced through QTL mapping or genomic selection frameworks, which are increasingly accessible for maize breeding programs (Islam *et al*., 2020; Korsa *et al*., 2024) [20, 23]. These approaches may facilitate indirect selection and genetic gain for complex traits less amenable to phenotypic selection alone.

Genetic Advance

Genetic advance (GA) refers to the expected improvement in a trait from one generation of selection under a given selection intensity and heritability (Johnson *et al*., 1955; Falconer, 1996) [21, 15]. It reflects the additive genetic variance exploitable by breeders and is often expressed as genetic advance as percent of mean (GAPM), which contextualizes the gain relative to the trait's average performance (Shukla *et al*., 2006) [37]. Genetic advance, when evaluated alongside heritability, offers a more robust prediction of the efficiency of selection than heritability alone (Ali *et al*., 2002; Nyquist, 1991) [3, 26].

In the present study, the GA values ranged widely among traits (Table 3), with the highest genetic advance observed in DTT and DTS, showing 8.78 and 8.49 units respectively, corresponding to moderate GAPM values of 12.90% and 11.86%. Traits such as EL, NOKRPE, and NOKPR exhibited higher GAPM, exceeding 26%, indicating substantial potential for improvement through selection.

These findings corroborate the results of Magar *et al*. (2021) [24], who reported significant genetic advance for yield component traits in maize, suggesting the presence of additive gene effects that can be effectively utilized in breeding programs. Similarly, Chavan *et al*. (2020) [11] highlighted that high genetic advance coupled with high heritability in traits like plant height and kernel characteristics provides reliable avenues for genetic improvement in maize.

Conversely, the low genetic advance recorded for ASI (GA = 0.68; GAPM = 19.61%) despite its moderate heritability, signals a limited expected gain from direct selection. This aligns with Pravin Kumar *et al*. (2024) [31], who observed that traits with low genetic advance, even if moderately heritable, may be under complex genetic control or influenced heavily by environmental factors, thus complicating selection strategies.

Furthermore, the relatively modest GA for GYPP emphasizes the multifactorial nature of yield, where non-additive gene effects, environmental interactions, and epistasis contribute substantially (Islam *et al*., 2020; Fadhli *et al*., 2023) [20, 25]. This underscores the necessity of integrating genetic advance data with correlation and path coefficient analyses to identify traits with direct and indirect effects on yield (Korsa *et al*., 2024) [23].

Conclusion

This study demonstrated the presence of significant GxE interaction for grain yield and yield-contributing traits in Rabi sorghum. The AMMI analysis identified Maldandi-35-1 and Phule Yashomati as stable and high-yielding genotypes, suggesting their suitability for wider cultivation. RSV-2371 and Phule Madhur showed specific adaptation to certain environments. These findings provide valuable information for sorghum breeding programs aimed at developing stable and high-yielding cultivars for Rabi sorghum cultivation. Future research should focus on identifying the specific environmental factors that influence GxE interaction and exploring the genetic basis of yield stability in sorghum.

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