Received: 08 Jan 2025 | Revised: 20 Mar 2025 | Accepted: 22 Mar 2025

Electronic Journal of Plant Breeding

Research Article

Selection of high-yielding and stable sugarcane (*Saccharum spp.* hybrids) clones across diverse seasons using WAASB and MGIDI methods

D. Adilakshmi[1*], P. V. Padmavathi[1], D. Purushotama Rao[1] and Ch. Mukunda Rao[2]

[1]Department of Plant Breeding, ANGRAU-Regional Agricultural Research Station, Anakapalle-531001
[2]Department of Crop Physiology, ANGRAU-Regional Agricultural Research Station, Anakapalle-531001
***E-Mail:** purushotamadatti@gmail.com

Abstract
Sugarcane is an important crop that significantly contributes to the production of sugar, jaggery, and bioethanol worldwide. One of the major challenges sugarcane breeders face is identifying superior clones that possess a combination of desirable agronomic and quality traits. This study evaluated the performance of 11 sugarcane clones across first plant, second plant and ratoon crops using the Randomized Block Design (RBD) with three replications during the 2020-21 and 2021-22 growing seasons at the Regional Agricultural Research Station, Anakapalle. Mean yield, phenotypic stability, and the ideotype distance among the clones were assessed by utilizing weighted average absolute scores of the Best Linear Unbiased Predictor stability index and the multi-trait genotype ideotype distance index (MGIDI). The results indicated that two clones, G3 (2017A236), and G2 (2017A65), exhibited stable yield performance across seasons, as evidenced by the WAASB biplot and WAASBY scores. Based on the MGIDI index, clones G3 (2017A236) and G2 (2017A65) were identified as demonstrating consistent performance across eleven yield and quality traits. The strength-weakness design analysis suggested that selected clones are shows weak contribution to all adoptable traits. Hence, these clones are considered to near ideal plant type, indicating their potential as superior elite lines for utilization in breeding programs.

Keywords: Sugarcane, BLUP, WAASB, WAASBY and MGIDI

INTRODUCTION

Sugarcane is one of the cash crops, which is cultivated abundantly in the tropical and subtropical regions of India. Currently, itis cultivated in 56.48lakh hectares and with an annual production of 446.43 million tonnes in India (E&S, DAC - *2nd Adv.Est.-2023-2).Tropical regions of the country are the major productive regions averaging 80 tonnes per hectare while subtropical regions account for more than 58% of the total sugarcane cultivation area, with a comparatively lower productivity of 78 tonnes per hectare (E&S, DAC - *2nd Adv.Est.-2023-2).In the state of Andhra Pradesh, sugarcane is grown on 0.27 lakh hectares, producing 2.10 million tonnes (E&S, DAC - *2nd Adv.Est.-2023-2). The main sugarcane-growing areas in Andhra Pradesh are located in the northern coastal zone of the state (Tyagi *et al.,* 2023).

In the breeding of sugarcane, genetic gain plays a critical role in developing an efficient selection strategy among clones. Relying on a limited number of traits for clonal selection is not the most effective approach, as it does not contribute to improvements in other equally important traits (Behera *et al.,* 2024). Therefore, plant breeders prioritize the enhancement of desirable traits, aiming to combine them into a single clone that demonstrates superior performance. In plant breeding, linear selection indexes like the Smith-Hazel (SH) index are widely used to identify promising genotypes (Klein *et al.,* 2023). Despite their utility, a significant challenge lies in accurately defining the economic value of traits and translating these into practical economic weightings, which often constrains breeders in selecting optimal genotypes. To address these limitations, Olivoto and Nardino (2020) introduced the multi-trait genotype ideotype distance index (MGIDI), a novel model that uses factor analysis to evaluate genotypes by calculating their distance from an ideal ideotype. This index focuses on selecting superior genotypes in breeding programs that involve multiple assessed traits. In the present study, both the WAASBY and MGIDI indexes were evaluated using data from main yield trials, which involved 11 clones evaluated over the ratoon, first and second plant crops for 11 yield and quality traits. These analyses enabled to identify clones with stable performance across desirable traits combination over different crop seasons.

MATERIALS AND METHODS

This study was carried out on 11 early mature sugarcane clones (**Table 1**) over two seasons under the Main Yield Trials. The first plant and ratoon crop investigation was conducted during the years 2020-22, while the second plant crop was carried out during 2021-22 at the Regional Agricultural Research Station, Anakapalle, India. Entries from three seasons were assessed by raised in a RBD with three replications. Each clone was planted in six rows, measuring six meters in length and 90 centimeters apart in each row. All the agronomic package of practices recommended for the crop growth season were uniformly followed throughout the three seasons (Sugeerthi *et al.,* 2018). Plantation crops were harvested at 10 months age (October 2nd fortnight) while ratoon crop were harvested at 9 months age (September) to ensure uniformity in data collection and analysis.

The study focused on 11 quantitative and quality traits of sugarcane, selected according to the descriptors and guidelines provided by PPV&FR, 2001 under the Distinctiveness, Uniformity, and Stability (DUS) criteria (Blakeney, 2001).Observations included yield and quality parameters such as the no. of shoots (×1000/ha) at 120 days after planting (NT120DAP) and 240 days after planting (NT240DAP), cane length (cm) (SL), single cane weight (kg) (SCW), and number of millable canes (NMC), all expressed in thousands per hectare ('000/ha). CCS yield (t/ha) (CCSY) was estimated using the formula (Cane yield × CCS %) / 100), and cane yield (t/ha) (CY) was recorded on a per-plot basis and subsequently calculated per hectare. Jaggery yield (t/ha) (JY), brix (%) (BP) and sucrose (%) (SP) were recorded, at the harvest stage. Commercial Cane Sugar percentage (CCSP) was determined as (Sucrose % × 1.022) – (Brix % × 0.292). The cane yield data for 11 clones across multiple crop seasons was analyzed using a joint analysis of variance. Genetic parameters based on Best Linear Unbiased Predictor and multi-trait genotype ideotype distance index were calculated utilizing the 'metan' package (Olivoto and Lucio, 2020) in R Studio (Posit Team, 2022) with R version 4.1.

Table 1. List of plant materials used in this experiment

Code	Clone	Pidgree
G1	2017A36	CoA12321 X Co775
G2	2017A65	CoA12321 X Co775
G3	2017A236	CoA13327 X CoH15
G4	2017A253	CoT8201 X Co94008
G5	2017A340	Co0235GC
G6	2017A396	CoV89101 X CoT8201
G7	2017A408	CoV89101 X CoT8201
G8	2017A457	CoV89101 X CoT8201
G9	2017A405	CoV89101 X CoT8201
G10	2017A553	CoV89101 X ISH69
G11	87A298 (S)	Co 7704 X CoC 671

RESULTS AND DISCUSSION

Analysis of clonal variance and men performance of cane yield over crop seasons: The development of highly efficient ratoon ability clones is essential for widespread adoption in extensive cultivation in sugarcane. Genotype-by-environment interaction plays a central role in selecting candidate clones through multi-environment and multi-season trials. The joint analysis of seasonal variance for cane yield across different crop seasons is presented in **Table 2**. This analysis revealed genotype (G), environment (E), and their interaction (GEI) of individual effect was significant ($P \leq 0.01$) and the significant GEI effect indicates that the mean performance of the clones responded differently to variations in seasonal conditions, and this variance is valuable for studying phenotypic stability and adaptability across diverse crop cycles. Similar conclusions have been drawn by Durai *et al.* (2025) and Mehareb *et al.* (2022).The candidate clones should demonstrate a high mean yield across these crop cycles. The mean performance for cane yield ranged from 84.4 t/ha in the ratoon season to 110.93 t/ha in the first plant crop. Among the 11 clones, 2017A236 (G3) recorded the top mean yield (123.6 t/ha) over the three crop seasons. Cane yields among the clones ranged from 64.19 t/ha (G8) to 137.47 t/ha (G1) during the ratoon to first plant crop.

BLUP-based genetic parameters: The BLUP (Best Linear Unbiased Predictor) is an advanced method used to identify stable performance clones across multiple environmental trials by estimating random effects within mixed models (Pezeshkpour *et al.,* 2024). It provides a clear understanding of the various factors that influence genotype-environment interactions (GEI). The success of crop breeding relies on the existing genetic variability

Table 2. Analysis of Variance for cane yield (t/ha) among eleven clones

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ENV	2	11856.69	5928.35	733.06	0.00
REP(ENV)	6	48.52	8.09	86.85	0.00
GEN	10	19947.05	1994.71	4.39	0.00
GEN:ENV	20	9096.73	454.84	4884.59	0.00
ENV/GEN	22	20953.42	952.43	10228.35	0.00
ENV/G1	2	2658.48	1329.24	14274.99	0.00
ENV/G10	2	1323.21	661.61	7105.15	0.00
ENV/G11	2	287.96	143.98	1546.21	0.00
ENV/G2	2	2533.12	1266.56	13601.87	0.00
ENV/G3	2	1339.64	669.82	7193.35	0.00
ENV/G4	2	4415.98	2207.99	23712.09	0.00
ENV/G5	2	4138.37	2069.19	22221.47	0.00
ENV/G6	2	300.64	150.32	1614.30	0.00
ENV/G7	2	2289.39	1144.70	12293.14	0.00
ENV/G8	2	873.05	436.53	4687.96	0.00
ENV/G9	2	793.59	396.79	4261.27	0.00
Residuals	60	5.59	0.09		
CV(%)	0.31				
MSR+/MSR-	2.14				
OVmean	96.43				

within a population and the heritability of the traits (Rao and Chaturvedi, 2024). A plant breeder must analyze the genetic variation present in the existing population to select desirable traits for modeling (Behera *et al.,* 2024, Sujitha *et al.,* 2024, Verma *et al.,* 2023 and Mohamed *et al.,* 2022). BLUP-based variance components for cane yield (t/ha) across different crop seasons are illustrated in **Table 3**.

The likelihood ratio test revealed significant effects ($p < 0.05$) for both genotype and genotype-by-environment interaction (GEI) concerning cane yield (t/ha) in this

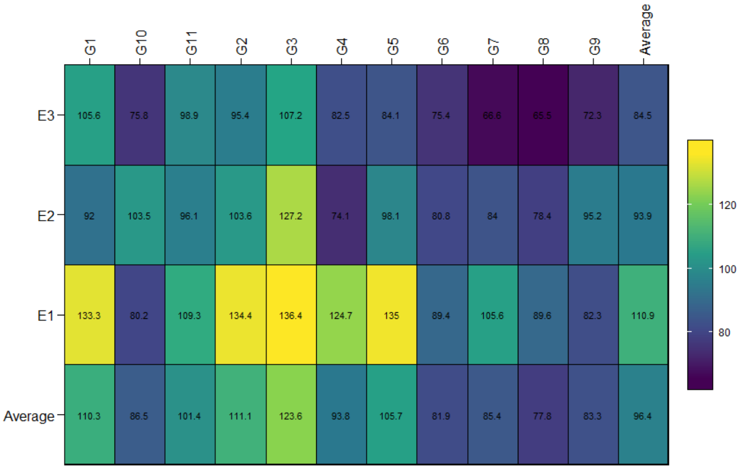
Table 3. BLUP-Based Variance Components for cane yield (t/ha) among eleven clones over crop seasons

Parameters	CY	Parameters	CY
Mean	96.44	Phenotypic variance	322.77
SE	2.05	Heritability	0.53
SD	20.34	GEIr^2	0.47
CV	21.2	h^2mg	0.77
Min	64.193$^{\#}$ (G8 in E3)	Accuracy	0.88
Max	137.47$^{\#}$ (G3 in E1)	rge	1.00
MinENV	E3 (84.49$^{\#}$)	CVg	13.56
MaxENV	E1 (110.93$^{\#}$)	CVr	0.32
MinGEN	G8 (77.83$^{\#}$)	CV ratio	42.87
MaxGEN	G3 (123.6$^{\#}$)		
LRT_g	7.88**		
LRT_{ge}	398.78**		

***significant at $p < 0.001$,LRT significance test is conducted against the Chi-square value; CY= cane yield (t/ha); LRT = Likelihood Ratio Test for the random effects; Heritability = Broad-sense heritability BLUP basis; GEIr^2= Coefficient of determination for the genotype-vs-environment interaction effects; h^2 mg = Heritability on the mean basis; Accuracy = Selective accuracy; rge = Genotype X environment correlation; CVg = Genotypic coefficient of variation; CVr = Residual coefficient of variation; CV = Ratio between genotypic and residual coefficient of variation. #= tonnes per hectare.

study. The significant GEI effect suggests that the clones demonstrate varying performance across different seasons, indicating that there is sufficient genetic variation for effective selection. Cane yield accounted for 53.01% of the genotypic variance, while the phenotypic variance was completely represented. Consequently, low estimates of broad-sense heritability were observed, suggesting that most of the significant variance is attributed to environmental factors rather than genetic ones (Pezeshkpour *et al.,* 2024). The genotypic coefficient of variation (CV) was 13.56%, which was notably higher than the residual CV of 0.32%. The genotypic accuracy of selection, defined as the correlation between predicted and actual values, was determined to be 0.88. These findings are useful for identifying superior clones over multiple seasons. Similar results were reported by other researchers, including Munda *et al.* (2023), Nataraj*et al.* (2021), and Shiri *et al.* (2024).

Evaluation of 11 sugarcane clones over crop seasons using the WAASB-based stability method: The WAASB index was utilized to select stable clones, while the WAASBY index was employed to identify stable clones with desirable mean traits. Both the indices were validated for cane yield across different crop seasons, as shown in **Fig 2**. In this study, based on WAASB scores the clones G8 (2017A457) and G7 (2017A408) were identified as stable. Notably, these clones exhibited lower mean values than the average for the population cane yield; therefore, they are not recommended for cultivation



	G1	G10	G11	G2	G3	G4	G5	G6	G7	G8	G9	Average
E3	105.6	75.8	98.9	95.4	107.2	82.5	84.1	75.4	66.6	65.5	72.3	84.5
E2	92	103.5	96.1	103.6	127.2	74.1	98.1	80.8	84	78.4	95.2	93.9
E1	133.3	80.2	109.3	134.4	136.4	124.7	135	89.4	105.6	89.6	82.3	110.9
Average	110.3	86.5	101.4	111.1	123.6	93.8	105.7	81.9	85.4	77.8	83.3	96.4

Fig 1. Cane yield (t/ha) of eleven clones over three seasons
E1= I plant crop, E2= second Plant ceop, E3= ratoon crop

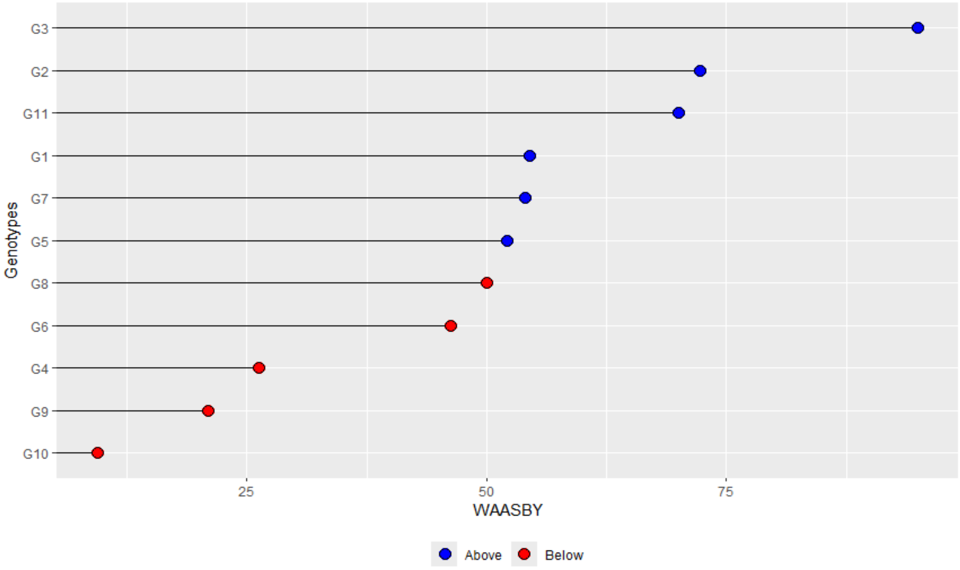


Fig. 2.The WAASBY mean performances of eleven clones for cane yield (t/ha) over the seasons

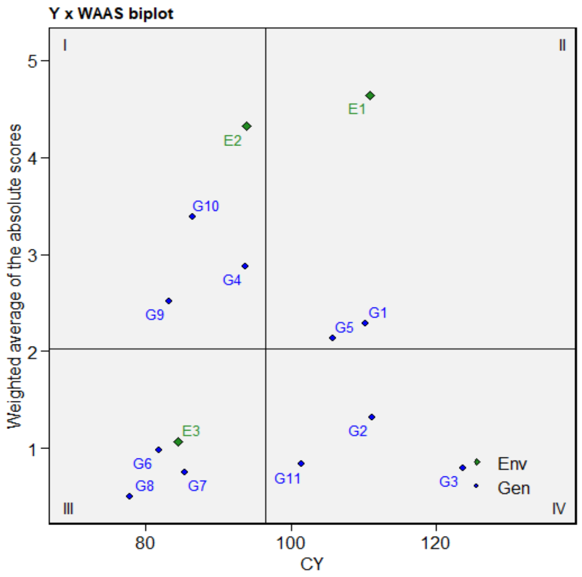


Fig 3. The Y X WAASB bi-plot mean performances of eleven clones for cane yield (t/ha) over the seasons

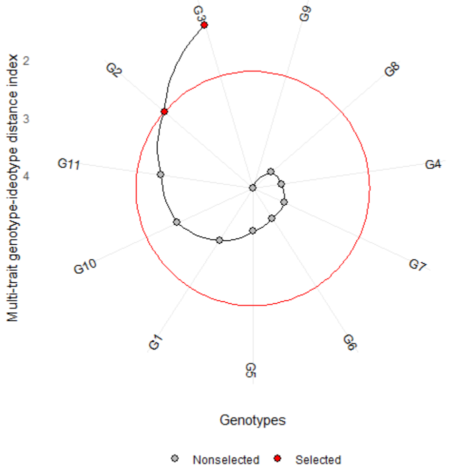


Fig 4. Ranking of eleven clones in ascending order based on MTSI index

or crop improvement programs. The WAASBY index revealed that clones G3 (2017A236) and G2 (2017A65) are stable and demonstrated high mean performance among the 11 clones examined over the crop seasons and it was illustrated in the **fig 2**. The Y × WAASB bi-plot categorizes the 11 clones and three seasons into four quadrants, allowing for a combined interpretation of stability and mean performance (**Fig. 3**). The clones G3, G11, and G2, fell within the fourth quadrant, indicating both high yield and stability. These clones are promising candidates for varietal recommendations for commercial cultivation in specific environments. Similar outcomes were reported by previous studies by Koundinya *et al.* (2021) in cassava and Li and Wu, (2023) in rapeseed.

*Selection of clones based on MGIDI index:*The MGIDI index demonstrated that clones with lower MGIDI values were closer to the ideotype and exhibited consistent high mean performance and stability across all studied traits and growing seasons. Among the 11 clones, G3 (2017A236) and G2 (2017A65) were selected as closest to the ideotype using a selection intensity of 15% across all investigated traits, with each clone receiving an 80% weightage of each trait in selection. The ranking of the genotypes was determined based on their MGIDI scores (**Table 4**) and is illustrated in **Fig. 4**.

Table 4. MGIDI Scores of eleven clones

S.No	Genotype	MGIDI
1	G3	1.27
2	G2	2.20
3	G11	2.62
4	G10	2.79
5	G1	3.16
6	G5	3.49
7	G6	3.61
8	G7	3.63
9	G4	3.72
10	G8	3.81
11	G9	4.24

Loadings and factor delineation: The results of the factor analysis using the WAASBY index for 11 yield and quality traits across 11 clones are summarized in **Table 4**, which includes eigenvalues and explained variance. Three principal components were retained, accounting for a cumulative variance of 86.95% (**Table 5**). After applying varimax rotation, the average communality (h) was found to be 0.86, with a maximum of 0.96 for the number of shoots at 240DAP and a minimum of 0.68 for jaggery yield. The maximum value of communality indicates that these factors can explain a significant portion of the variance in each trait analyzed. The yield and quality traits were categorized into three factors based on their communality values. Factor 1 (FA1) is associated with agronomic and yield traits, including NT 120DAP, NT 240DAP, NMC, SL, CY, and CCSY. Factor 2 (FA2) relates to sugar quality characteristics, such as BP, SC, and CCSP. Factor 3 (FA3) includes traits related to SCW and JY. These results aligned with the findings of Ahsan *et al.* (2024) in sesame and Klein *et al.* (2023) in oats.

Predicted genetic gains under selection based on MGIDI The selection differential and predicted genetic gains for yield and quality traits are illustrated in **Table 6**. The

Table 5. Factor analysis using MGIDI method for eleven traits across eleven clones

S.No.	Character	FA1	FA2	FA3	Communality	Uniquenesses
1	No. of shoots at 120 DAP (x 1000/ha)	-0.906	-0.033	0.030	0.822	0.178
2	No. of shoots at 240 DAP (x 1000/ha)	-0.980	-0.044	-0.049	0.964	0.036
3	No. of millable canes (000'/ha)	-0.863	-0.001	-0.441	0.939	0.061
4	Stalk length (cm)	-0.882	-0.127	0.190	0.830	0.170
5	Single cane weight (kg)	0.147	0.121	-0.827	0.721	0.279
6	Cane yield (t/ha)	-0.759	-0.049	-0.587	0.922	0.078
7	CCS yield (t/ha)	-0.742	-0.319	-0.511	0.914	0.086
8	Jaggery yield (t/ha)	-0.327	-0.345	-0.678	0.685	0.315
9	Brix (%)	0.158	-0.933	-0.019	0.895	0.105
10	Sucrose (%)	-0.202	-0.954	-0.037	0.953	0.047
11	CCS (%)	-0.162	-0.943	-0.059	0.919	0.081
	PC	PC1	PC2	PC3		
	Eigenvalues	5.41	2.62	1.54		
	Variance (%)	49.15	23.83	13.96		
	Cum. variance (%)	49.15	72.98	86.95		

Table 6. Evaluation of selection differential and genetic gains for eleven traits

S.No.	Character	Factor	Xo	Xs	SD	SDperc	h2	SG	SGperc	sense	goal
1	No. of shoots at 120 DAP (x 1000/ha)	FA1	118.53	130.40	11.88	10.02	0.68	8.08	6.81	increase	100.00
2	No. of shoots at 240 DAP (x 1000/ha)	FA1	103.41	116.86	13.45	13.01	0.75	10.07	9.73	increase	100.00
3	No. of millable canes (000'/ha)	FA1	93.90	105.80	11.90	12.68	0.66	7.85	8.36	increase	100.00
4	Stalk length (cm)	FA1	284.83	325.12	40.29	14.15	0.91	36.81	12.92	increase	100.00
5	Cane yield (t/ha)	FA1	96.44	114.81	18.37	19.05	0.71	12.96	13.44	increase	100.00
6	CCS yield (t/ha)	FA1	11.83	14.42	2.58	21.82	0.79	2.05	17.30	increase	100.00
7	Brix (%)	FA2	18.45	18.76	0.31	1.69	0.54	0.17	0.91	increase	100.00
8	Sucrose (%)	FA2	16.97	17.34	0.37	2.18	0.59	0.22	1.29	increase	100.00
9	CCS (%)	FA2	12.01	12.28	0.27	2.28	0.60	0.16	1.37	increase	100.00
10	Single cane weight (kg)	FA3	0.94	0.93	0.00	-0.35	0.79	0.00	-0.27	increase	0.00
11	Jaggery yield (t/ha)	FA3	10.58	12.80	2.22	21.01	0.64	1.42	13.42	increase	100.00
			variable	**min**	**mean**	**max**	**sum**	**sd**	**sense**		
			SDperc	-0.34629	10.68479	21.817	117.5327	8.171763	increase		
			SGperc	-0.27286	7.753853	17.30144	85.29238	6.174031	increase		

Xo = mean for WAASBY index of the original population; Xs = mean for WAASBY index of the selected genotypes; SD and SD perc, The selection differential and selection differential in percentage; SG and SG perc, The selection gains and selection gains in percentage

MGIDI Index effectively identified desirable traits using the WAASBY method, achieving an 80% success rate. A positive selection differential (SD) was noted for 10 out of the 11 agronomic and quality traits assessed. All yield and quality traits demonstrated positive selection differentials, except for single cane weight, which had a value of -0.003, indicating undesired selection. The average selection differential (%) and selection gains are 10.68% and 7.75%, respectively. The CCS yield exhibited the highest SD% and SG% at 21.81% and 17.31%, while single cane weight recorded the lowest at -0.34% for SD% and -0.27% for SG%. Based on the WAASBY index for these traits, the selected genotypes displayed greater stability. The higher percentage of positive selection differentials and percentage genetic gain under selection enhances the breeding program, indicating significant improvement toward the desired characteristics and suggesting that the selection process is quite effective. Similar findings were reported by Benakanahalli *et al.* (2021) in guar.

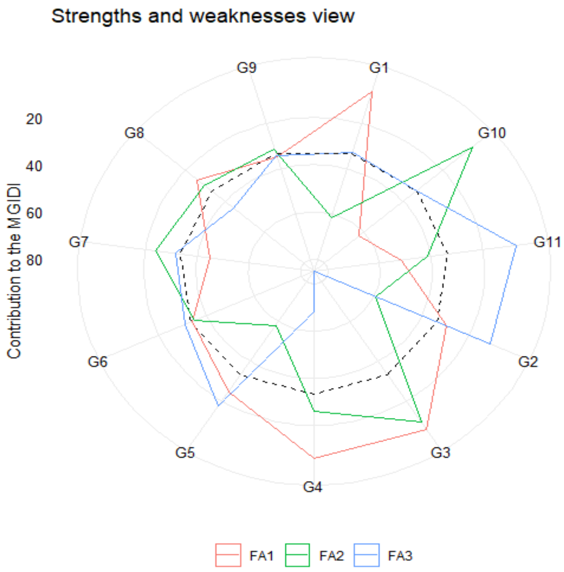


Fig. 5. The strengths and weaknesses view of all clones under study

The strength-weakness perspectives of all clones based on the MGIDI index are illustrated in **Fig. 5**. Each factor contributing to the MGIDI index is categorized into two groups: those that contribute the least are shown at the edge of the plot, while the factors with significant contributions are displayed in the center. The dashed line represents the theoretical value if all factors contributed equally. The selected clones, G3 and G2, are considered stable and close to the ideal type, as they exhibit three factors that have weak contributions to all the adoptable traits.

Overall, this investigation compared the results from various stability analysis modules, including BLUPs, WAASBY, and the MGIDI index, and concluded that the clone 2017A 236 (G3) and 2017A 65 exhibited stable performances in terms of yield across three crop cycles. The WAASB assesses clonal stability using multi-environment trial data, while the MGIDI method simultaneously selects the performance of genotypes and their stability in relation to multiple traits. This approach helps identify high-yielding clones with desirable trait combinations. Consequently, the MGIDI method aids plant breeders in making precise decisions to identify ideal plant genotypes with the desired traits, thereby supporting breeding programs designed to improve the cane yield.

REFERENCES

Ahsan, A.F.M.S., Alam, Z., Ahmed, F., Akter, S. and Khan, M.A.H. 2024. Selection of waterlogging tolerant sesame genotypes (*Sesamum indicum* L.) from a dataset using the MGIDI index. *Data in Brief*, **53**: 110176. [Cross Ref]

Behera, P.P., Singode, A., Bhat, B.V., Ronda, V., Borah, N., Yue, H. and Sarma, R.N. 2024. WAASB-based stability analysis and simultaneous selection of forage sorghum for forage yield traits. *Euphytica*, **220**(9): 145. [Cross Ref]

Benakanahalli, N.K., Sridhara, S., Ramesh, N., Olivoto, T., Sreekantappa, G., Tamam, N. and Abdelmohsen, S.A. 2021. A framework for identification of stable genotypes based on MTSI and MGDII indexes: An example in guar (*Cymopsistetragonoloba* L.). *Agronomy*, **11**(6): 1221. [Cross Ref]

Blakeney, M. 2001. Protection of plant varieties and farmers' rights. *European Intellectual Property Review*, **24**: 9-19.

Durai, A.A., Amaresh, Kumar, R.A. and Hemaprabha, G. 2025. Elucidating the GXE interaction using AMMI, AMMI stability parameters, and GGE for cane yield and quality in sugarcane. *Tropical Plant Biology*, **18**(1): 3. [Cross Ref]

Klein, L.A., Marchioro, V.S., Toebe, M., Olivoto, T., Meira, D., Meier, C. and Finatto, J.L.B. 2023. Selection of superior black oat lines using the MGIDI index. *Crop Breeding and Applied Biotechnology*, **23**(3): e45112332. [Cross Ref]

Koundinya, A.V.V., Ajeesh, B.R., Hegde, V., Sheela, M.N., Mohan, C. and Asha, K.I. 2021. Genetic parameters, stability, and selection of cassava genotypes between rainy and water stress conditions using AMMI, WAAS, BLUP, and MTSI. *ScientiaHorticulturae*, **281**: 109949. [Cross Ref]

Li, Z. and Wu, W. 2023. Genotype recommendations for high performance and stability based on multiple traits selection across a multi-environment in rapeseed. *European Journal of Agronomy*, **145**: 126787. [Cross Ref]

Mehareb, E.M., Osman, M.A.M., Attia, A.E., Bekheet, M.A. and Abo Elenen, F.F. 2022. Stability assessment for selection of elite sugarcane clones across multi-environment based on AMMI and GGE-biplot models. *Euphytica*, **218**(7): 95. [Cross Ref]

Mohamed, M. M., Darwish, M. A., Abd El-Rady, A. G., Ghalab, E. and Elfanah, A. M. 2022. Estimation of AMMI and GGE biplots for some bread and durum wheat genotypes. *Journal of Plant Production*, **13**(3): 75-83. [Cross Ref]

Munda, S., Paw, M., Saikia, S., Begum, T., Baruah, J. and Lal, M. 2023. Stability and selection of trait-specific genotypes of *Curcuma caesia*Roxb. using AMMI, BLUP, GGE, WAAS, and MTSI model over three years evaluation. *Journal of Applied Research on Medicinal and Aromatic Plants*, **32**: 100446. [Cross Ref]

Nataraj, V., Bhartiya, A., Singh, C.P., Devi, H.N., Deshmukh, M.P., Verghese, P. and Gupta, S. 2021. WAASB-based stability analysis and simultaneous selection for grain yield and early maturity in soybean. *Agronomy Journal*, **113**(4): 3089-3099. [Cross Ref]

Olivoto, T. and Lúcio, A.D. 2020. Metan: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution*, **11**: 783–789. doi: 10.1111/2041-210X.13384. [Cross Ref]

Olivoto, T. and Nardino, M. 2021. MGIDI: Toward an effective multivariate selection in biological experiments. *Bioinformatics*, **37**: 1383–1389. [Cross Ref]

Pezeshkpour, P., Amiri, R., Karami, I. and Mirzaei, A. 2024. Evaluation of seed yield stability of lentil genotypes based on REML/BLUP and Multi-Trait Stability Index (MTSI). *Journal of Crop Breeding*, **16**(2): 42-52. [Cross Ref]

Posit Team. 2022. RStudio: Integrated development environment for R. *Posit Software, PBC*, Boston, MA. URL: http://www.posit.co/.

Rao, D. P. and Chaturvedi, H. P. 2024. Identification of foxtail millet (*Seteria italica* (L.) P. Beauv.) genotypes for multi-season adaptability using GGE biplot analysis in Foothills of Nagaland. *Electronic Journal of Plant Breeding*, **15**(3): 650-659. [Cross Ref]

Shiri, M., Moharramnejad, S., Estakhr, A., Fareghi, S., Najafinezhad, H., KhavariKhorasani, S. and Mohseni, M. 2024. Determining the stability of new maize hybrids with WAASBY and MTSI indices. *Journal of Crop Breeding*, **16**(2): 14-28. [Cross Ref]

Sugeerthi, S., Jayachandran, M.and Chinnusamy, C. 2018. Effect of planting materials and integrated nutrient management on yield of sugarcane seed crop. *Madras Agricultural Journal,***105**. [Cross Ref]

The Second Advance Estimates of production of Foodgrains, Oilseeds and Other Commercial Crops for the year 2023-24 released by the Directorate of Economics and Statistics (E&S) within the Department of Agriculture and Cooperation (DAC), Ministry of Agriculture, Government of India.

Tyagi, S., Chandra, S. and Tyagi, G. 2023. Statistical modelling and forecasting annual sugarcane production in India: Using various time series models. *Annals of Applied Biology*, **182**(3): 371-380. [Cross Ref]

Sujitha, R., Iyanar, K., Ravikesavan, R., Chitdeshwari, T., Boopathi, N. M. and Rasitha, R. 2024. Insights into yield stability: A comparative analysis of regression, AMMI indices and Biplot Methods in pearl millet. *Electronic Journal of Plant Breeding*, **15**(1): 42-52. [Cross Ref]

Verma, A., Verma, R. P. S., Singh, J., Kumar, L. and Singh, G. P. 2023. Parametric and Non Parametric measures to compare fixed and random effects of malt barley genotypes. *Electronic Journal of Plant Breeding*, **14**(2): 646-654. [Cross Ref]