



Selection of superior fodder maize (*Zea mays*) parental inbreds using multi trait genotype ideotype distance index (MGIDI) and multi trait stability index (MTSI)

S PALANIYAPPAN¹, K N GANESAN^{1*} and N MANIVANNAN²

Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu 641 003, India

Received: 21 November 2023; Accepted: 15 October 2024

ABSTRACT

Fodder maize (*Zea mays* L.) is one of the highly nutritious and palatable forage crop among the cereal fodders. For identifying the superior parents for hybridization, breeders have to identify the best performing inbreds by evaluating different plant variables. However, selecting a genotype that excels across multiple traits is a complex and challenging task. The most widely used selection index method is Smith-Hazel model mainly based on phenotypic covariance matrices inversion. In this multi trait selection method, the presence of multicollinearity leads to inefficient estimates of selection gain. Therefore, the new genetic statistical selection indices like multi trait genotype ideotype distance index (MGIDI) and multi trait stability index (MTSI) were employed in the present experiment for selection of superior and stable performing genotypes among the 28 fodder maize inbreds. The MGIDI analysis in 28 fodder maize inbreds evaluated in three different seasons namely rainy (*khari*) 2022, winter (*rabi*) 2022 and summer 2023, revealed that African Tall, TNFM 139-1 and GETM 25 identified as superior genotypes across the three different seasons consistently. Similarly, MTSI analysis pertaining to the stability of genotypes indicated genotypes, viz. UMI 1201, N-09-160-2, GETM 25, 52485, UMI 1210 and N 66 to be superior and stable. The identified superior fodder maize inbreds could be used in breeding programme to develop heterotic single cross fodder maize hybrids.

Keywords: Fodder maize, Inbreds, MGIDI, MTSI

Maize (*Zea mays* L.) is considered as a staple food crop and widely used in most of the countries for animal feed, biofuel production (Choudhary *et al.* 2020). Due to its superior nutritive values, it is considered good green fodder in cattle diet (Tahir and Habib 2013). Its fodder is highly nutritious, tasty, and succulent, and animals, especially milch animals prefer to consume it. The amount of green fodder produced by a plant is influenced by several traits. It is necessary to understand how these advantageous attributes are related to other qualities in order to select better genotypes that produce more green fodder coupled with nutritional quality (Borkhatariya *et al.* 2022).

One of the key objectives of breeding programme is to select best performing genotypes and the linear selection index models which helps to address these issues (Ceron and Crossa 2018). The most widely using linear model of phenotypic selection index is Smith-Hazel model (Smith

1936, Hazel 1943). But the primary issue with this method is multicollinearity and it leads to inefficient estimates of selection gain (Olivoto *et al.* 2021a). Most selection in multi-environment trials is based on a single variable at a time, such as in AMMI or GGE biplot analysis. However, selection within an environment remains challenging because user preferences are not based on a single trait (Azrai *et al.* 2023). To overcome all of these weaknesses, Olivoto *et al.* (2021a) proposed a selection index called Multi trait genotype ideotype distance index (MGIDI) using BLUP (Best Linear Unbiased Prediction) values.

The appropriate understanding about Genotype × Environment interaction (GEI) in diverse environment might be helpful in screening and identification of superior and stable genotypes (Kumar *et al.* 2024). The additive main effect and multiplicative interaction (AMMI) is a univariate analysis graphical tools used for analysing multi environment trials (MET) (Gauch 2013). The other important method is BLUP that has the potential to enhance the predictive accuracy of random effects (Olivoto *et al.* 2019a). So, the newly developed method called multi-trait stability index (MTSI) based on WAASBY; includes both WAASB (weighted average of absolute scores from the singular value decomposition of the matrix of BLUP) index and the

¹Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu; ²Centre of Excellence in Molecular Breeding, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu. *Corresponding author email: knganesan71@gmail.com

weighting of response variables performance (Y). Hence, the current study explored MGIDI and MTSI approaches to select superior and stable fodder maize genotypes.

MATERIALS AND METHODS

Experimental material, seasons and design: An experiment was conducted during three different seasons, viz. rainy (*kharif*) 2022 (E1), winter (*rabi*) 2022–2023 (E2) and summer 2023 (E3) at Tamil Nadu Agricultural University, Coimbatore (11° N, 77° E and 427 m amsl), Tamil Nadu to evaluate 28 fodder maize inbred lines (Supplementary Table 1). Each genotype was evaluated in randomized complete block design (RCBD) with two replications in all the environments. Every genotype was grown in two rows of 4 m length with 30 cm spacing between rows and 15 cm between plants and the crop was successfully maintained following all the recommended agronomic practices.

Trait phenotyping: The experiment mainly focused towards forage yield and 50% flowering was considered as harvesting stage uniformly for all the genotypes. A total of 11 biometrical traits were measured namely days to 50% flowering (DFF), plant height (PH), cob placement height (CH), leaf length (LL), leaf breadth (LB), number of leaves (NL), number of nodes (NN), stem girth (SGR), internode length (IL), leaf stem ratio (LSR) and green fodder yield (GFY). The observations were recorded with five randomly selected plants in both the replications. After that, these plants were harvested and shade dried upto complete drying to measure the dry matter yield (DMY). After drying, samples were milled completely by Wiley mill to make powdered sample of each genotype. The forage quality traits like crude protein (CP), crude fiber (CF), acid detergent fiber (ADF) and neutral detergent fiber (NDF) were analysed using standard protocol prescribed by Association of Official Analytical Collaboration (1970) in 65 samples. These data were then used for the standardization of the NIR (Near Infrared Spectrophotometer) model SpectraAlyser ZEUTECH. After calibration with a standard graph, further analysis was carried out using an NIR instrument.

Statistical analysis

Selection of genotypes within the environment by MGIDI: Olivoto *et al.* (2020a) proposed the multi-trait genotype-ideotype distance index (MGIDI) to select genotypes which performs superior for most of the studied variables in single environment. Theoretically MGIDI index includes four steps, viz. rescaling the variables, computing the factor analysis, planning of ideotypes and calculation of distance between genotype and ideotype. The selection of genotypes within each environment by MGIDI was done by using all the 16 variables.

1) **Rescaling of the variables:** The rescaling of each variables was done by using following equation:

$$rX_{ij} = \frac{\eta_{nj} - \varphi_{nj}}{\eta_{oj} - \varphi_{oj}} \times (\theta_{ij} - \eta_{oj}) + \eta_{nj}$$

where η_{nj} and φ_{nj} , Rescaled maximum and minimum values of variables; η_{oj} and φ_{oj} , Maximum and minimum original values of traits, respectively; θ_{ij} , Original value of the i^{th} variable of the j^{th} genotype.

Factor analysis: The BLUP (Best Linear Unbiased Prediction) values of both studied variables and genotypes were used for recalling and computation of factor analysis. After that, for each genotypes the factorial score was estimated by following formula:

$$X = \mu + Lf + \xi$$

where μ , f and ξ are $p \times 1$ vector of standardized mean, common factors and residues, respectively; $L = p \times f$ is matrix factorial loading, p and f are number of variables and retained common factors, respectively. Based on this the correlation matrix for all the variables computed and eigen values and vectors were retained. Initial loading vectors were obtained from eigen values with greater than one.

Ideotype planning and MGIDI estimation: The ideotype has the maximum of rescaled value for all the studied variables. The final one is estimation of MGIDI index by using the following formula:

$$MGIDI_i = \sqrt{\sum_{j=1}^f (F_{ij} - F_j)^2}$$

where F_{ij} is i^{th} genotype score for j^{th} factor ($i = 1, 2, \dots, g$; $j = 1, 2, \dots, f$), g and f stated as total number of genotypes and their factors. The MGIDI were performed in R studio 4.2.1. with “metan” package version 1.18.0 (Olivoto *et al.* 2020b) using the ‘gamem’ and ‘mgidi’ functions.

Simultaneous selection based on mean performance and stability (MPS): Identification of superior genotypes based on simultaneous selection for mean performance and stability is done by utilizing the index called WAASBY. In this method, weighting between both the stability (WAASB) and the mean performance of response variables (Y), and it was performed by following the formula proposed by Olivoto *et al.* (2019a):

$$WAASBY_i = \frac{(rY_i \times \theta_y) + (rW_i \times \theta_w)}{\theta_y \times \theta_w}$$

where $WAASBY_i$ is the selection index for genotypes by weighting between MPS, rY_i and rW_i are the rescaled values of response variable and WAASB respectively. θ_y and θ_s are the weightage given to variable and WAASB respectively. The other statistical estimations for selection of stable genotypes are similar to MGIDI. The final step for the selection of stable genotypes based on multi traits is computation of multi trait stability index (MTSI) proposed by Olivoto *et al.* (2019b)

$$MTSI_i = \left[\sum_{j=1}^f (F_{ij} - F_j)^2 \right]^{0.5}$$

Here, the genotypes with lower MTSI were identified as close to ideotype planned and having the greater performance and stability among all the studied variables. The selection differential was estimated for both mean and WAASBY

index with selection intensity of 20%. MTSI was analysed by R software using “mtsi” package (Olivoto *et al.* 2019b).

RESULTS AND DISCUSSION

Selection of superior inbreds within seasons by MGIDI index

Factor delineation: The factor analysis of 16 variables (Supplementary Table 2) revealed that first four PCs had eigen value greater than one which cumulatively accounted for 78.60 and 76.30% variation in E1 and E2 conditions, respectively. In E3 condition first five PCs contributed for 81.50% total variation with greater than 1 eigen value. Based on factor analysis (Table 1), the 16 variables grouped into four factors in E1, E2 and five factors in E3 conditions. The importance of this factor analysis is to group the correlated variables into single factor (FA) and each selected genotypes has the strength and weakness of different FA. In the E1 condition, FA1 includes PH, LL, IL and GFY, FA2 enclosed with CP, CF, ADF, NDF and DMY, in FA3 the traits LB, LSR and FA4 includes DFF, CH, NL, NN and SGR. In E2 condition, the four factors are follows, FA1 (IL, CP, CF, ADF and NDF), FA2 (DFF, CH, NL and NN), FA3 (LSR, DMY and GFY) and FA4 (PH, LL, LB and SGR). In E3 environment, the five factors are FA1 (CH, PH, LL, IL, DMY and GFY), FA2 (CF and NDF), FA3 (DFF, NL and NN), FA4 (LB and SGR) and FA5 (LSR, CP and ADF).

Ranking of genotypes according to MGIDI index: Among the 16 studied variables, a total of 14, 14 and 15

traits displayed positive desired selection gain in E1, E2 and E3, respectively (Table 1). The highest per cent of selection gain of 23.10, 47.80 and 28.40% was recorded with CH in E1, E2 and E3 conditions, respectively. Only few variables namely LSR (-3.17, -2.08), CP (-4.24, -6.53) under E1 and E2 conditions and LSR (-9.61) under E3 condition showed negative selection gain. In the present experiment, the heritability was highest (99%) for DFF and LSR in E1 and NDF (99%) in E2 and both PH and LSR (98%) in E3 condition. Similar approaches were utilised for selection of superior genotypes in strawberry (Olivoto *et al.* 2021b) and maize (Uddin *et al.* 2021) by the earlier scientists.

The selection pressure of 20% was applied for selection of top performing genotypes among the 28 fodder maize inbreds. With this selection pressure six genotypes were identified as top ranked genotypes and this ranking is based on the MGIDI index values. The green circle indicating the selection pressure of 20% and the genotypes with green dots are the selected genotypes (Supplementary Fig. 1). The genotypes with a lower MGIDI index are considered closer to the ideotype, making them as ideal genotypes (Al-Ashkar *et al.* 2023). In the present study, the genotypes GETM 25, UMI 1205, N 66, TNFM 139-1, UMI 1210 and African Tall were selected as top genotypes in E1. Among the genotypes, the MGIDI (Supplementary Table 3) ranged from 2.88 (GETM 25) to 5.97 (N-10-86). In case of E2 situation, the inbreds such as African Tall, TNFM 139-1, DM 74-2, UMI 1210, GETM 25 and UMI 120 were the selected inbreds (Supplementary Fig. 2) and the index

Table 1 Selection gain of 16 traits based on MGIDI index of fodder maize inbreds

Kharif 2022 (E1)				Rabi 2022 (E2)				Summer 2023 (E3)			
Trait	Factors	SG	h ²	Trait	Factors	SG	h ²	Trait	Factors	SG	h ²
PH	FA1	17.80	0.97	IL	FA1	10.30	0.88	CH	FA1	28.40	0.97
LL	FA1	13.30	0.93	CP	FA1	-6.53	0.91	PH	FA1	20.00	0.98
IL	FA1	18.70	0.85	CF	FA1	4.53	0.95	LL	FA1	11.90	0.93
GFY	FA1	17.30	0.94	ADF	FA1	1.70	0.94	IL	FA1	7.93	0.92
CP	FA2	-4.24	0.98	NDF	FA1	8.74	0.99	DMY	FA1	22.00	0.94
CF	FA2	2.85	0.90	DFF	FA2	4.98	0.96	GFY	FA1	20.10	0.93
ADF	FA2	4.12	0.96	CH	FA2	47.80	0.98	CF	FA2	6.16	0.95
NDF	FA2	0.08	0.97	NL	FA2	12.00	0.88	NDF	FA2	4.16	0.97
DMY	FA2	3.56	0.93	NN	FA2	11.00	0.88	DFF	FA3	2.16	0.93
LB	FA3	3.93	0.83	LSR	FA3	-2.08	0.95	NL	FA3	4.82	0.85
LSR	FA3	-3.17	0.99	DMY	FA3	5.05	0.63	NN	FA3	4.45	0.86
DFF	FA4	7.32	0.99	GFY	FA3	7.90	0.85	LB	FA4	8.28	0.97
CH	FA4	23.10	0.97	PH	FA4	27.50	0.98	SGR	FA4	8.97	0.93
NL	FA4	7.13	0.90	LL	FA4	9.93	0.88	LSR	FA5	-9.61	0.98
NN	FA4	8.23	0.94	LB	FA4	3.98	0.88	CP	FA5	1.90	0.90
SGR	FA4	13.10	0.79	SGR	FA4	10.50	0.90	ADF	FA5	3.43	0.94

MGIDI, Multi-trait Genotype Ideotype Distance Index; SG, Selection gain; PH, Plant height; LL, Leaf length; IL, Internode length; GFY, Green fodder yield; CP, Crude protein; CF, Crude fiber; ADF, Acid detergent fiber; NDF, Neutral detergent fiber; DMY, Dry matter yield; LB, Leaf breadth; LSR, Leaf stem ratio; DFF, Days to 50% flowering; CH, Cob placement height; NL, Number of leaves; NN, Number of nodes; SGR, Stem girth.

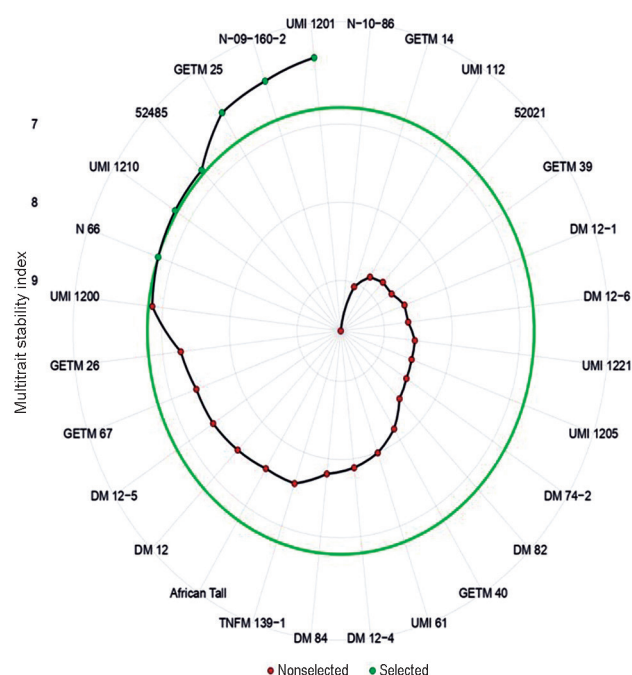


Fig. 1 MTSI index for selection of fodder maize inbreds.

ranged from 1.47 (African Tall) to 5.46 (52021). In the E3 environment, the inbreds namely, GETM 25, GETM 26, DM 74-2, African Tall, DM 12-6 and TNFM 139-1 were identified as best genotypes (Supplementary Fig. 3). The fodder maize inbreds GETM 25 and N-10-86 were found with minimum and maximum index value of about 1.96 and 6.17, respectively. The inbred lines African Tall, TNFM 139-1 and GETM 25 were identified as superior in all three environments.

Strength and weakness of selected genotypes: The superior genotypes were ranked on the basis of their MGIDI score and the contributions of different factors towards their index were classified as most and least contributing factors (Olivoto *et al.* 2021b). Factors which are placed in the centre to plot and edge to the plot are the most and least contributing factors, respectively (Supplementary Fig. 4a–4c). In E1 condition, FA4 is the most contributing factor responsible for selection of genotypes and FA2 is the least contributing factor. The inbred line GETM 25 has strength of FA1 and weakness of FA4. This indicated that this genotype performs better for GFY, PH, LL and IL. In E2 situation, the best genotype had strength of FA4 and FA3 which includes all the yield related traits. Among the five factors formed in E3 condition, GETM 25 has the strength of FA1, FA4 and FA5. These factors were completely accounted with the yield component variables.

Selection of stable fodder maize inbreds by MTSI: The commercialisation of any cultivar developed through any breeding programme primarily depends on their adaptability over the diverse changing environments. Conducting stability analysis on inbred lines is essential as it helps in identifying parental lines with reliable and consistent performance, thus ensuring the dependability of hybrid

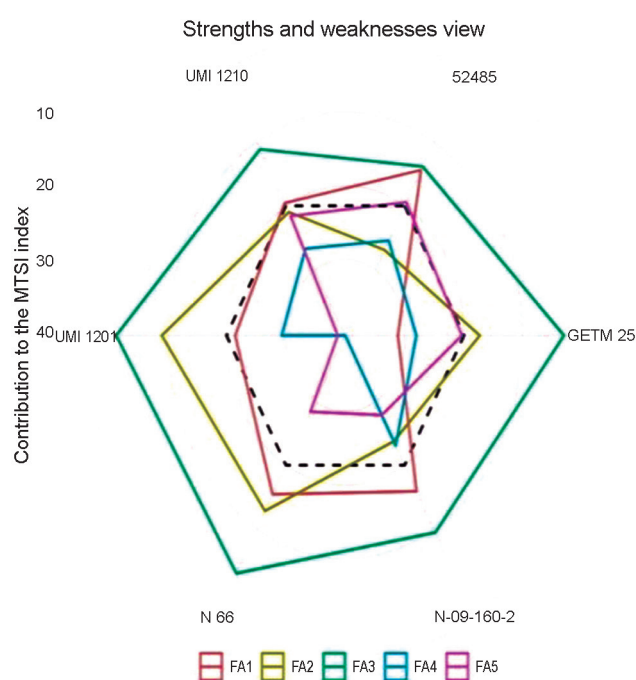


Fig. 2 Strength and weakness of selected inbreds based on MTSI.

results. The WAASBY method developed by Olivoto *et al.* (2019a) was employed for analysis of multi environmental trials. MTSI is the best tool for identification of superior and stable genotypes by utilizing multi trait performance of genotypes. Based on WAASBY values, the variables with high magnitude of correlation were grouped into a factor. The exploratory factor analysis of 16 variables resulted into first five PCs (with eigen value of more than one) with 69.70% cumulative variance (Supplementary Table 4). The 16 variables were grouped into five factors (Table 2) by WAASBY values and the factors are FA1: (IL, LSR, CP, CF, ADF, NDF and GFY), FA2: (NL and NN), FA3: (DFF), FA4: (CH, PH and DMY), FA5: (LL, LB and SGR). The communality (h) was computed after varimax rotation and it defined as the shared variance of individual variance by the factors (Hussain *et al.* 2021). It ranged from 0.379 (LSR) and 0.934 (NL) with an average of 0.696.

The selection differential (Table 2) based on mean and WAASBY was positive for most of the traits. The range of selection differential varied from -7.99 (PH) to 28.50 (NDF) for WAASBY. Whereas, it was from -5.81 (CF) to 8.25 (NL) for mean performance. The negative selection differential was observed with only few variables namely GFY, PH, IL for WAASBY and IL, CF, ADF and NDF for mean performance. The negative selection differential is primarily due to the mean values of the selected genotypes (X_s) being lower than the mean of the original population (X_o). The heritability varied among the genotypes from 21% (DMY) to 95% (DFF). The trait GFY has registered about 59%.

MTSI was helpful to select genotypes possessing wider adaptability along with higher mean performance based on all the studied variables (Memon *et al.* 2023). The genotypes

Table 2 Factor analysis and selection differential for mean and WAASBY for 16 variables

Variable	Factor	Selection differential for the WAASBY index			Selection differential for the mean of the variables			
		Xo	Xs	SD	Xo	Xs	SD	h ²
IL	FA 1	55.4	53.8	-2.91	13.9	13.7	-1.20	0.72
LSR	FA 1	50.7	58.8	16	0.276	0.28	4.13	0.36
CP	FA 1	58.1	74.1	27.4	12.5	13.4	7.23	0.73
CF	FA 1	55.6	69.9	25.7	25.1	23.7	-5.81	0.75
ADF	FA 1	54.4	65.3	20.2	31.7	30.1	-5.11	0.64
NDF	FA 1	50.1	64.4	28.5	50.1	48.1	-3.87	0.64
GFY	FA 1	49.8	46.7	-6.35	34	35.1	3.19	0.59
NL	FA 2	52.8	66.9	26.5	13.4	14.5	8.25	0.78
NN	FA 2	53.4	62.3	16.7	13.9	14.9	7.36	0.77
DFF	FA 3	60.4	67.5	11.7	57.9	58.9	1.66	0.95
CH	FA 4	53.9	61.6	14.2	93.4	94.6	1.30	0.91
PH	FA 4	49.3	45.4	-7.99	201	206	2.88	0.91
DMY	FA 4	55.3	60.3	9.01	7.64	8.04	5.19	0.21
LL	FA 5	54.8	62.2	13.6	79.8	82.7	3.63	0.83
LB	FA 5	60.6	69.3	14.3	7.79	8.36	7.31	0.70
SGR	FA 5	52.4	60.1	14.6	5.09	5.5	8.12	0.68

WAASBY, Weighted average of absolute scores by yield; Xo, Mean of the original population; Xs, Mean of the selected genotype; SD, Standard deviation; IL, Internode length; LSR, Leaf stem ratio; CP, Crude protein; CF, Crude fiber; ADF, Acid detergent fiber; NDF, Neutral detergent fiber; GFY, Green fodder yield; NL, Number of leaves; NN, Number of nodes; DFF, Days to 50% flowering; CH, Cob placement height; PH, Plant height; DMY, Dry matter yield; LL, Leaf length; LB, Leaf breadth; SGR, Stem girth.

were ranked according to their MTSI index values, applying a selection intensity of 20%. Genotypes with the lowest MTSI index were identified as stable with superior mean performance (Fig. 1). In this study, six genotypes such as UMI 1201, N-09-160-2, GETM 25, 52485, UMI 1210 and N 66 exhibited the lowest MTSI index. Hence these are selected as stable and highest mean performing genotypes among the 28 inbred lines studied. The MTSI index score (Supplementary Table 3) ranged from 6.13 (UMI 1201) to 9.64 (N-10-86) for the inbred lines selected.

The strength and weakness based on MTSI of selected genotypes (Fig. 2) revealed that the highly stable inbreds had strength of FA3 which is related to flowering. The selected inbred line UMI 1201 had greater strength of FA2 which included the variables contributing for greater fodder yield like NN and NL. However, it showed the weakness of FA5. It simplifies that it requires the desired gain for FA5. Among the factors FA4 has been identified as most contributing factor for selection of these superior genotypes. The selection of stable performing genotypes by using this approach was also done by Zuffo *et al.* (2020) in soybean, Sellami *et al.* (2021) in lentil and Lee *et al.* (2022) in rice.

This study demonstrated the use of latest biometrical tool multi trait selection indices such as MGIDI and MTSI to select the superior and stable genotypes. Based on MGIDI, the genotypes namely African Tall, TNFM 139-1 and GETM were identified as most superior among 28 fodder maize inbred lines evaluated during three different environments. Similarly, the genotypes UMI 1201, N-09-160-2, GETM

25, 52485, UMI 1210 and N 66 were identified to be most stable genotypes possessing greater performance for all studied variables over environments. So, these inbred lines can be targeted to develop synthetic/composite varieties or used as parents for developing superior single cross heterotic combinations for enhanced fodder production.

REFERENCES

- Al-Ashkar I, Sallam M, Almutairi K F, Shady M, Ibrahim A and Alghamdi S S. 2023. Detection of high-performance wheat genotypes and genetic stability to determine complex interplay between genotypes and environments. *Agronomy* **13**(2): 585.
- Azrai M, Aqil M, Efendi R, Andayani N N, Makkulawu A T, Iriany R N, Suarni, Yasin M, Suwardi, Zainuddin B, Salim, Sitaresmi T, Bahtiar Paesal and Suwarno W B. 2023. A comparative study on single and multiple trait selections of equatorial grown maize hybrids. *Frontiers in Sustainable Food Systems* **7**: 1185102.
- Borkhatariya T H, Gohil D P, Sondarava P M, Patel R and Akbari K M. 2022. Character association and path coefficient analysis among diverse genotypes of forage maize (*Zea mays* L.). *Biological Forum—An International Journal* **14**(3): 829–33.
- Ceron-Rojas J J and Crossa J. 2018. *Linear Selection Indices in Modern Plant Breeding*, pp. 256. Springer Nature.
- Choudhary M, Singh A, Gupta M and Rakshit S. 2020. Enabling technologies for utilization of maize as a bioenergy feedstock. *Biofuels, Bioproducts and Biorefining* **14**(2): 402–16.
- Gauch H G. 2013. A simple protocol for AMMI analysis of yield trials. *Crop Science* **53**(5): 1860–69.
- Hazel L N. 1943. The genetic basis for constructing selection indexes. *Genetics* **28**: 476–90.

- Hussain T, Akram Z, Shabbir G, Manaf A and Ahmed M. 2021. Identification of drought tolerant Chickpea genotypes through multi trait stability index. *Saudi Journal of Biological Sciences* **28**(12): 6818–28.
- Kumar B, Choudhary M, Kumar P, Kumar S, Sravani D, Vinodhana N K and Rakshit S. 2024. GGE biplot analysis and selection indices for yield and stability assessment of maize (*Zea mays* L.) genotypes under drought and irrigated conditions. *Indian Journal of Genetics and Plant Breeding* **84**(2): 209–15.
- Lee S Y, Lee H S, Lee C M, Ha S K, Park H M, Lee S M, Jeung Y K J and Mo Y. 2023. Multi-environment trials and stability analysis for yield-related traits of commercial rice cultivars. *Agriculture* **13**(2): 256.
- Memon J, Patel R, Parmar D J, Kumar S, Patel N A, Patel B N, Patel D A and Katba P. 2023. Deployment of AMMI, GGE-biplot and MTSI to select elite genotypes of castor (*Ricinus communis* L.). *Heliyon* **9**(2).
- Olivoto T, Lucio, A D, Silva J A, Marchioro V S, Souza V Q and Jost E. 2019a. Mean performance and stability in multi-environment trials I: Combining features of AMMI and BLUP techniques. *Agronomy Journal* **111**: 2949–60.
- Olivoto T, Lucio A D, Da Silva J A, Sari B G and Diel M I. 2019b. Mean performance and stability in multi-environment trials II: Selection based on multiple traits. *Agronomy Journal* **111**(6): 2961–69.
- Olivoto T and Nardino M. 2020a. MGIDI: A novel multi-trait index for genotype selection in plant breeding. *BioRxiv* 2020–07.
- Olivoto T and Lucio A D C. 2020b. Metan: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution* **11**(6): 783–89.
- Olivoto T and Nardino M. 2021a. MGIDI: Toward an effective multivariate selection in biological experiments. *Bioinformatics* **37**(10): 1383–89.
- Olivoto T, Diel M I, Schmidt D and Lucio A D. 2021b. Multivariate analysis of strawberry experiments: Where are we now and where can we go? *BioRxiv* 2020–12. 2030.424876
- Sellami M H, Pulvento C and Lavini A. 2021. Selection of suitable genotypes of lentil (*Lens culinaris* Medik.) under rainfed conditions in South Italy using multi-trait stability index (MTSI). *Agronomy* **11**(9): 1807.
- Smith H. 1936. A discriminant function for plant selection. *Annals of Eugenics* **7**: 240–50.
- Tahir A and Habib N. 2013. Forecasting of maize area and production in Pakistan. *Crop Production* **2**(2): 44–48.
- Uddin M S, Azam M G, Billah M, Bagum S A, Biswas P L, Khaldun A B M, Hossain N, Gaber A, Althobaiti Y S and Abdelhadi A A. 2021. High-throughput root network system analysis for low phosphorus tolerance in maize at seedling stage. *Agronomy* **11**(11): 2230.
- Zuffo A M, Steiner F, Aguilera J G, Teodoro P E, Teodoro L P R and Busch A. 2020. Multi-trait stability index: A tool for simultaneous selection of soya bean genotypes in drought and saline stress. *Journal of Agronomy and Crop Science* **206**(6): 815–22.