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Identification and Validation of Stable Horse Gram [*Macrotyloma uniflorum* (Lam.) Verdc.] Genotypes using Multi-trait based Selection Indices in Multi-environment Experiments

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ABSTRACT

Background: Horse gram is an underutilized legume but possesses multi-utilities. The narrower genetic base warrants targeted crop improvement attempts. Induced mutagenesis evolved a few promising mutants for yield whose breeding potency through multiple environment experiments (MEEs) was assessed.

Methods: The stability of the high-yielding mutants was assessed through MEEs (six environments in two cropping years) using multiple trait-based selection indices (SIs). The coincidence index was utilized to identify the most common stable genotypes identified by SIs. The effectiveness of the SIs was assessed using the selection differential (SDs).

Result: The multi trait-based SIs namely MGIDI, FAI-BLUP and SH index facilitated the selection of superior and stable horse gram mutant genotypes. The results of both preliminary (PT) and confirmatory trials (CT) were analysed using the coincidence index and identified the most common stable mutant genotypes G1, G3, G27 and G22. Based on the SDs for yield-related traits, it is inferred that the SI MGIDI can be relied upon to enhance the genetic gain for yield-associated traits improvement. The SIs, FAI-BLUP and the SH shall be utilized to improve growth-related traits in horse gram.

Key words: FAI-BLUP, Horse gram, MGIDI, Selection index, Smith-hazel, Stability.

INTRODUCTION

Legumes are versatile and highly adaptable to diverse climatic conditions and play a crucial role in food security. They can thrive in low-input farming systems, providing sustainable nutrition with high protein content and offering other health benefits for a growing global population. In southern India, legumes are predominantly cultivated during the *Kharif* and *Rabi* seasons (Sudhagar *et al*., 2022). *Rabi* legumes account for 63% of the total legume-growing area and contribute 53% to overall legume production (Krishna *et al*., 2022). Among *Rabi* legumes, horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] also known as *Dolichos uniflorus* Lam. or *Dolichos biflorus*, is a significant crop grown after the North-East monsoon. Belonging to the subkingdom Tracheobionta, division Magnoliophyta and family Fabaceae (Chahota *et al*., 2013), horse gram is widely cultivated by marginal farmers in southern India, particularly under rainfed and dryland conditionsand is well-suited to marginal soils. Despite its importance, the average yield potential of horse gram cultivars is relatively low. To overcome this limitation, targeted breeding programs aimed at improving yield-related traits are critical. Considering this, efforts have been initiated through induced mutagenesis aimed at creating genetic variation for important traits (Priyanka *et al*., 2023). Through a series of breeding trials and comprehensive evaluations of the genetic variability in the mutant populations, several mutants exhibiting significantly higher yields than the parents have been

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identified (Pushpayazhini *et al*., 2022). However, the performance of these genotypes may vary significantly across environments due to genotype-environment interactions (GxE), therefore necessitates its estimation before commercializing these better-performing mutants (Vaishnavi *et al*., 2023). Breeders generally conduct multi-environmental experiments (MEEs) to evaluate genotypic performances over environments to ascertain their true breeding potential (Ligarreto-Moreno and Pimentel-Ladino, 2022). The results arrived at after analysing MEEs are used as inputs for various selection indices to select best-performing genotypes with stability. A selection index (SI) is a statistical tool used in the selection of individuals based on several traits simultaneously. These indices facilitate the evaluation of genotypes based on their trait performance in diverse environments and help in achieving specific breeding goals. Plant breeders utilize various SI(s) to effectively identify and select the best-performing genotypes from a given population (Ceron-Rojas and Crossa, 2018). Commonly adopted multivariate selection tools in the context of MEEs include the (i) Multi-trait genotype-ideotype distance index (MGIDI): It analyses information from multiple traits, condenses it into a single valueand ranks genotypes based on their proximity to an ideal genotype (Olivoto and Nardino, 2021); (ii) Factor analysis and ideotype based BLUP (FAI-BLUP) index: It combines multiple environments and traits at once. It considers the genetic correlations between the target traits of the genotype and the ideotype without considering multicollinearity or economic weights; and (iii) Smith-Hazel index (SH): It assigns optimal weights to each trait based on their economic importance and genetic potential, allowing breeders to select genotypes that maximize overall genetic gain. The genetic values of genotypes estimated using BLUPs are utilized in the aforementioned SI(s) (Daba *et al*., 2023). This approach provides more reliable results by ensuring unbiased predictions of genetic values and making valid inferences about genotypic performance through robust statistical principles (Aboye and Edo, 2024). Previously Ambrosio *et al*. (2024); Rocha *et al*. (2018) and Costa *et al*. (2023) showed the efficiency of these indices in selecting superior genotypes. After genotype selection using SI, the coincidence index (CI) helps to determine the most frequently identified stable genotypes across stability indices (Behera *et al*., 2024). Subsequently, the selection differential (SD) is calculated. SD refers to the difference between the average trait value of the selected individuals and the average trait value of the entire population, providing insights into the genetic gain achievable from these selected genotypes (Behera *et al*., 2024).

Given this context, the present study was designed to select stable horse gram mutant genotypes based on multiple traits using various SI(s). The coincidence index was used to identify common stable genotypes among the promising genotypes identified by various SIs. The SDs obtained from each index were used to identify the most suitable index for selecting promising horse gram mutant genotypes.

Materials and Methods

Experimental materials

Thirty horse gram genotypes, comprising 29 mutants and their parent cultivar PAIYUR 2, were evaluated in this study. The mutant population was developed from the variety PAIYUR 2 using various combinations of mutagens (Sudhagar *et al*., 2022). From 2016 to 2019, under the funding of the Board of Research in Nuclear Sciences, Government of India (BRNS-GOI), the potential of the resulting mutant population was rigorously assessed following standard plant-breeding protocols. Subsequently in 2020, with the support of the Department of Science and Technology-Science and Engineering Research Board (DST-SERB), 29 promising mutants from the homogenized population were tagged for further investigation. In the current experiment, the stability and yielding potential of these 29 horse gram mutants were assessed by utilizing the biometrical data of six environments with multiple trait-based SI(s). The biometrical data of these 29 test genotypes were recorded in two multi-environment experiments (MEE). The first experiment otherwise the preliminary trial (PT) was conducted in three environments during the cropping season 2021-2022. The set of experiments otherwise the confirmatory trial (CT) was conducted in the same environments during the 2023-2024 cropping season to confirm the findings of the PT.

Study location, design and analyses

Both the PT and CT were conducted in three environments E1, E2 and E3. The E1 was the legume research field belonging to the Centre for Plant Breeding and Genetics (Department of Pulses), Coimbatore, Tamil Nadu Agricultural University in Coimbatore located at 11.02°N latitude and 76.92°E longitude. The E2 was the research field of Sugarcane Research Station, Melalathur, Tamil Nadu Agricultural University, Vellore district, positioned at 12.91°N latitude and 78.87°E longitude. The E3 was a farmer's field in Krishnagiri district, Tamil Nadu with coordinates of 12.34°N latitude and 78.13°E longitude. The experiments were conducted in a randomized block design (RBD) with three replications per environment, with each genotype sown in 5-meter rows spaced at 45 cm×15 cm. Standard agronomic practices were employed throughout the study. In all the environments, for each genotype, data for ten traits collected from ten randomly selected plants per replication. The traits were days to maturity (DAM), number of clusters per plant (NC), plant height (PLH), days to 50% flowering (DAF), pods per plant (NP), seeds per pod (NS), yield per hectare (YD), pods per cluster (NPC), primary branches (NB) and hundred seed-weight (HS) as outlined by Mahajan *et al*. (2007). Data for DAM and DAF were taken at the appropriate developmental stages, while the remaining traits were measured at post-harvest.

Multi-trait genotype-ideotype distance index (MGIDI) analysis

The MGIDI was used to evaluate genotypes that performed well across multiple environments, by calculating the distance between genotype and ideotype, which is assumed to have the highest value for all traits. To determine this, MGIDI performs (i) an all-trait data rescaling for all genotypes and (ii) factor analysis (FA). After FA, the distance of each genotype from an ideal genotype is calculated (Olivoto and Nardino, 2021). The MGIDI was calculated using the formula,

$$MGIDI_j = \left[\sum_{j=1}^{f} (\gamma_{ij} - \gamma_j)^2\right]^{0.5}$$

Where,

γ_{ij} = Represents the score of the i^{th} genotype for the j^{th} factor (i = 1, 2, …, g; j = 1, 2, …, f).

γ_j = Denotes the score of the ideotype for the j^{th} factor.

Factor analysis and ideotype based BLUP (FAI-BLUP) analysis

The FAI-BLUP index was calculated using factor analysis and genotype-ideotype design, following the approach of Rocha *et al*. (2018). This index is based on structural equation models, which integrate both exploratory (for dimension reduction) and confirmatory factor analysis (for genotype-ideotype comparison) to assess the relationship between genotypes and the ideal ideotype. It is calculated as follows:

$$P_{ij} = \frac{\frac{1}{d_{ij}}}{\sum_{i=1;j=1}^{i=n;j=m} \frac{1}{d_{ij}}}$$

Where,

P_{ij} = Represents the probability that the i^{th} genotype (i = 1, 2,…, n) is similar to the j^{th} ideotype (j = 1, 2,…, m), while d_{ij} = Refers to the distance between the i^{th} genotype and the j^{th} ideotype, calculated using the standard mean of Euclidean distance.

Smith-hazel (SH) index analysis

The SH index uses the genotypic and phenotypic variance-covariance matrices to select the genotypes by assigning the economic weights to determine an individual genotype's genetic worth. It is computed using the formula,

$$b = p^{-1} Aw$$

Where,

B= Vector of index coefficients.

P= Phenotypic covariance matrix.

A= Genetic covariance matrix.

W= Vector of economic weights.

The genetic worth of a genotype is computed based on,

$$I = b_x G_x + b_y G_n + ... + b_n G_n$$

Where,

I= Genetic worth (breeding value of a genotype).

b = Index coefficient for the traits x, y, ..., n.

G = BLUPs for the traits x, y, ..., n (Smith, 1936).

Identification of most common stable genotypes using the coincidence index (CI)

From the genotypes selected by various selection indices, the coincidence index was applied to identify the common stable genotypes as described by Hamblin and Zimmermann (1986).

Calculating the selection differentials (SD) for indices

Genotype selection was performed across different environments using MGIDI, FAI-BLUP, SH index values, applying a selection intensity of about 20% (Al- Ashkar *et al*., 2023). The selection differential as a percentage of the population mean (SD%) for individual traits was calculated using the following formula:

$$\text{Selection differential (SD)\%} = \left(\frac{x_s - x_0}{x_0}\right) \times 100$$

Where:

Xs= Mean of the selected genotypes.

Xo= Population mean.

All the indices were computed using the METAN package (version 4.1.1) in R Studio (https://cran.r-project.org/).

Results and Discussion

Horse gram is a valuable legume known for its nutrient density and climate resilience. However, the lack of genetic variability has hindered its improvement through classical breeding programmes. To address this, induced mutagenesis was employed and successfully significant genetic variability, particularly for growth and yield-related traits was generated. To maximize the potential of these mutants, it is essential to evaluate their stability across different environments, as G×E can impact their performance. Multi-trait selection indices, which allow for the simultaneous evaluation of multiple traits, play a key role in identifying stable, good-performing genotypes, ensuring consistent yield and adaptability across environments.

Genotypes evaluation based on MGIDI index

The MGIDI simplifies multi-trait selection by consolidating various trait data into a single index and ranking genotypes based on their proximity to an ideotype. It uses factor analysis to ascertain how different traits are connected or influence one another. MGDI thus, maintains the original correlation structure and supports effective ideotype planning (Olivoto and Nardino, 2021). Based on the selection intensity, the genotype(s) with the lowest MGIDI score is (are) chosen as the selected genotype(s), indicating its (their) proximity to the ideotype. The selected mutant genotypes using the MGIDI index from both PT and CT are shown in Fig 1A and 2A. In PT, genotype G1 (2.80) had the lowest MGIDI score followed by G25 (2.85), G22

(2.85), G3 (3.08), G27 (3.39) and G17 (3.47); whereas in the CT, the genotypes G8, G22, G3, G25, G27 and G1 emerged as top performers with MGIDI scores of 1.15, 1.16, 1.44, 1.59, 1.75 and 1.76 respectively. The genotypes G1, G3, G22 and G25 consistently performed well in both trials, indicating their adaptability and stability to changing environmental conditions. Similarly, MGIDI has been effectively used in other crops to identify superior genotypes based on multiple traits. For instance, Maranna *et al*. (2021); Aruna *et al*. (2024) and Amin *et al*. (2024) employed the MGIDI index to identify the superior genotypes targeting stability in soybean, disease resistance in mung beanand adaptability in lentils respectively. These studies demonstrate the utility of MGIDI in enhancing breeding efforts across different crops.

Genotypes evaluation based on the FAI-BLUP index

FAI-BLUP utilizes BLUPs to derive genetic values and eliminates the influence of experimental errors in the data (Costa *et al*., 2023). Like MGIDI, the FAI-BLUP also use factor analysis to select superior genotypes based on multi-trait performance; however, they differ in their selection formulae. Based on the FAI-BLUP index, the experimented horse gram mutant genotypes were ranked (Fig 1B and 2B). The index indicated that six mutant genotypes (G27, G22, G1, G3, G16, G10) performed well in the PT (Fig 1B). In the CT, G3 outperformed the others, along with notable performances from G29, G1, G22, G27 and G7 (Fig 2B). From these results, it is notable that G10, G16 and G27 exhibited varied performances in CT suggesting its sensitivity to environmental conditions. The ability of FAI-BLUP to enhance genotype selection has been highlighted by Woyann *et al*. (2020) for soybean and Rocha *et al*. (2019) for common beans.

Genotypes evaluation based on SH index

In SH index, the genotypes are selected based on their genetic potential using phenotypic values and genetic covariances (trait's correlation) since the exact genetic values are not directly known (Rocha *et al*., 2018). The genotypes G1, G22, G27, G25, G8 and G3 were identified stable genotypes in the PT (Fig 1C). Interestingly, the same set of genotypes were selected in the CT as well (Fig 2C), with a slight variation in their order of selection (G1, G3,

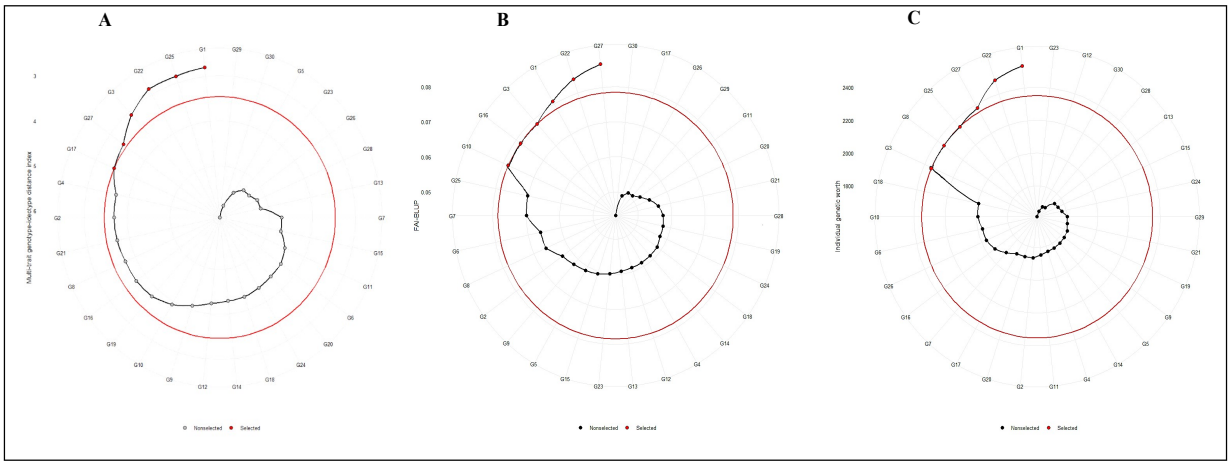


Fig 1: MGIDI index (A), FAI-BLUP index (B) and Smith-Hazel index (C) for horse gram mutant genotypes in preliminary trial.

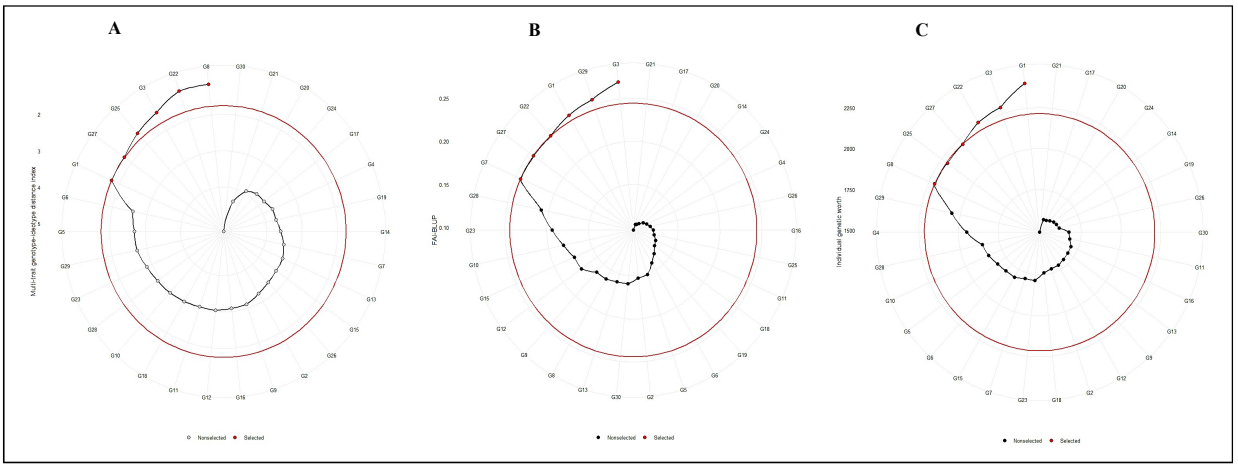


Fig 2: MGIDI index (A), FAI-BLUP index (B) and Smith-Hazel index (C) for horse gram mutant genotypes in confirmatory trial.

G22, G27 G25 and G8). It may be due to the changes in the environmental factors between two experimental years. Notably, the SH index consistently ranked genotype G1 in the same position in both trials, highlighting its stable performance. Earlier, Ambrósio *et al*. (2024) applied the SH index to successfully select superior lines in black bean, while Jahufer *et al*. (2015) utilized it for selecting superior lines in switchgrass.

Coincidence of common genotypes across multi-trait stability indices

Coincidence index (CI) is the metric that quantifies the overlap of genotypes commonly selected across different indices. A higher CI indicates a larger number of genotypes selected in common between indices (Behera *et al*., 2024). In both trials, the highest CI was observed between the MGIDI and SH indices. In the PT, the coincidence index was 79.17%, with both indices sharing five common genotypes (Table 1). In the CT, the coincidence index reached 100%, with six common genotypes (Table 2). The common genotypes selected by all three indices (MGIDI, FAI-BLUPand SH) are depicted through the Venn diagram (Fig 3). The genotypes G1, G3, G27and G22 were consistently selected across all three indices in both the PT and CT (Fig 3). This consistency highlights that these genotypes demonstrated superior and stable performance across MEEs and years, irrespective of the index used for selection. The robustness of these genotypes, which are not sensitive to the specific analysis approach of each index, emphasizes their high adaptability and overall stability.

Initially in horse gram, Jafarullakhan *et al*. (2024) identified G1, G3, G25 and G27 as stable genotypes using

Table 1: Common genotypes of preliminary trial identified using coincidence index in horse gram mutant genotypes.

Selection indices		Coincidence index (%)	No of common genotypes	List of common genotypes	Genotypes common to all selection indices
MGIDI	FAI-BLUP	59.33	4	G1, G22, G3, G27	G1, G22, G3, G27
MGIDI	Smith Hazel	79.17	5	G1, G25, G22, G3, G27	
FAI-BLUP	Smith Hazel	59.33	4	G27, G22, G1, G3	

Table 2: Common genotypes of confirmatory trial identified using coincidence index in horse gram mutant genotypes.

Selection indices		Coincidence index (%)	No of common genotypes	List of common genotypes	Genotypes common to all selection indices
MGIDI	FAI-BLUP	58.33	4	G22, G3, G27, G1	G22, G3, G27, G1
MGIDI	Smith Hazel	100.00	6	G8, G22, G3, G25, G27, G1	
FAI-BLUP	Smith Hazel	58.33	4	G3, G1, G22, G27.	

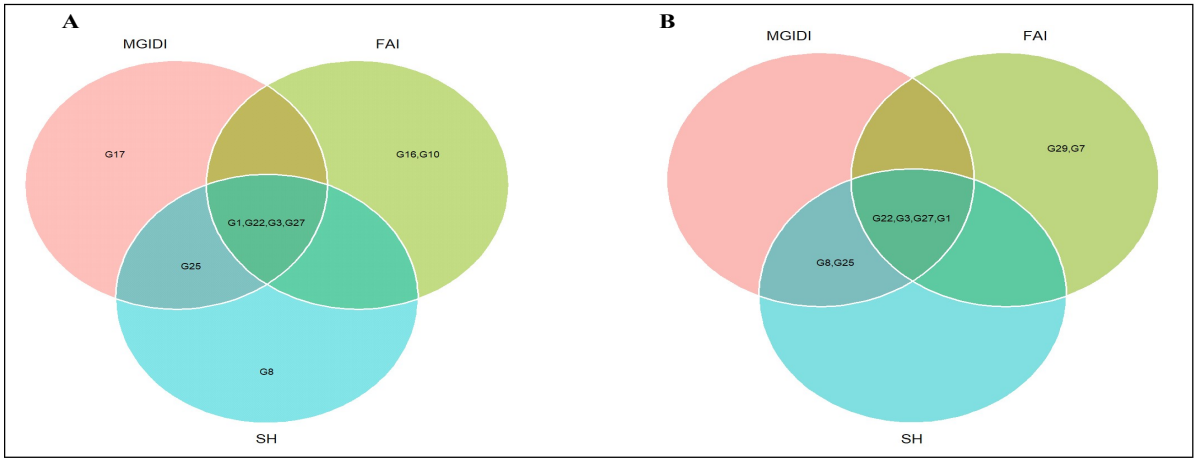


Fig 3: Venn diagram with the selected genotypes by the multi-trait genotype-ideotype distance (MGIDI) index, FAI-BLUP index and Smith-Hazel (SH) index for horse gram genotypes in preliminary trial (A) and confirmatory trial (B).

yield-related traits based on AMMI and GGE models. To confirm this finding, in the current study, we expanded the genotypic evaluation by including multiple traits comprised of growth, phenological and reproductive traits using a broader set of selection indices: MGIDI, FAI-BLUP and SH. In both PT and CT, the same genotypes G1, G3, G27and G22 were consistently selected by all three indices, reconfirming their stability across a wide range of environmental conditions.

Comparison of SDs arrived from various selection indices in PT and CT

SDs indicate the level of improvement in the traits achieved by selecting genotypes from the initial population using each index. In this study, the SDs derived from three indices were compared in the PT (Table 3). Such comparison of the SDs of each index will help in determining the efficiency of an index in selecting the genotypes for trait improvement. The SD results were cross-validated in the successive

Table 3: Selection differentials arrived from multi-trait selection indices for morphological traits of horse gram mutants in preliminary trial

Traits	MGIDI				FAI-BLUP				Smith-Hazel		
	Factor	Xo	Xs	SD%	Factor	Xo	Xs	SD%	Xo	Xs	SD%
Growth related traits											
PLH	FA3	150.10	163.00	8.59	FA3	150.00	161.00	7.33	150.00	168.00	12.00
NB	FA1	9.43	10.47	11.06	FA1	9.43	10.2	8.16	9.43	10.40	10.29
DAF	FA4	58.50	58.75	0.42	FA4	58.60	58.50	-0.21	58.50	59.30	1.37
DAM	FA1	118.10	120.80	2.28	FA1	119.00	121.00	1.68	121.00	121.00	0.03
Yield related traits											
NC	FA2	135.60	154.70	14.06	FA2	136.00	143.00	5.14	136.00	142.00	4.41
NPC	FA2	3.84	4.11	7.03	FA2	3.85	3.99	3.63	3.85	4.02	4.41
NP	FA1	405.40	530.70	30.91	FA1	405.00	506.00	24.93	405.00	496.00	22.46
NS	FA1	4.99	5.52	10.62	FA1	5.00	5.26	5.26	5.00	5.08	1.69
HS	FA3	3.68	3.79	2.98	FA3	3.68	3.81	3.53	3.68	3.87	5.16
YD	FA1	964.80	1324.00	37.26	FA1	965.00	1231.00	27.56	965.00	1181.00	22.38

DAM = Days to maturity, NC = Number of clusters per plant, PLH = Plant height, DAF = Days to 50% flowering, NP = Pods per plant, NS = Seeds per pod, YD = Yield per hectare, NPC = Pods per cluster, NB = Primary branches and HS = Hundred seed-weight.

Xs = Mean of selected genotypes; Xo = Mean of original population; SD% = Selection differential (%).

MGIDI = Multi-trait genotype-ideotype distance index; FAI-BLUP = Factor analysis and ideotype based BLUP index; SH = Smith-hazel index.

Table 4: Selection differentials arrived from multi-trait selection indices for morphological traits of horse gram mutants in confirmatory trial.

Traits	MGIDI				FAI-BLUP				Smith -Hazel		
	Factor	Xo	Xs	SD%	Factor	Xo	Xs	SD%	Xo	Xs	SD%
Growth related traits											
PLH	FA2	156.50	167.80	7.22	FA2	157.00	163.00	3.82	157.00	167.00	6.36
NB	FA2	9.68	10.08	4.13	FA2	9.68	9.81	1.34	9.68	9.94	2.69
DAF	FA2	58.59	59.01	0.71	FA2	58.60	57.50	-1.87	58.60	59.20	1.02
DAM	FA3	120.90	121.70	0.67	FA3	120.00	121.00	0.83	121.00	123.00	1.47
Yield related traits											
NC	FA1	160.90	204.00	26.79	FA1	161.00	201.00	24.84	161.00	194.00	20.50
NPC	FA1	3.44	3.88	12.79	FA1	3.44	3.82	11.04	3.44	3.73	8.43
NP	FA1	410.80	528.10	28.55	FA1	411.00	521.00	26.76	411.00	484.00	17.76
NS	FA1	5.55	6.03	8.64	FA1	5.55	6.06	9.18	5.55	6.00	8.10
HS	FA3	3.79	3.89	2.69	FA3	3.79	3.82	0.79	3.79	3.88	2.37
YD	FA1	945.40	1241.00	31.29	FA1	945.00	1215.00	28.57	945.00	1165.00	23.28

DAM = Days to maturity, NC = Number of clusters per plant, PLH = Plant height, DAF = Days to 50% flowering, NP = Pods per plant, NS = Seeds per pod, YD = Yield per hectare, NPC = Pods per cluster, NB = Primary branches and HS = Hundred seed-weight.

Xs = Mean of selected genotypes; Xo = Mean of original population; SD% = Selection differential (%).

MGIDI = Multi-trait genotype-ideotype distance index; FAI-BLUP = Factor analysis and ideotype based BLUP index; SH = Smith-hazel index.

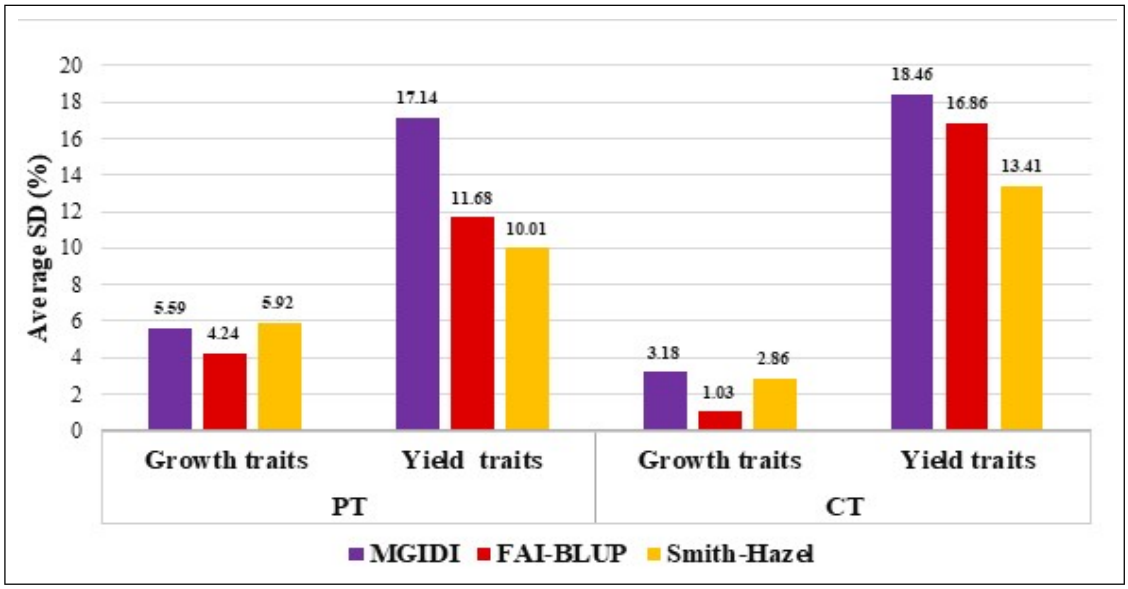


Fig 4: Comparison of selection differentials derived from different indices in preliminary trial (PT) and confirmatory trial (CT).

year through the CT (Table 4). This cross-validation helped in assessing the robustness of these indices and ensured the reliability of selection across environments. In both PT and CT, the mean of selected genotypes was higher across all traits and indices. The MGIDI and SH demonstrated positive SDs for all traits, while FAI-BLUP exhibited a negative SD for DAF in both PT and CT. Negative SD is useful when the breeding goal is to decrease the trait value in designing the ideal genotype (Behera *et al*., 2024).

The interpretation of SDs will be more meaningful when comparing growthand yield traits across the indices. To improve the understanding of the effectivity of the index on genotype selection, we performed a comparative analysis of SDs arrived at for the evaluated traits based on various indices (Fig 4). The three selection indices, MGIDI, FAI-BLUPand SH demonstrated varying levels of effectiveness in achieving genetic gain across the genotypes. Accordingly, in PT, the SH index displayed a higher percentage of SD (5.92%) for growth-related traits such as PLH, NB, DAFand DAM, followed closely by MGIDI (5.59%) and FAI-BLUP (4.24%). However, for yield-attributing traits such as NC, NPC, NP, NS, HSand YD, the MGIDI showed the highest SD (17.14%) followed by FAI-BLUP (11.68%) and SH (10.01%). This shows that the utility of MGIDI will be an ideal SI for yield improvement in horse gram. When considering the average SDs for all traits, MGIDI appears to be the most effective selection index for improving stable genotypes in horse gram. In the CT, slight variations in the order of SDs were observed across indices for growth-related traits. MGIDI (3.18%) exhibited higher SD, whereas SH (2.86%) and FAI-BLUP (1.03%) showed relatively similar SDs for these traits. However, for yield-related traits, MGIDI once again outperformed the other indices, with the highest SD of 18.46%, followed by FAI-BLUP (16.86%) and SH (13.41%). These results suggest that MGIDI is the most effective index for selecting superior genotypes in the CT.

Altogether, by combining the results of both PT and CT, MGIDI consistently produced the highest SDs for yield and its related traits, suggesting that it is the most effective index in identifying high-performing genotypes. After that, FAI-BLUP showed strong performance for yield-related traits but it showed less SD for growth-related traits. SH exhibited moderate yet consistent selection differentials, making it a reliable but less effective method compared to MGIDI and FAI-BLUP. These results suggest that MGIDI will be the best-suited index for maximizing genetic gain when prioritizing multiple traits, especially those contributing to yield, while FAI-BLUP and SH offer balanced results, better suited for more specific selection goals.

Conclusion

The multi trait-based SIs namely MGIDI, FAI-BLUP and SH index facilitated the selection of superior and stable horse gram mutant genotypes. The results of both preliminary (PT) and confirmatory trials (CT) were analysed using the coincidence index and identified the most common stable mutant genotypes G1, G3, G27 and G22. Based on the SDs for yield-related traits, it is inferred that the SI MGIDI can be relied upon to enhance the genetic gain for yield-associated traits improvement. The SIs, FAI-BLUP and the SH shall be utilized to improve growth-related traits in horse gram.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institution. The authors are responsible for the accuracy and completeness of the information provided but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

All animal procedures for experiments were approved by the Committee of Experimental Animal Care and handling techniques were approved by the University of Animal Care Committee.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article.

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