Received: 06 Aug 2024 | Revised: 12 Nov 2024 | Accepted: 12 Nov 2024

Electronic Journal of Plant Breeding

Research Article

Optimizing rice (*Oryza sativa* L.) yield and lodging resistance using MGIDI and conventional selection indices

Durga Prasad Mullangie[1],Kalaimagal Thiyagarajan[1*],Manonmani Swaminathan[2], Sritharan Natarajan[2] and Senthilkumar Govindan[2]

[1]Department of Genetics and Plant Breeding, Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University, Coimbatore- 641003
[2]Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641003
***E-Mail**: kalaimagal.t@tnau.ac.in

Abstract

To deal with the changing climate there is a necessity to develop climate resilient varieties without compromising yield. Hence concentrating on all the traits is essential to select genotypes. On utilization of the selection indices SI 1, SI 2, SI 3, and MGIDI we have observed that the modern selection indices such as MGIDI are superior over the Smith Index as MGIDI reported a gain of 2% in yield in F_5 which simultaneously improved lodging resistance with a gain of 39.6% for section modulus and 34.7% for bending stress. In BC_1F_4, a selection gain of 5.80% for yield with simultaneous improvement in culm diameter at 5.89% gain was observed. Hence MGIDI was found to be superior over conventional indices, which improved both lodging resistance and yield.

Keywords: Smith Hazel Index; Genetic Weights; Section Modulus; Bending Stress; Multicollinearity.

INTRODUCTION

Rice (*Oryza sativa* L.) occupies a major share of the Indian Agriculture system, and people throughout the country depend on rice for their daily calorie requirements. However, the changing climate has made the agricultural system prone to decreased yields. Hence developing varieties to deal with the changing climate without compromising the yield is the prerequisite (Kambale *et al.,* 2022). Crop improvement cannot be based on a single trait i.e., either exclusively concentrating on yield or biotic stress resistance, each trait results from several other traits, especially yield which shows a low to medium heritability with the environment highly influencing it. Hence there is a great requirement for a selection method that is not based on one trait alone and should be based on all the traits under study i.e., all the component traits (Smith *et al.,* 1981). Smith selection Index was one of the pioneer indices based on multiple traits. However, it is said that the multi-collinearity seen in the data will highly influence the results (Olivoto and Nardino, 2021) derived and breeders have reported the inefficiency of the Smith Index because of multi-collinearity. The novel selection indices which include the multi-trait index based on factor analysis and genotype-ideotype distance (FAI-BLUP), Multi-Trait Stability Index (MTSI), and Multi-Trait Genotype Ideotype Distance Index (MGIDI) are found to deal with multicollinearity (Olivoto *et al.,* 2019, 2022). The FAI-BLUP and MTSI are utilized when there is multi-season or multi-location data and the MGIDI can be applied even for single-season or single-environment data (Benakanahalli *et al.,* 2021). MGIDI is a multi-trait-based index that is based on genotype-ideotype distance. Developing lodging-resistant cultivars is an utmost need for the country as there are recurrent rains, storms, and winds all of which lead to heavy loss both in quality and quantity of the produce, bending stress (BS), section modulus (SM) and culm diameter (CD) are the major traits which govern the lodging resistance, high SM, BS and CD all are said to improve the lodging resistance.

The Japanese cultivar Habataki is highly lodging resistant because of the presence of *SCM 1*, and *SCM2*. Hence, crossing India's mega varieties with Habataki (Japanese bold *indica* rice) to select recombinants for yield and lodging resistance is a prerequisite. However, most Indians prefer slender grain, hence backcross breeding to select the background of the slender grain parent is essential. In the current study, CO 51 is a slender grain type high yielder and Habataki has a bold type grain. To select background of CO 51 backcross breeding was carried out and to select recombinants with agronomic traits of both the parents' pedigree was carried out. The present work deals with the stabilized recombinants of the cross-involving the popular CO-51(Robin *et al.*, 2019) and Habataki to select the best families in F_5 and BC_1F_4 for forwarding them further for varietal trials, we have utilized both conventional selection indices and MGIDI to concentrate on several traits to have high selection gain.

MATERIALS AND METHODS

To develop a lodging-resistant and high-yielding cultivar a cross-involving CO 51 and Habataki was made by previous workers. The female parent CO 51 is a slender type medium duration high-yielding and popular cultivar (Robin *et al.,* 2019) and the male parent Habataki is a lodging-resistant bold-seeded Japanese cultivar (*indica*). The crossed seed (F_1) was forwarded till F_5 through pedigree breeding and simultaneously the crossed seed was backcrossed to CO 51 to generate BC_1F_1 which was forwarded till BC_1F_4. Thirty-two stabilized families of F_5 and 35 stabilized families of BC_1F_4 were selected based on marker-assisted selection for *SCM 2* (a marker for lodging resistance) in the previous generation (i.e., F_4 and BC_1F_3) and those found to be positive for the Habataki allele were evaluated in RCBD in the Department of Rice, TNAU, Coimbatore in *Rabi* 2023-24 along with parents and commercial promising cultivars such as BPT 5204, CO 52 and ADT 43 as checks. The progeny along with parents and checks were raised in 4 rows each, each row with 12 plants hence in total 48 plants were maintained per family.

Days to 50% flowering (DFF), plant height (PH), panicle length (PL), flag leaf length (FLL), flag leaf width (FLW), the total number of productive tillers (TPT), culm diameter (CD), number of grains per panicle (NGP), L/W ratio, 1000 grain weight (W), section modulus (SM), bending stress (BS), bending moment at breaking (M) and yield per plant (YPP) are the traits under study evaluated on F_5 progeny, of which traits such as SM, BS, and M are considered as lodging pertaining traits and remaining being yield traits. In regards to the BC_1F_4 population, the families were evaluated for only yield traits. Smith-Hazel Index I, SH 2, Selection Index 3 with variable genetic weights (SH 3), and MGIDI, were computed for selecting the best families. The study is intended to compare different selection indices and utilize the advantage derived from the modern selection indices which deal with multi-collinearity problems. All the statistical analyses were carried out in the metan package of R software (Olivoto & Lúcio, 2020).

The bending moment at breaking (M) is a critical parameter used to screen for lodging resistance. It is calculated by multiplying the section modulus (SM) by the bending stress (BS). The SM is derived from the cross-section of the rice culm using the formula

$$\frac{\pi}{32} \times \frac{a_1^3 b_1 - a_2^3 b_2}{a_1}$$

where a_1 and b_1 represent the outer diameters of the major and minor axes, respectively, while a_2 and b_2 denote the inner diameters of the major and minor axes of the rice culm. The parameters a_1 and b_1 were measured using a vernier calliper, while a_2 and b_2 were obtained through stereo-microscopic measurements.

Bending stress (BS) is measured using a Universal Testing Machine (UTM) [Easy MESUR Version 2.0.1]. For this measurement, a two-week-old rice culm was used. The culm was cut 20 cm above the ground and placed between two fulcrums spaced 4 cm apart. A load of 0.5 kN was applied at a speed of 200 mm/s to measure bending stress (BS). A genotype with a high bending moment at breaking (M) is considered lodging-resistant (Nomura *et al*., 2019; Ookawa *et al.,* 2016).

Computation of selection indices: Smith Index/Selection Index 1 was computed using equal genetic weights for all traits. The function `non-collinear vars()` from the **metan** package in R software was employed to detect traits that contribute to multicollinearity. Upon eliminating these traits, a new selection index, referred to as Selection Index 2, was calculated. Both SI 1 and SI 2 utilize equal genetic weights. To enhance genetic gain, path analysis was conducted for yield, and traits were assigned scores of 2, 1.5, and -0.5 based on their high direct effect, moderate effect, and negative effect, respectively. This scoring method for Selection Index 3 follows the guidelines set by Palaniyappan *et al.* (2024). The Multi-Trait Genotype Ideotype Distance Index (MGIDI) was calculated according to Olivoto & Nardino (2021) which involves four major steps as indicated: rescaling the original variables between 0 to 100, principal component analysis (PCA), factorial analysis, and finally calculation of Euclidian distances. All selection indices were computed using the **metan** package in R software. Using these indices, the Coincidence Index (CI) was determined (Janick, 1986), and the gains obtained from various selection indices were represented through a bar chart.

RESULTS AND DISCUSSION

All the traits under study in F_5 and BC_1F_4 except the L/W ratio of grain in BC_1F_4 were found to be significant for the mean sum of square for genotype in ANOVA which indicates the presence of variability within the F_5 and BC_1F_4 families suggesting the potentiality to impose selections to select the best family. Heritability ranged from 92.2% for DFF to 28% for PL in F_5. High heritability was reported for DFF, PH, TPT, SM, S, and M, moderate heritability for FLL, FLW, CD, NGP, W, and YPP, and low heritability for PL and L/W ratios in F_5. High heritability in lodging-pertaining traits such as SM, BS, and M suggests the future scope to improve and do effective selections for lodging resistance. Heritability in percentage ranged from 91.5 for DFF to 5.37 for L/W ratio in BC_1F_4. Most traits under study in BC_1F_4 reported high heritability, except NGP, W, and YPP with moderate heritability and L/W ratio with low heritability. **Fig. 1** illustrates the proportion of variation attributed to genotype and residual factors, with the residual encompassing both block effects and error. A high proportion of genetic variance suggests that the observed variability is true to the type to the genotype.

Selection Accuracy: The selection accuracy was high for most of the traits in both the populations under study. Yield per plant recorded a selection accuracy of 80.3 % in F_5 and 87.4 % in BC_1F_4. The traits related to lodging resistance such as SM, S, and M reported an accuracy of more than 90 % indicating fruitfulness for imposing selections (**Table 1**, **Table 2)**.

Detection of Multicollinearity: Multicollinearity is known to decrease the precision of analyses and was detected in the dataset using the code `cold2 <- colindiag(Data[...]).` The parameters used to detect multicollinearity include the Variance Inflation Factor (VIF), the Generalized Variance Inflation Factor (GVIF), and the condition number. The code displays the number of traits that exceed the VIF threshold of 10, where a VIF greater than 10 indicates the presence of multicollinearity (Cheng *et al*., 2022), bending moment at breaking (M) in F5 crossed the VIF threshold of 10, while no traits in BC_1F_4 exceeded this limit.

A GVIF of 1 indicates a lack of multicollinearity, whereas a value greater than 1 suggests its presence (Kim, 2019). In this study, a GVIF of 1.78 was observed in F_5, while BC_1F_4 showed a GVIF of 2.005. Additionally, a condition number greater than 10 indicates multicollinearity. The code reported a condition number of 68.111 in F_5 and 14.59 in BC_1F_4. These results collectively indicate the existence of multicollinearity; therefore, Selection Indices (SI) 2 and 3 were computed, both of which eliminated variables with a VIF greater than 10. The desired ideotype for rice in this study is a dwarf plant with high culm strength and section modulus, along with high yield. Consequently, genetic weights were assigned accordingly in the selection indices, and rescaling was performed in the Multi-trait Genotype Ideotype Distance Index (MGIDI) to achieve maximum selection gain (SG).

Smith Index: The Smith Index is a pioneering multi-trait index that allows breeders to select genotypes based on all traits under study by assigning equal genotypic weight to each trait. Using the **metan** package, Selection Index I (SI 1) was developed, based on the equation Pb=Gg where P is the phenotypic variance-covariance matrix, b is the phenotypic weights, G is the genotypic variance-covariance matrix, and g represents the genotypic weights. The goal is to find the phenotypic regression coefficient ($b=P^{-1}G$) that maximizes the phenotype in relation to the genotype. Regression coefficients for all traits in both populations are presented in **Table 3.** However, the benefits of the Smith Index can be compromised by multicollinearity. In this study, the bending moment at breaking (M) in F_5 and plant height (PH) in BC_1F_4 were identified as contributors to multicollinearity.Consequently, new Smith indices were computed, referred to as Smith Index 2 (Selection Index 2).

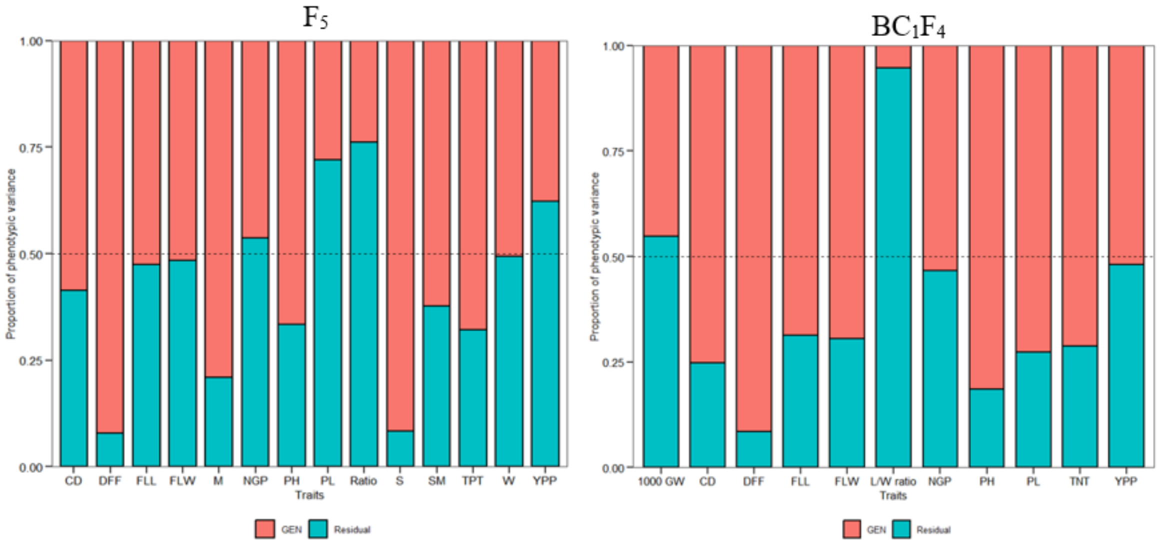

Fig. 1. Variance components in F_5 and BC_1F_4 (The residual also includes block variance)

Table 1. Variance components in F_5

	Gv	G(%)	Rv	R(%)	Pv	H2	Acc	Cvg	Cvr	CVR
DFF	36.1	92.2	3.07	7.85	39.1	92.2	98.6	6.57	1.92	3.43
PH	42.1	66.6	21.1	33.4	63.2	66.6	92.6	7.38	5.23	1.41
PL	1.05	28	2.70	72.5	3.75	28	73.4	4.67	7.49	0.62
FLL	26.1	52.5	23.6	47.5	49.7	52.5	87.7	21.3	20.3	1.05
FLW	0.02	51.6	0.02	48.4	0.04	51.6	87.3	13.8	13.4	1.03
TPT	19.3	67.8	9.18	32.2	28.5	67.8	92.9	23.9	16.5	1.45
CD	0.46	58.6	0.32	41.4	0.78	58.6	90	14.9	12.5	1.19
NGP	474	46.3	551	53.7	1025	46.3	84.9	20.8	22.4	0.92
L/W	0.05	23.8	0.18	76.2	0.24	23.8	69.6	8.27	14.8	0.55
W	7.86	50.6	7.68	49.4	15.5	50.6	86.9	12.6	12.5	1.01
SM	6.83	62.4	4.12	37.6	10.9	62.4	91.2	50.4	39.1	1.29
S	35290	91.6	3223	8.37	38513	91.6	98.5	46.9	14.2	3.31
M	32863	79.1	8702	20.9	41565	79.1	95.9	81.5	41.9	1.94
YPP	42.2	37.7	69.7	62.3	112	37.7	80.3	18.9	24.3	0.77

DFF. Days to 50% Flowering, PH. Plant Height, PL. Panicle Length, FLL. Flag leaf length, FLW. Flag Leaf width, TPT. Total Number of Productive tillers, CD. Culm Diameter, NGP. Number of Grains Per Panicle, L/W. Length/ Width Ratio, W. 1000 Grain Weight, SM. Section modulus, S. Bending Stress, M. Bending Moment at Breaking, YPP. Yield Per Plant, Gv. Genetic Variance, G(%). Genetic variance in percentage, Rv. Residual Variance, R(%). Residual Variance (%), Pv. Phenotypic Variance, H2. Heritability, Acc. Accuracy of selection, Cvg. Genotypic coefficient of variation, Cvr. Residual coefficient of variation, CVR. The ratio between genotypic and residual coefficient of variation.

Table 2. Variance components in BC_1F_4

	Gv	G(%)	Rv	R(%)	Pv	H2	Acc	Cvg	Cvr	CVR
DFF	20.5	91.5	1.91	8.52	22.4	91.5	98.5	5.02	1.53	3.28
PH	53.3	81.5	12.1	18.5	65.4	81.5	96.4	8.55	4.08	2.10
PL	8.72	72.7	3.27	27.3	12.0	72.7	94.3	14.7	9.01	1.63
FLL	25.3	68.6	11.6	31.4	36.9	68.6	93.2	18.9	12.8	1.48
FLW	0.01	69.4	0.00	30.6	0.02	69.4	93.4	12.6	8.39	1.51
TPT	35.6	71.3	14.3	28.7	49.9	71.3	93.9	25.6	16.3	1.58
CD	0.62	75.2	0.20	24.8	0.83	75.2	94.9	20.4	11.7	1.74
NGP	670	53.4	585	46.6	1255	53.4	88.0	25.6	23.9	1.07
L/W	0.01	5.37	0.32	94.6	0.34	5.37	38.2	4.71	19.7	0.23
W	6.80	45.2	8.24	54.8	15.0	45.2	84.4	11.5	12.7	0.90
YPP	15.4	51.9	14.3	48.1	29.7	51.9	87.4	11.1	10.7	1.04

DFF. Days to 50% Flowering, PH. Plant Height, PL. Panicle Length, FLL. Flag leaf length, FLW. Flag Leaf width, TPT. Total Number of Productive tillers, CD. Culm Diameter, NGP. Number of Grains Per Panicle, L/W. Length/ Width Ratio, W. 1000 Grain Weight, YPP. Yield Per Plant.

On analysis Habataki, CO 52, G 32, G 31, and G 30 were ranked the top 1 to 5 for SI 1 among the 32 F_5 families however excluding the M from the analysis as it is leading to multicollinearity, the new selection index called, SI 2, revealed CO 52, G 32, Habataki, G 24, G 25 as the top rankers. The genotypes G 32, Habataki, and CO 52 were found to be common for both SI 1 and SI 2. As the Smith Index had equal genotypic weights, equal importance was given for both lodging-resistant traits and yield traits. Genotypes such as CO 51, despite its high yield potential, exhibit significant susceptibility to lodging, characterized by low section modulus and bending stress. Consequently, CO 51 ranked 24th and 27th in Selection Index I (SI 1) and Selection Index II (SI 2), respectively. In contrast, the donor genotype Habataki achieved the highest rankings of 1st and 2nd in SI 1 and SI 2. This analysis indicates that both SI 1 and SI 2 primarily emphasize the improvement of

Table 3. Regression coefficients (b) derived from genotypic and phenotypic variance and co-variance matrix

S.No	Traits	SI(1) F_5	SI(2) F_5	SI(1) BC_1F_4	SI(2) BC_1F_4	a	SI(3) F_5	a	SI(3) BC_1F_4	a
1	DFF	2.26	1.42	0.65	0.75	1	0.80	1.5	-0.60	-0.5
2	PH	2.95	1.18	0.54	-	1	-0.411	-0.5	-	-0.5
3	PL	3.47	5.02	2.63	1.97	1	2.64	1.5	1.18	2
4	FLL	-0.01	0.85	1.52	1.20	1	1.37	1.5	0.00	-0.5
5	FLW	-47.34	-41.76	44.98	36.12	1	-47.3	-0.5	18.11	-0.5
6	TPT	1.62	1.88	1.19	1.26	1	1.41	-0.5	1.64	2
7	CD	37.64	19.75	-1.87	-1.51	1	17.70	-0.5	0.75	2
8	NGP	0.25	0.25	0.62	0.63	1	1.13	2	0.03	0
9	L/W	-13.50	6.69	-9.05	-5.72	1	4.43	2	3.01	-0.5
10	W	3.57	0.97	-0.19	-0.08	1	0.71	2	0.23	0
11	SM	3.62	3.31			1	3.65	0	-	-
12	BS	1.00	0.90			1	-0.05	0	-	-
13	M	0.76	-			1	-	-	-	-
14	YPP	0.19	-0.511	1.14	0.99	1	0.05	2	1.48	2

SI (1): Selection Index 1 with equal genotypic weights without removing the variable causing multicollinearity, SI (2): Selection Index 2 with equal genotypic weights without the variable which causes multicollinearity, SI (3): Selection Index 3 where the genetic weights are defined based on path analysis: higher direct effect. Genotypic weight is 2, negative direct effect. Genotypic Weight is set as -0.5

lodging resistance while inadequately addressing yield characteristics. Based on path analysis DFF, PL, FLL, NGP, L/W, and W were found to have a high direct effect on yield and hence were given weightage of 1.5 and 2, the traits such as NGP and W having direct influence on yield were allotted weightage of 2. Traits having a negative direct effect on yields such as PH, FLW, TPT, and CD were allotted genetic weightage of -0.5, subsequently, following the fresh values for "a" (genotypic weights), "b" (regression coefficients) were recalculated using the same procedure applied for Selection Index I (SI 1) and Selection Index II (SI 2). The genotypes CO 52, G 26, G 23, G 20, and G 27 were ranked 1st in genetic worth. The check CO 52 was common for all the selection indices, which raised the issue of whether the F5 families succeeded in reaching the target yield levels in comparison to available varieties (**Table 4**). The genotypes CO 52, G 17, G 24, G 26, G 23, and ADT 43 were top rankers in BC_1F_4 through SI 1, while in SI 2, G 17, CO 52, G 24, G 26, G 23, and G 30 were observed to be top-ranked. Hence both SI 1 and SI 2 selected common genotypes, SI 3 selected G 30, G 17, G 35, ADT 43, and G 32. The genotype G 17 was found to be commonly selected in all the above selection indices (**Table 5**).

Multi-Trait Genotype Ideotype Distance Index (MGIDI):In MGIDI, the ideotype of genotypes was defined by rescaling the original means between 0 to 100 values. Traits that we aim to improve are assigned a maximum value of 100 and a minimum value of 0. In contrast, traits for which we seek a negative gain, such as days to 50% flowering (DFF) and plant height (PH), are assigned a maximum value of 0 and a minimum value of 100. The principal component analysis is a dimensionality reduction technique that converts the corrected variables into uncorrelated principal components (PCs), five PCs have been found to cross the eigenvalue of 1 which collectively explained 71.6% variance in F_5, four PCs have crossed the eigenvalue of 1 which collectively explained 70.30% of the variance in BC_1F_4 (**Table 6**). Considering the presence of five and four PCs in F_5 and BC_1F_4 crossing the eigenvalue of 1, five factors have been created in F_5 and four in BC_1F_4. FA1 included DFF, CD, SM, and S, in F_5 similarly PH, PL, and W were grouped under FA 2, TPT, and NGP are part of FA3, FLL, FLW are part of FA4, and L/W ratio, and YPP are part of FA5. Traits of lodging importance were grouped in FA1 along with DFF, yield belonging to FA5. In BC_1F_4, PH, PL, CD, and NGP were grouped under FA1, FLL, FLW is part of FA2, TPT, L/W ratio, and 1000 GW part of FA3, DFF, and YPP are part of FA4 (**Table 7 and Table 8**). The rescaled values are utilized to calculate the MGIDI score. On calculating the MGIDI scores, the genotypes with the lowest MGIDI scores are considered to be close to the Ideotype. CO 52, G 32, G 31, ADT 43, G 27, and G 1 are selected in F_5, and CO 52, G 25, G 17, G 21, G 30, and G 23 are selected in BC_1F_4 (**Fig. 2**). On visualizing the radar graph, the genotypes found outside the circle are said to have low MGIDI scores and they are selected at 15% selection intensity, genotypes lying on the circle are said to possess special qualities i.e., G 1, CO 52 in F_5 and G 13 in BC_1F_4.

Analyzing Strengths and Weaknesses: The strengths and Weaknesses plot is a unique feature of MGIDI which gives

Table 4. Ranking of genotypes of F_5 families based on selection indices

S.no	Genotype	Index Score	Rank	Index Score	Rank	Index score	Rank
		Smith Index 1		Smith Index 2		Selection Index 3	
1	Habataki	2272.00	1	1231.51	2	307.03	28
2	CO 52	2262.25	2	1315.23	1	397.57	1
3	G 32	2025.16	3	1217.35	3	347.00	10
4	G 31	1885.00	4	1104.19	7	350.17	9
5	G 30	1719.96	5	1105.08	6	333.66	15
6	BPT 5204	1681.60	6	1035.94	10	338.05	13
7	G 24	1669.52	7	1168.24	4	363.34	7
8	G 25	1603.99	8	1127.73	5	315.42	22
9	G 28	1550.84	9	1039.09	9	341.82	11
10	ADT 43	1502.37	10	932.70	11	350.17	8
11	G 20	1499.28	11	863.20	14	378.80	4
12	G 29	1498.75	12	1047.26	8	302.68	30
13	G 27	1492.599	13	853.37	15	373.27	5
14	G 16	1410.25	14	820.10	22	310.36	25
15	G 2	1366.77	15	910.488	13	284.83	36
16	G 11	1354.25	16	828.80	18	308.36	26
17	G 6	1338.94	17	839.73	16	302.64	31
18	G 19	1335.63	18	922.90	12	321.23	19
19	G 17	1280.30	19	820.45	21	366.20	6
20	G 1	1269.60	20	823.29	20	301.22	32
21	G 23	1206.81	21	828.28	19	379.32	3
22	G 13	1185.19	22	837.66	17	314.22	24
23	G 26	1134.24	23	765.07	24	385.45	2

Selection gain: 15%

Table 5. Ranking of genotypes of BC_1F_4 families based on selection indices

S.no	Genotype	Index Score	Rank	Index Scores	Rank	Index Score	Rank
	Smith Index 1			**Smith Index 2**		**Selection Index 3**	
1	CO 52	414.98	1	333.13	1	101.35	18
2	G 17	407.88	2	332.70	2	121.66	2
3	G 24	402.76	3	318.16	5	109.14	7
4	G 26	399.22	4	319.43	3	106.03	10
5	G 23	396.09	5	318.16	4	101.52	17
6	ADT 43	380.30	6	306.44	9	112.85	4
7	G 25	377.02	7	306.45	8	100.14	21
8	G 4	370.42	8	308.38	7	98.46	24
9	G 21	366.47	9	300.70	10	105.28	11
10	G 30	364.94	10	308.98	6	139.73	1
11	BPT 5204	354.37	11	298.65	11	106.54	9
12	G 5	351.76	12	292.74	14	100.31	20
13	G 7	350.79	13	289.15	16	107.89	8
14	G 32	347.93	14	294.13	13	109.59	5
15	G 31	347.65	15	291.05	15	109.14	6
16	G 2	344.18	16	285.34	18	102.63	14
17	G 35	343.02	17	296.96	12	113.98	3

Selection gain: 15%

Table 6. Principal component analysis in F_5 and BC_1F_4 of the cross CO 51 x Habataki

PC	EV	V (%)	CuV (%)	EV	V(%	CuV(%)
		F_5			BC_1F_4	
PC1	3.71	26.5	26.5	3.14	28.5	28.5
PC2	2.17	15.5	41.9	1.71	15.5	44.0
PC3	1.68	12	53.9	1.48	13.5	57.5
PC4	1.41	10.1	64	1.41	12.8	70.3
PC5	1.23	8.77	72.8	0.98	8.92	79.2
PC6	0.88	6.28	79	0.79	7.2	86.4
PC7	0.77	5.47	84.5	0.52	4.76	91.1
PC8	0.56	4.01	88.5	0.46	4.16	95.3
PC9	0.5	3.6	92.1	0.33	3	98.3
PC10	0.37	2.63	94.8	0.11	1.01	99.3
PC11	0.33	2.33	97.1	0.08	0.7	100
PC12	0.21	1.53	98.6			
PC13	0.16	1.12	99.8			
PC14	0.03	0.24	100			

EV. Eigenvalue, V(%). Variance explained, CuV(%). Cumulative variance explained

Table 7. Factorial loadings in F_5 population

	FA1	FA2	FA3	FA4	FA5
DFF	0.57	-0.13	-0.4	-0.28	0.23
PH	0.23	0.77	0.06	-0.14	-0.13
PL	-0.16	-0.8	0.33	-0.1	-0.06
FLL	-0.13	-0.19	0.11	0.9	-0.04
FLW	-0.31	-0.47	0.13	-0.71	-0.07
TPT	0.06	-0.02	0.87	0.08	-0.01
CD	-0.74	-0.2	0.23	-0.18	-0.06
NGP	-0.26	0.01	0.52	-0.04	-0.01
L/W	0.05	-0.08	0.41	-0.11	0.76
W	-0.22	0.7	0.26	0.04	-0.1
SM	-0.78	0.02	-0.2	-0.01	0.4
BS	-0.73	-0.11	0.28	0.06	-0.37
M	-0.96	-0.07	-0.01	0.02	0.01
YPP	0.01	-0.11	-0.39	0.11	0.73

Table 8. Factorial loadings in the BC_1F_4 population

VAR	FA1	FA2	FA3	FA4
DFF	0.16	-0.14	-0.05	0.85
PH	0.88	-0.26	0.24	-0.11
PL	-0.92	-0.03	-0.12	0.03
FLL	-0.14	0.91	0.02	-0.03
FLW	-0.54	-0.69	0.15	-0.32
TPT	0.18	0.37	0.66	-0.27
CD	-0.66	-0.25	0.20	-0.40
NGP	-0.63	-0.05	0.31	-0.06
L/W	0.16	-0.16	0.62	0.37
W	0.26	0.08	-0.64	0
YPP	-0.1	0.20	0.09	0.66

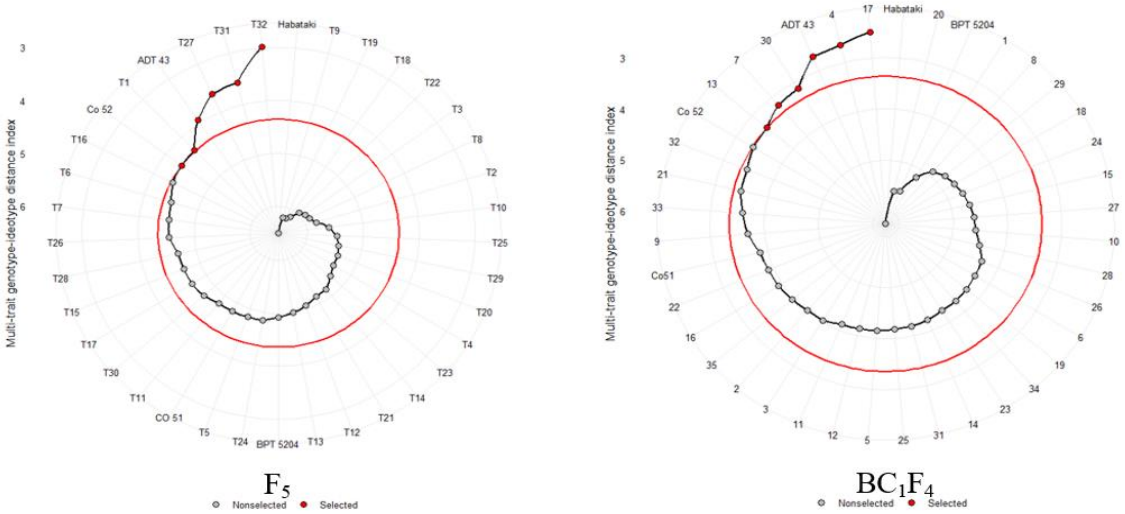

Fig. 2. Genotype ranking order for the MGIDI index in F_5 and BC_1F_4 populations.

the weaknesses and strengths of the selected genotypes. Genotypes that are close to the circumference of the circle are said to be least contributed by that particular factor and the genotype shows high performance for the traits included in that factor. And a genotype close to the center of the plot is most contributed by that factor and the genotype performance is less for the traits belonging to that factor. In the strength and weakness plot of F_5, FA 1 and FA 5 are important to us as FA 1 included lodging resistant pertaining traits and FA 5 included yield. G 31 and the check CO 52 showed the radar to be close to the circumference indicating FA 1 has the least contribution to these genotypes are good in performance for SM and M, whereas G1 and ADT 43 are most contributed by FA 1 suggesting the genotypes are lodging in nature which is the weakness of these genotypes. FA 5 radar was close to the outer circumference for G 27 indicating the least contribution of FA 5 and it is good in performance for yield and slender grain type. The lodging-resistant G 31 was relatively least contributed by FA 5 in comparison to CO 52 hence it is more in yield in comparison to the check CO 52. Hence, G 31 can be promoted further for trails according to the strengths and weaknesses plot as it is good for both yield and lodging resistance. On analyzing strengths and weaknesses plots of BC_1F_4, G 17, and ADT 43 are the least contributed by FA 1 hence these both are good for culm diameter (CD), number of grains per panicle (NGP), PL, and dwarf PH. G 30 and G 4 are more contributed by FA 1 hence least in importance for lodging resistance as their performance for CD is not good. G 4 and G 30 are least contributed by FA 4 hence their performance is good for yield and they also have a dwarf stature, hence these genotypes can be further promoted for preliminary yield trials (**Fig. 3**).

Selection Gain: Selection gain (SG) in percent for the F_5 population was negative for yield for SI 1, 2, and 3. As in SI 1 and SI 2, there was a very high gain for lodging-resistant traits i.e., SM and S. Improvement for lodging was at the expense of yield. However, in SI 3 where genetic weights were differentially given, 0 weight was given for lodging resistant pertaining traits the SG in percent for yield was -1.65 % which was better in comparison with -6.79% seen for SI 1 and -5.07 % seen in SI 2. MGIDI resulted in a positive gain of 2% under selection for yield which also improved lodging-resistant traits with a 39.6 % gain for SM and a 34.7 % gain for S. Hence unlike SI 1, 2, and 3 which could not improve yield and lodging resistance simultaneously, MGIDI could improve both. In BC_1F_4 selection gain of 2.02 and 1.88 % was seen for SI 1 and 2, however, in SI 3 where the weights were differentially given, and in MGIDI the selection gain for yield was high and promising, 5.84 % SG was reported in SI 3 and MGIDI showed 5.80 % gain. Both SI 3 and MGIDI could show a negative gain for the duration hence there is a possibility to select short duration lines to be forwarded further (**Table 9, Table 10,** and **Fig. 4**).

Coincidence Index: To know the level of agreement between different selection indices, the coincidence index is computed using the formulae $CI = \frac{A-C}{M-C} \times 100$,

where A is a number of genotypes common several selection indices, M is the total number of genotypes selected, C is number of genotypes included by a chance event (M x 0.15). In both F_5 and BC_1F_4, a high level of agreement of 52.94 and 80.39 was reported between SI 1 and SI 2. The level of agreement between MGIDI and conventional selection indices is less ranging from 29.41% to 5.88% in F_5 and 21.57% to 41.18% in BC_1F_4 suggesting that the novel MGIDI has been selecting a different subset of genotypes in comparison to conventional indices (**Table 11 and 12**).

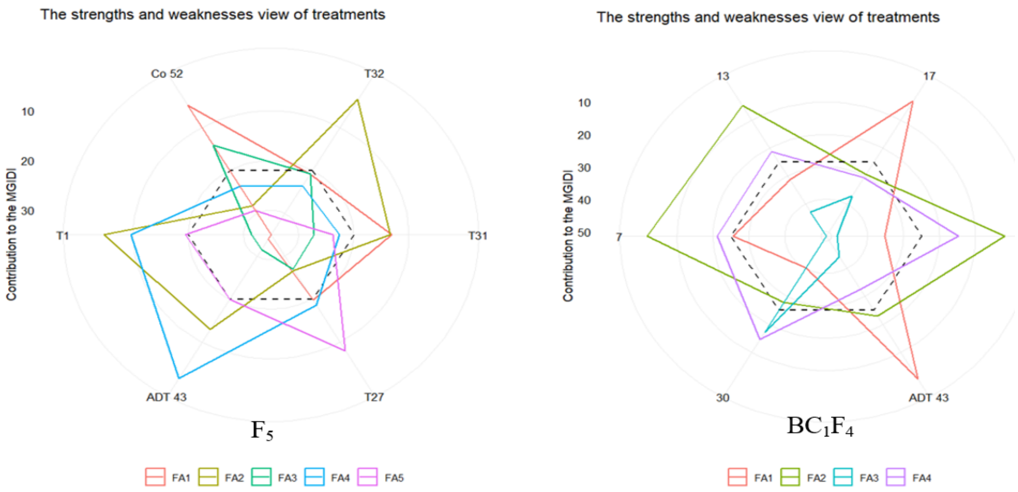

Fig. 3. Visualization of Strengths and Weaknesses of the selected genotypes in stabilized F_5 and BC_1F_4 families.

Table 9. Selection gain through conventional indices in F_5 and BC_1F_4 families of the cross CO 51 x Habataki

S.No	Trait	SG% (SI 1)	SG% (SI 2)	SG%(SI 3)	SG% (SI 1)	SG% (SI 2)	SG% (SI3)
			F_5			BC_1F_4	
1	DFF	9.02	6.49	2.91	0.57	2.14	-0.52
2	PH	2.39	0.90	-1.18	11.6	-	-
3	PL	1.42	1.01	0.11	16.6	13.84	-3.31
4	FLL	0.07	11.25	9.05	11.1	14.48	4.85
5	FLW	7.88	-0.08	-4.53	7.47	4.01	0.08
6	TPT	7.62	10.10	3.57	-0.33	16.18	31.59
7	CD	16.04	10.75	6.14	18.7	16.94	8.54
8	NGP	2.68	3.26	16.42	27.2	21.51	10.37
9	L/W	-0.42	-0.993	1.20	-0.12	-0.14	0.10
10	W	1.90	1.95	4.36	-3.36	-1.28	-2.69
11	SM	34.53	13.91	31.35	-	-	-
12	BS	68.08	76.80	1.44	-	-	-
13	M	123.2	-	-	-	-	-
14	YPP	-2.82	-5.074	-1.65	2.02	1.88	5.84

SG(%). Genetic Gain in % for Selection Index 1, 2, and 3.

Table 10. Selection gain (%) in F_5 and BC_1F_4 derived through MGIDI based selection

Trait	SG (%)	Ideotype	Trait	SG (%)	Ideotype
DFF	4.43	Decrease	DFF	-3.19	Decrease
PH	6.06	Decrease	PH	1.63	Decrease
PL	1.59	Increase	PL	6.52	Increase
FLL	9.04	Increase	FLL	-3.0	Increase
FLW	6.57	Increase	FLW	3.19	Increase
TPT	8.52	Increase	TPT	9.87	Increase
CD	10.70	Increase	CD	5.89	Increase
NGP	5.03	Increase	NGP	16.6	Increase
L/W	2.87	Increase	L/W	0.22	Increase
W	-0.61	Increase	W	-6.08	Increase
SM	39.60	Increase	-	-	
BS	34.70	Increase	-	-	
M	84.60	Increase	-	-	
YPP	2.00	Increase	YPP	5.80	Increase

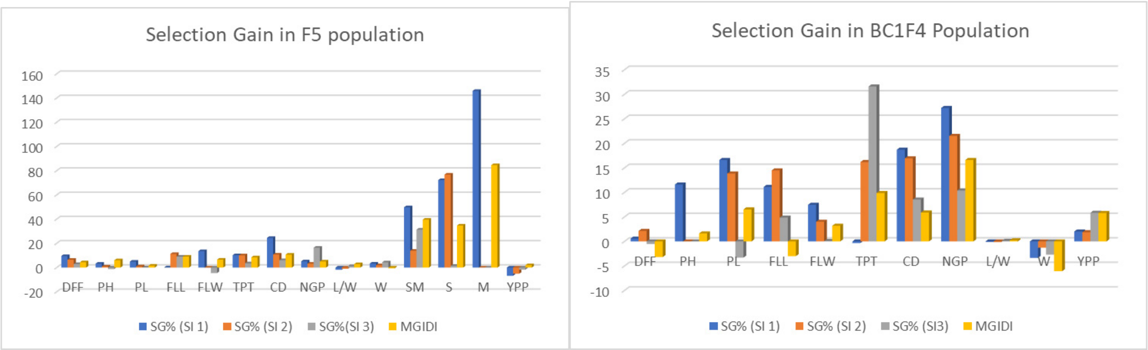

Fig. 4. Selection gain in F_5 and BC_1F_4

Table 11. Coincidence index and common genotypes in F_5

S.No	V1	V2	Index	Common genotypes
1	MGIDI	Selection Index 1	29.41	G 32, G 31
2	MGIDI	Selection Index 2	5.88	G 32
3	MGIDI	Selection Index 3	5.88	G 27
4	Selection Index 1	Selection Index 2	52.94	Habataki, CO 52, G 32
5	Selection Index 1	Selection Index 3	5.88	CO 52
6	Selection Index 2	Selection Index 3	29.41	CO 52

Table 12. Coincidence index and common genotypes in BC_1F_4

S.No	V1	V2	Index	Common genotypes
1	MGIDI	Selection Index 1	21.57	G 17, ADT 43
2	MGIDI	Selection Index 2	21.57	G 17, G 30
3	MGIDI	Selection Index 3	41.18	G 17, ADT 43, G 30
4	Selection Index 1	Selection Index 2	80.39	CO 52, G 17, G 24, G 26, G 23
5	Selection Index 1	Selection Index 3	21.57	G 17, ADT 43
6	Selection Index 2	Selection Index 3	21.57	G 17, G 30

Improving lodging resistance and yield simultaneously was the goal of the work, however, the conventional indices showed a selection gain of 68.08% and 76.80% for lodging-pertaining traits at the expense of a decrease in the yield of 2.82% and 5.07% in the F_5 population. However, on assigning the differentially the genetic weights in SI 3, showed a gain of 31.35% for section modulus and 1.44% for bending stress, and yield showed a decrease of 1.65%. However, using MGIDI, 2% increase in yield was recorded which also did not compromise the section modulus and bending stress which showed a gain of 39.6% and 34.7% respectively. Gain of 2.02, 1.88, and 5.84 for yield was achieved through SI 1, SI 2, and SI 3 in BC_1F_4. MGIDI achieved a gain of 5.88% for yield and 5.89% for culm diameter which also showed a decrease in duration at 3.99 % which could not be achieved through the conventional selection indices. Hence it was felt that MGIDI is superior as a selection criterion in comparison to the conventional indices however SI 3 was comparable to MGIDI. On analyzing the strengths and weaknesses along with various selection indices, G 27 of F_5 was found to be more desirable for both yield and lodging resistance hence it can be forwarded further, and G 32, and G 31 can also be considered however in this generation G 32, and G 31 are less is yield compared to G 27 and checks however considering their high performance for lodging resistance they can be further forwarded to check for yield stability in future trails. In BC_1F_4 G 4 and G 30 are more desirable for yield and can be forwarded further.

ACKNOWLEDGMENT

We acknowledge the paddy breeding station for giving the facilities to do high throughput phenotyping for lodging resistance and providing all the required facilities to carry out the research work.

REFERENCES

Benakanahalli, N. K., Sridhara, S., Ramesh, N., Olivoto, T., Sreekantappa, G., Tamam, N., Abdelbacki, A. M., Elansary, H. O. and Abdelmohsen, S. A. 2021. A framework for identification of stable genotypes basedon MTSI and MGDII indexes: An example in guar (*Cymopsis tetragonoloba* L.). *Agronomy*, **11**(6): 1221. [Cross Ref]

Cheng, J., Sun, J., Yao, K., Xu, M. and Cao, Y. 2022. A variable selection method based on mutual information and variance inflation factor. *Spectrochimica Acta Part A: Molecular and Biomolecular Spectroscopy*, **268**(1): 120652. [Cross Ref]

Kambale, R., Raveendran, M., Bharathi, A. and Ramalingam, J. 2022. Genetic improvement of drought tolerance in North Eastern chakhao amubi rice through marker-assisted selection. *Madras Agricultural Journal*, **109**(1-3): 107-111. [Cross Ref]

Kim, J. H. 2019. Multicollinearity and misleading statistical results. *Korean Journal of Anesthesiology.*, **72**(6): 558–569. [Cross Ref]

Nomura, T., Arakawa, N., Yamamoto, T., Ueda, T., Adachi, S., Yonemaru, J., Abe, A., Takagi, H., Yokoyama, T. and Ookawa, T. 2019. Next-generation long-culm rice with superior lodging resistance and high grain yield, Monster Rice 1. *PLoS One.*, **14**(8). [Cross Ref]

Olivoto, T., Diel, M. I., Schmidt, D. and Lúcio, A. D. 2022. MGIDI: A powerful tool to analyze plant multivariate data. *Plant Methods*, **18**(1): 121. [Cross Ref]

Olivoto, T. and Lúcio, A. D. 2020. metan: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution.*, **11**(6): 783–789. [Cross Ref]

Olivoto, T., Lúcio, A. D. C., Da Silva, J. A. G., Sari, B. G. and Diel, M. I. 2019. Mean performance and stability in multi-environment trials II: Selection based on multiple traits. *Agronomy Journal.*, **111**(6): 2961–2969. [Cross Ref]

Olivoto, T. and Nardino, M. 2021. MGIDI: Toward an effective multivariate selection in biological experiments. *Bioinformatics*, **37**(10): 1383–1389. [Cross Ref]

Ookawa, T., Aoba, R., Yamamoto, T., Ueda, T., Takai, T., Fukuoka, S., Ando, T., Adachi, S., Matsuoka, M. and Ebitani, T. 2016. Precise estimation of genomic regions controlling lodging resistance using a set of reciprocal chromosome segment substitution lines in rice. *Scientific Reports.*, **6**(1): 30572. [Cross Ref]

Ookawa, T., Hobo, T., Yano, M., Murata, K., Ando, T., Miura, H., Asano, K., Ochiai, Y., Ikeda, M. and Nishitani, R. 2010. New approach for rice improvement using a pleiotropic QTL gene for lodging resistance and yield. *Nature Communications.*, **1**(1): 132. [Cross Ref]

Palaniyappan, S., Arunachalam, P., Banumathy, S. and Muthuramu, S. 2024. Introspection of discriminate function analysis and MGIDI selection index for selection to improve yield in rice (*Oryza sativa* L.). *Indian Journal of Genetics and Plant Breeding*, **84**(02): 202–208. [Cross Ref]

Pallavi, M., Prasad, B. M., Shanthi, P., Reddy, V. L. N. and Kumar, A. N. 2024. Multi trait genotype-ideotype distance index (MGIDI) for early seedling vigour and yield related traits to identify elite lines in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding.*, **15**(1): 120–131. [Cross Ref]

Robin, S., Mohanasundaram, K., Manonmani, S., Rajeswari, S., Jeyaprakash, P., Pushpam, R., Thiagarajan, K., Rabindran, R., Suresh, S. and Ravichandran, V. 2019. TNAU Rice CO 51 (IET 21605)-A high-yielding short-duration fine-grain rice variety for Tamil Nadu. *Electronic Journal of Plant Breeding*, **10**(2): 324–333. [Cross Ref]

Smith, O. S., Hallauer, A. R. and Russell, W. A. 1981. Use of index selection in recurrent selection programs in maize. *Euphytica*, **30**(3): 611–618. [Cross Ref]