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RESEARCH ARTICLE

Introspection of discriminate function analysis and MGIDI selection index for selection to improve yield in rice (*Oryza sativa* L.)

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Abstract

In order to improve the grain yield the different selection indices were constructed based on a discriminate function using 36 rice genotypes. Two types of Smith and Hazel selection methods namely equal (Selection Index I) and differential weightage (Selection Index II) were used to construct the selection index using 17 quantitative traits, resulting in 94.34 and 95.88% genetic advance, respectively. The genotypes M7-1, M7-4, M7-6, M7-8, and M7-11 proved their top rankings based on index scores in both cases. To know better understand the selection and identification of superior genotypes the MGIDI were engaged. Based on 15% selection pressure the genotypes F_5-5, M_4-2, Anna (R) 4, M_4-8 and M_4-9 were identified as superior performing genotypes for all the studied variables. However, the ranking of genotypes by MGIDI was not similar to the ranking of Smith Hazel method because this method does not include the variables' correlation structure. Comparing the classical method of selection index the MGIDI were more advantageous to identify the best performing genotypes based on the factorial analysis of BLUP values and more helpful to identify the traits responsible for selection of superior genotypes.

Keywords: Rice, selection index, discriminate function, genetic advance, relative efficiency, MGIDI

Introduction

Rice is the most important stable crop in world population. One of the primary dependent traits is grain yield and its improvement through direct selection is very slow because of its intricate control nature. Mainly, grain yield depends on a number of yield contributing component characters. So the selection index is one of the suitable methods to improve efficiency compared to straight selection for grain yield in rice. The method proposed by Smith's (1936) classical selection index on the basis discriminant function of Fisher (1936) was the desirable approach to discriminate the anticipated genotype from a group of undesirable populations. Hazel and Lush (1942) and Robinson et al. (1951) showed that the selection based on such index was more efficient than selecting individually for the various characters. Normally in seriatim selection, breeders have possible to select single attribute for improvement at the time and so on for further one in succeeding generations. However, the selection index method helps to select superior genotypes based on the simultaneous selection of a combination of traits called discriminate function analysis. Bos and Caligari (2008) also stated that simultaneous selection with related or desirable traits is a tactic to improve the grain yield. Since this selection method has the problem of inversion of phenotypic variance, multicollinearity affects the genetic gain estimation. Apart from dealing with the issue of multicollinearity, breeders commonly confront challenging decisions in expressing the economic significance of traits and requiring the conversion

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of these trait values into tangible economic weightings (Bizari et al. 2017). Olivoto and Nardino (2021) developed a new genetic analysis called multi trait genotype ideotype distance index (MGIDI) to overcome these difficulties. The MGIDI index's performance is assessed through Monte Carlo simulations, wherein the effectiveness of selecting traits with desired gains is calculated across multiple scenarios involving variations in the number of genotypes and traits under evaluation. In this investigation, the Smith and Hazel selection index and MGIDI were performed for the selection of superior genotypes based on 17 quantitative traits. The main objective of this study is to compare the Smith and Hazel selection index with the MGIDI selection index for the identification of superior genotypes in rice. Additionally, this experiment employed these techniques to identify superior homozygous lines for further varietal evaluation

Table 1. The details of genetic materials and their code

S. No.	Pedigree	Code	Generation	Parentage/ Treatment
1	M_7–T_5 85 – 6- 1- 3-30	M_7-1	M_7	100mM (EMS)
2	M_7–T_5 85 – 3- 2- 5-25	M_7-2	M_7	100mM (EMS)
3	M_7–T_5 85 – 6- 1- 3-37	M_7-3	M_7	100mM (EMS)
4	M_7–T_5 84 – 1- 2- 3-27	M_7-4	M_7	100mM (EMS)
5	M_7–T_5 85 – 3- 2- 5-24	M_7-5	M_7	100mM (EMS)
6	M_7–T_6 151 – 4- 16- 8-1	M_7-6	M_7	110mM (EMS)
7	M_7–T_5 85 – 6- 1- 3-34	M_7-7	M_7	100mM (EMS)
8	M_7–T_6 151 – 1- 15- 8-35	M_7-8	M_7	110mM (EMS)
9	M_7–T_5 81 – 2- 1- 5-22	M_7-9	M_7	100mM (EMS)
10	M_7–T_5 85 – 3- 2- 5-33	M_7-10	M_7	100mM (EMS)
11	M_7–T_6 151 – 11- 1- 9-28	M_7-11	M_7	110mM (EMS)
12	M_7–T_6 151 – 1- 15- 8-27	M_7-12	M_7	110mM (EMS)
13	F_5 - C_{13} -10- 30- 34	F_5-1	F_5	MDU 6 X *Jaldi Dhan* 6
14	F_5 - C_{13} -10- 4- 15	F_5-2	F_5	MDU 6 X *Jaldi Dhan* 6
15	F_5 - C_{13} -10- 4- 3	F_5-3	F_5	MDU 6 X *Jaldi Dhan* 6
16	F_5 - C_{13} -10- 22- 34	F_5-4	F_5	MDU 6 X *Jaldi Dhan* 6
17	F_5 - C_{13} -12- 3- 45	F_5-5	F_5	MDU 6 X *Jaldi Dhan* 6
18	F_5 - C_{13} -19- 20- 30	F_5-6	F_5	MDU 6 X *Jaldi Dhan* 6
19	F_5 - C_{13} -19- 2- 18	F_5-7	F_5	MDU 6 X *Jaldi Dhan* 6
20	F_5 - C_{17} -6- 16- 24	F_5-8	F_5	TKM 6 X *Jaldi Dhan* 6
21	GT_1- 24- 3- 1- 8	M_4-1	M_4	100 Gy Gamma Rays
22	GT_1- 45- 7- 2- 9	M_4-2	M_4	100 Gy Gamma Rays
23	GT_1- 46- 3- 1- 6	M_4-3	M_4	100 Gy Gamma Rays
24	GT_1- 46- 4- 1- 6	M_4-4	M_4	100 Gy Gamma Rays
25	GT_1- 129- 15- 2- 4	M_4-5	M_4	100 Gy Gamma Rays
26	GT_2- 14- 15- 2- 7	M_4-6	M_4	150 Gy Gamma Rays
27	GT_2- 73- 17- 1- 2	M_4-7	M_4	150 Gy Gamma Rays
28	GT_2- 82- 1- 1- 2	M_4-8	M_4	150 Gy Gamma Rays
29	ET_1- 37- 6- 2- 6	M_4-9	M_4	100 Gy Electron Beam
30	ET_1- 64- 3- 2- 4	M_4-10	M_4	100 Gy Electron Beam
31	ET_1- 79- 29- 2- 6	M_4-11	M_4	100 Gy Electron Beam
32	ET_1- 91- 23- 1- 6	M_4-12	M_4	100 Gy Electron Beam
33	ET_2- 51- 13- 2- 7	M_4-13	M_4	150 Gy Electron Beam
34	ET_2- 62- 4- 1- 9	M_4-14	M_4	150 Gy Electron Beam
35	ET_2-118- 19- 1- 3	M_4-15	M_4	150 Gy Electron Beam
36	Anna (R) 4	Anna (R) 4	Variety	Pantdhan 10 / IET 9911

and segregant lines for advancement.

Materials and methods

The present experimental research was conducted at the Agricultural College and Research Institute, Madurai. The main aim focused in this study is to select the suitable genotypes that are ultimately favourable to rainfed situations with all suitable parameters. For that, we select the experimental material of 35 genotypes, which includes 12 advanced breeding lines (M_7 generation) derived from Anna (R) 4 EMS-induced mutant lines, 7 homozygous lines (F_5 generation) of MDU 6 x *Jaldi Dhan* 6 and one homozygous line (F_5 generation) of TKM 6 x *Jaldi Dhan* 6 and 15 mutant lines (M_4 generation) of Anna (R) 4 irradiated entries derived from gamma ray irradiation (8 entries) and Electron beam irradiation (7 entries) (Table 1). The EMS mutants included in this study achieved homozygosity during the M3 and M4 generations. The initial selection focused on the short slender grain mutation, and further advancements up to the M7 generation were evaluated for grain yield. These 35 genotypes were evaluated with the check variety Anna (R) 4 and the breeding materials were early maturing genotypes with drought tolerance. The crop was raised in *kharif* 2019 with a 25 X 15 cm spacing in Randomized Block Design (RBD). Two replications of this evaluation consist of three rows with 3m length for all genotypes. Each genotype was assessed by evaluating 15 plants per replication for all the variables. A total of 17 quantitative traits were recorded at different crop stages (Table 2).

In this study, the type of selection index proposed by Smith (1936) called the classical selection index model, were used to identify better genotypes and the Fisher (1936) discriminant functions were used for making a simultaneous selection of several characters and discriminating the desirable genotypes from group of genotypes based on phenotypic performance. The different parameters utilized to derive the index score are given below

$$\underset{A}{\begin{bmatrix} x_{11} & x_{12} & x_{13} \\ x_{21} & x_{22} & x_{23} \\ x_{31} & x_{32} & x_{33} \end{bmatrix}} \text{x} \underset{B}{\begin{bmatrix} b_1 \\ b_2 \\ b_2 \end{bmatrix}} = \underset{C}{\begin{bmatrix} G_{11} & G_{12} & G_{13} \\ G_{21} & G_{22} & G_{23} \\ G_{31} & G_{32} & G_{33} \end{bmatrix}} \text{x} \underset{D}{\begin{bmatrix} a_1 \\ a_2 \\ a_2 \end{bmatrix}}$$

where, $B = A^{-1}CD$, A = phenotypic variance and covariance matrix, B = Regression coefficients, C = genotypic variance and covariance matrix, and D = weights

Selection indices (I)

$I = b_1 x_1 + b_2 x_2 + \ldots\ldots\ldots\ldots\ldots\ldots + b_n x_n$

$x_{1,}\ x_{2\ldots.}\ x_n$ are the phenotypic value of different characters, by using b_i values, selection indices was worked out for individual genotypes. Finally, based on this index, the rank was given and selection of top-ranked genotypes for further breeding programs. The genetic advance and the relative efficiency of each discriminate function were analyzed and

Table 2. Selection index - Weightage of different traits and their regression coefficients

S. No.	Traits	Different selection index based on economic weightage			
		Selection index I		Selection index II	
		Equal weights to different traits	Regression coefficient (b_i)	Differential weights to different traits based on direct effects	Regression coefficient (b_i)
1	Plant height at 50th day	1	1.598	2	-49.820
2	Days to fifty per cent flowering	1	-5.590	0.5	-16.439
3	SPAD value	1	3.010	2	83.205
4	Plant height	1	1.866	0.5	58.096
5	Panicle length	1	2.708	0.5	1.579
6	Flag leaf length	1	-2.057	2	-7.821
7	Flag leaf breadth	1	37.044	0.5	-2.912
8	Total tillers	1	2.596	0.5	-73.361
9	Productive tillers	1	-2.876	2	-75.756
10	Days to maturity	1	2.589	2	7.562
11	Panicle weight	1	-10.665	0.5	4.140
12	No. of grains per panicle	1	1.330	0.5	1499.753
13	Filled grains per panicle	1	-0.067	1.5	1349.465
14	Grain length	1	-52.747	0.5	-8.793
15	Grain breadth	1	-68.032	0.5	-5.736
16	Hundred seed weight	1	30.784	2	-12.864
17	Grain yield per plant	1	1.188	2	203.461

grain yield is our primary dependent variable, so the relative efficiency of this attribute is fixed as 100%. The formula for genetic advance is GA= $KW/(V_p)^{1/2}$. Where K is selection differential for 10% (1.76), $W = \sum\sum a_i G_{ij} b_j$ and $V_p = \sum\sum b_i P_{ij} b_j$ and for relative efficiency given by Brim *et al.* (1959) is RE= (Genetic advance of individual index/Genetic advance of grain yield) x 100 used for estimation.

Statistical analysis

Initially, the genotypes were ranked using equal economic weightage (W1) to calculate all seventeen quantitative traits and genetic advances (Selection Index I). Secondly, the selection indices II were worked out based on the direct effect of the different characters from path analysis used as weightage (W_2). The weightage is fixed by those traits having very high direct effect. The weight (A) is given as 2, for traits with high direct effect as 1.5. For traits with a negative effect, the weight is taken as 0.5; finally, 2 is given for the grain yield trait. All calculations were done with a Microsoft Excel worksheet by using different selection index parameters.

Selection of superior performing genotypes by MGIDI

The MGIDI is based on the principle of rescaling of variables, factorial analysis of BLUP (Best Linear Unbiased Prediction) values, ideotype planning and MGIDI estimation. The MGIDI was estimated based on the formula given below.

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

where, F_{ij} is i^{th} genotype score for j^{th} factor *(i = 1, 2, ..., g; j = 1, 2, ..., f)*, *g* and *f* are a number of genotypes and their factors. The MGIDI were analyzed by using "metan" package version 1.18.0 (Olivoto and Nardino (2021) in R studio 4.2.1. with the 'gamem' and 'mgidi' functions.

Result and discussion

Discriminate function by all traits (uniform vs differential weightage)

The relative economic weights and their regression coefficients (b_i) for both equal weightage (W_1) and differential weight (W_2) are presented in Table 2. In the equal weightage selection index (I) highest regression coefficient (b) value was derived for flag leaf breadth (37.04) followed by hundred seed weight (30.78), whereas the grain yield it was low (1.18). As to b values obtained from differential weightage, the number of grains per panicle (1499.75) and filled grains (1349.65) had the highest values. Among 17 traits, the highest weight 2 was given to seven traits and out of these, grain yield was recorded as peak coefficient value (203.46).

Index score was derived by multiplying the coefficient values (b_i) with the mean values of each trait with respective genotypes and these genotypes were ranked based on the index score (Table 3). In the first selection index system, the highest index score was recorded with the genotype of M_7-4, so it was ranked first and followed by M_7-1 (186.20), and M_7-11 (184.84) was documented as second and third

Table 3. Selection index score and ranking of 36 rice genotypes

S. No.	Genotypes	Selection index I		Selection index II	
		Index score	Rank	Index score	Rank
1	M_7-1	186.620	2	230.603	1
2	M_7-2	159.429	9	190.221	8
3	M_7-3	152.087	11	187.829	10
4	M_7-4	191.009	1	216.945	2
5	M_7-5	123.513	15	156.733	14
6	M_7-6	181.002	5	202.105	4
7	M_7-7	150.343	12	179.790	12
8	M_7-8	181.316	4	201.110	5
9	M_7-9	162.123	8	195.379	7
10	M_7-10	174.099	6	195.670	6
11	M_7-11	184.844	3	215.156	3
12	M_7-12	154.984	10	186.554	11
13	F_5-1	110.795	21	145.027	18
14	F_5-2	69.434	29	103.231	28
15	F_5-3	79.925	26	110.149	27
16	F_5-4	99.630	24	120.943	24
17	F_5-5	93.968	25	144.156	19
18	F_5-6	44.457	32	75.381	32
19	F_5-7	22.833	34	42.711	35
20	F_5-8	13.307	35	45.583	34
21	M_4-1	117.681	19	149.106	17
22	M_4-2	169.526	7	189.918	9
23	M_4-3	115.853	20	140.896	20
24	M_4-4	102.384	23	119.149	25
25	M_4-5	120.674	17	138.261	22
26	M_4-6	78.143	27	112.397	26
27	M_4-7	22.896	33	46.820	33
28	M_4-8	132.801	13	156.146	15
29	M_4-9	68.531	30	87.603	30
30	M_4-10	128.414	14	162.256	13
31	M_4-11	119.098	18	140.078	21
32	M_4-12	2.069	36	33.154	36
33	M_4-13	106.778	22	127.143	23
34	M_4-14	57.525	31	75.942	31
35	M_4-15	72.995	28	102.499	29
36	Anna (R) 4	122.548	16	156.071	16
Genetic advance			94.349	95.886	

rank, respectively. In order to compare with 35 genotypes Anna (R) 4 ranked as 16 and the value of index score was 122.54. The genotype M_4-12 had a very low score value (2.069) and was trapped with the rank of 36. In this equal weightage selection index situation, the genetic advance was calculated as 94.34% with the respective of over 17 quantitative traits.

In the differential weightage system, the highest score value is imprisoned with M_7-1 (230.60) genotype, followed by M_7-4 (216.94) and ranked first and second, respectively. The check variety Anna (R) 4 had an index score of 156.07 and obtained the same rank 16 as in the first system of selection index. In both cases, the EMS-derived Anna (R) 4 mutants were got top ranks. In the ranking of I & II selection index, M_7-4 and M_7-1 evidenced as first and second rank alternatively and the genotype, M_4-12 imprisoned with last rank which was irradiated mutant of Anna (R) 4, since most of the traits of these two genotypes proved their distinctness from M_4-12 such as maturity dates, panicle weight, grains per panicle, filled grains and grain yield. Finally, the genetic advance also increased at a very low level from equal weightage system and was 95.88%. The differential weightage increased/changed the index score, not the genotypes' ranks, compared to uniform weightage. The correlation between the uniform and differential weightage ranks of genotypes shows a strong correlation ($R^2 = 0.914$). This indicates that generalized SI with a uniform score help to differentiate the genotype by its functional value of (b) traits.

The selection indices, based on an even and differential weightage system, revealed that there is no significant difference observed in the ranking of the genotypes. Therefore, the differential weights of the traits didn't change the ranks of the genotypes, but they did influence the index score. The non-significant ranking between selection indices I and II may be due to the inclusion of component variables of grain yield, leading to increased relative efficiency, which isn't reflected in the ranking (Rathod et al., 2013). Hazel and Lush (1942) also accepted that the inclusion of more variables increases the superiority of selection based on the index. Moreover, calculating the SH index involves the inversion of a phenotypic covariance matrix encompassing multiple traits. The existence of closely correlated traits may lead to biased index coefficients. So, the traits used in the selection index are highly correlated, and changes in weighting may not lead to substantial alterations in the rankings. To maximize grain yield, 14 selection indices were constructed using equal weights and direct effects of different attributes and correlation values give better results in the selection index (Sabouri et al. 2008). The relative efficiency and genetic advance were increased with the combination of attributes over the direct selection of a single trait performed by Hadavani et al. (2018) in Indian beans.

Selection of superior genotypes by MGIDI

The principal component analysis showed that the first five components were observed with more than one eigenvalue, accounting for 83.20% of the cumulative variance (Table 4). The main aim of rice breeding programme is to target increased yield and its primarily controlled quantitative nature leads to low heritability in nature. So, the straight selection of genotypes is not appropriate and doesn't

Table 4. MGIDI selection index - Factor analysis, selection gain

S. No	PC	Eigen values	Variance (%)	Cumulative variance (%)	Variables	Factor	h2	SG (%)
1	PC1	4.93	29.00	29.00	FG	FA1	0.81	-1.89
2	PC2	3.64	21.40	50.40	GL	FA1	0.91	3.59
3	PC3	2.45	14.40	64.80	GB	FA1	0.91	1.09
4	PC4	1.89	11.10	75.90	HSW	FA1	0.98	13.00
5	PC5	1.24	7.29	83.20	TT	FA2	0.73	5.97
6	PC6	0.87	5.10	88.30	PT	FA2	0.61	2.98
7	PC7	0.57	3.34	91.60	PH-50th day	FA3	0.96	3.65
8	PC8	0.39	2.30	94.00	PH	FA3	0.81	0.48
9	PC9	0.34	2.01	96.00	PL	FA3	0.85	5.95
10	PC10	0.19	1.13	97.10	FL	FA3	0.85	2.91
11	PC11	0.17	1.00	98.10	SPAD	FA4	0.88	-1.85
12	PC12	0.11	0.68	98.80	PW	FA4	0.30	1.67
13	PC13	0.09	0.52	99.30	NGPP	FA4	0.83	3.44
14	PC14	0.06	0.35	99.60	GYP	FA4	0.12	0.19
15	PC15	0.03	0.20	99.80	DFF	FA5	0.95	0.28
16	PC16	0.02	0.11	100	FB	FA5	0.94	4.51
17	PC17	0.01	0.05	100	DTM	FA5	0.89	0.57

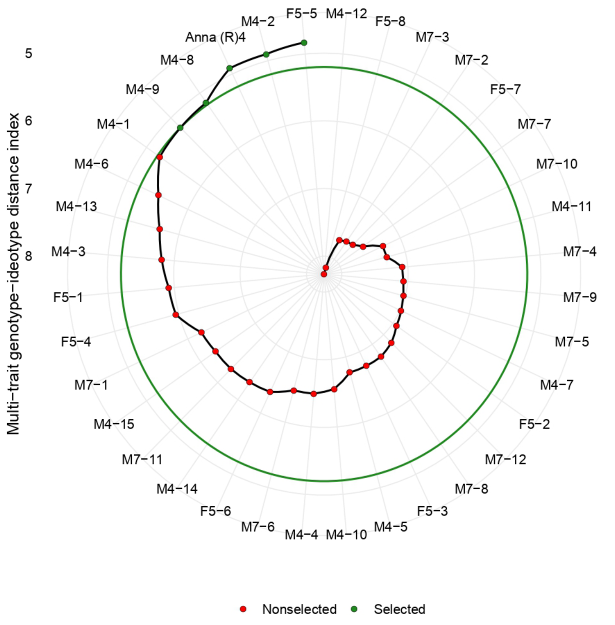

Fig. 1. MGIDI based selected and non-selected genotypes of rice

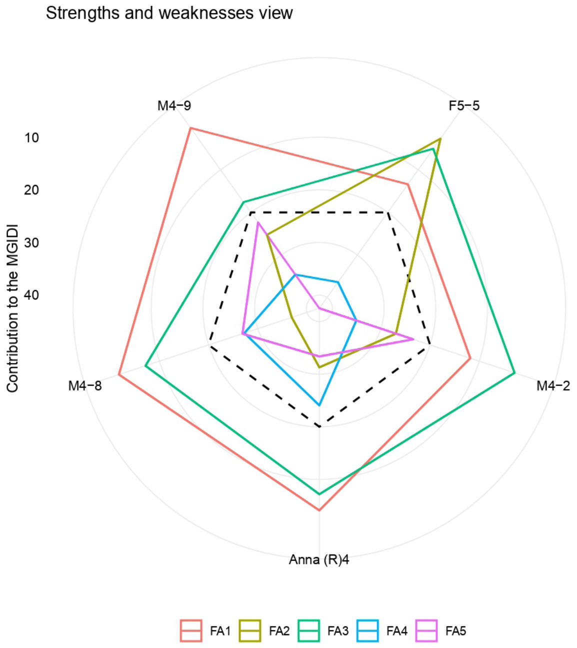

Fig. 2. Strenght and weakness view of selected genotypes

explain the genotypic variation fully. Hence, including component variables to select superior genotypes is more helpful. The MGIDI selection is based on the factorial analysis and includes the correlation of component variables for selection. So, this factorial analysis is useful for differentiating the genotypes specifically performed for the variables included in the factors (FA). The factor analysis revealed that a total of five different factors were grouped from 17 variables. The FA1 includes filled grains, grain length, grain breadth and hundred seed weight; FA2 includes total tillers and productive tillers; FA3 includes plant height at 50th day, plant height, panicle length and flag leaf length; FA4 includes SPAD value, panicle weight, number of grains per panicle and grain yield per panicle; FA5 includes days to 50% flowering, flag leaf breadth and days to maturity. The heritability percent varied from 12 (GYP) to 98 (HSW) and almost most of the variables exhibited greater heritability. Significant heritability values ($h^2 > 0.8$) were noted except TT, PT, PW and GYP, suggesting that traits with higher heritability have favorable possibilities for achieving selection gains. However, the estimation of selection gain for individual variables is not possible in the Smith and Hazel method. But, it is possible to estimate the genetic gain for individual traits by MGIDI selection index and also to know the strengths and weaknesses of individual traits for the selection of superior genotypes. In the present study, except FG and SPAD values, the selection gain exhibited positive selection gain and differed from -1.89 (FG) to 13% (HSW).

The selection intensity of 15% was engaged for the selection of superior-performing genotypes among the 36 rice cultures. The MGIDI score selected five genotypes F5-5, M4-2, Anna (R) 4, M4-8 and M4-9 (Fig. 1) as superior performing genotypes for 17 studied variables. The genotypes identified as superior through the Smith-Hazel method differed completely from those identified through the MGIDI selection. This is because MGIDI selection method specifically considers the distance between genotypes and their ideotype across all variables included in the study. Factor analysis (FA) was employed in the MGIDI index to address the correlation structure. This was facilitated by the rescaling procedure, which preserved the original correlation structure of the data, enabling the straightforward planning of an ideotype. According to Al-Ashkar et al. (2023), the genotype with the least score of MGIDI had greater performance and was selected as a superior genotype. In this study F_5-5 had least MGIDI sore, about 4.83 followed by M_4-2 with 4.90. The genotype with the minimum MGIDI value indicates a closer genetic distance between the genotype and ideotype. This distance is computed using the Euclidean distance. Therefore, the strength of the selected genotypes can be easily identified by the variables in that particular FA. In contrast, the Smith and Hazel method is based on genotypic and phenotypic variance and does not include the correlation between variables. The selection of best-performing genotypes by using MGIDI approach was also done earlier in different crops, such as strawberries (Olivoto and Nardino 2021), soybean (Maranna et al. 2021), guar (Benakanahalli et al. 2021), maize (Uddin et al. 2021), and barley (Pour-Aboughadareh et al. 2021).

The selection of genotypes primarily depends on the selection with correlated variables. The strength and weakness view of selected genotypes (Fig. 2) is useful to know the different variables which contribute for the selection. The FA line located near the center is said to be a greater contributing variable and *vice versa* (Olivota et al. 2021). According to this, variables presents in FA4 were the most contributing traits for the selection of these superior genotypes. In case of considering individually selected genotypes F_5-5 had the greatest strength of FA2 and weakness of FA5. Similarly, M_4-2 had strength of FA3 and Anna (R) 4 had FA1 and FA3, M_4-8 had FA1 and M_4-9 had FA1. This strength and weaknesses of genotypes have been highlighted earlier (Benakanahalli et al. 2021; Pour-Aboughadareh et al. 2021; Olivoto and Nardino 2021). The MGIDI method utilizes a comprehensive assessment of multiple characteristics along with an examination of strengths and weaknesses, the treatment ranking proves to be a potent tool for directing researchers toward more effective treatment recommendations. So, comparing the conventional method, MGIDI selection based on multiple traits is more effective for the identification of best-performing genotypes.

Authors' contribution

Conceptualization of research (PA); Designing of the experiments (SP, PA, SB, SM); Contribution of experimental materials (PA); Execution of field/lab experiments and data collection (SP); Analysis of data and interpretation (SP, PA); Preparation of the manuscript (SP, PA, SB, SM).

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