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Discerning ideal blackgram (*Vigna mungo*) genotypes using multi-trait genotype ideotype distance index

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ABSTRACT

Meticulous identification of ideal parental types with most of the improved traits is essential to develop superior varieties. The recently developed genotype-ideotype distance based selection index furnished an improved way in selection of ideal genotypes in plant breeding. The present experiment was conducted during rainy (*kharif*) seasons of 2021 and 2022 at research farm of Agricultural College (Acharya N. G. Ranga Agricultural University), Bapatla, Andhra Pradesh to identify potential blackgram [*Vigna mungo* (L.) Hepper] genotypes with majority of the improved traits. A total of 127 blackgram genotypes were analyzed by using Multi-trait Genotype Ideotype Distance Index (MGIDI) to select superior genotypes with improved traits. MGIDI provided selection differential and selection gain for all the traits with desired values. After varimax rotation, 10 traits were grouped under 4 factors, which cumulatively explained about 76.4% of total variance with eigen value more than 1. Out of 127 studied blackgram genotypes, MGID index identified 6 superior genotypes (GAVT 12, GAVT 7, TBG 106, VBG 13-003, GBG 12 and MBG 1046) at 5% selection intensity. Per cent contribution of factors towards the MGIDI values indicated that, the factor 3 which includes days to maturity, plant height and pod length contributed least and factor 1 which includes grain yield/plant, clusters/plant, pods/plant and seeds/pod contributed most. These selected genotypes with superior *per* se performance for multiple traits based on the MGIDI can be used as genitors in any hybridization programme to develop superior varieties in turn improving the blackgram productivity.

Keywords: Blackgram, Factor contributions, Multicollinearity, Multi-trait genotype ideotype distance index, Phenotypic selection, Selection gain

Blackgram [*Vigna mungo* (L.) Hepper] is an important short duration, self-pollinated tropical legume crop belonging to family Fabaceae, having diploid chromosome number of 2n=2x=22 with an estimated genome size of 574 Mbp (Arumuganathan and Earle 1991). It is highly nutritious with 25–26% of easily digestible and good quality protein, 60% of carbohydrates, 1.5% fat, minerals, amino acids and vitamins (Jeberson *et al*. 2018). It is also used as fodder for milch animals (Fery 2002). During 2021–2022, more than 2.77 Mt of blackgram was produced from 4.63 Mha in India with an average unit production of 599 kg/ha (Ministry of Agriculture 2021–2022). Even though, India is the largest producer of blackgram the average productivity is less due to lack of new potential/stable genotypes or varieties specific to local conditions, unavailability of suitable ideotype and lack of resistance to biotic and abiotic stresses (Chauhan *et al*. 2018). Hence to get an ideal genotype with improved production, there is a need to identify or develop superior blackgram genotypes with diverse gene complexes and genetic relationships among traits.

Effective utilization of available germplasm and identification of superior genotypes with significantly distinguishing traits as genitors for crop improvement requires systematic evaluation and characterization of germplasm. Among several basic selection methods which are employed for selecting several characters simultaneously, Smith-Hazel index (Smith 1936, Hazel 1943) is widely accepted method. The SH index requires inverting a phenotypic covariance matrix (Smith 1936), lead multicollinearity when several traits are assessed which in turn results in poorly conditioned matrices and biased index coefficients, thus, affecting the estimates of genetic gains. The Multi-trait Genotype Ideotype Distance Index (MGIDI) proposed by Olivoto and Nardino (2020) overcome the above defects of traditional selection index methods (Benakanahalli *et al*. 2021). MGIDI utilizes factor analysis, hence, the genotype scores are free from multicollinearity (Dormann *et al*. 2013) due to production of orthogonal axes among the factors. Hence, the present study was carried out

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to identify ideal genotypes with favourable genetic gains by constructing MGIDI to each genotype.

MATERIALS AND METHODS

Experimental location, layout and plant material: An experiment was conducted during rainy (*kharif*) seasons of 2021 and 2022 at the research farm of Agricultural College, (Acharya N. G. Ranga Agricultural University), Bapatla (15.54°N latitude, 80.47°E longitude and 5.49 m amsl), Andhra Pradesh. A total of 127 blackgram genotypes belonging to 14 different states of India were evaluated in randomized complete block design (RCBD) with two replications. In each replication each genotype was accommodated in two rows of 4 m length with 30 cm row-row spacing and 10 cm plant-plant spacing in each row. All the recommended cultural practices were taken up to raise a healthy crop.

Determination of quantitative traits: Data on 10 traits, viz. days to 50% flowering, plant height (cm), branches/plant, clusters/plant, pods/plant, pod length (cm), seeds/pod, test weight (g), grain yield/plant (g) and days to maturity recorded over two seasons were subjected to pooled ANOVA after validating the homogeneity of error variance through the Bartlett test (Gomez and Gomez 1984).

Statistical analysis: Statistical analysis was performed using R software version 4.3.2 (R Core Team 2023) of metan package (Olivoto and Lucio 2020). The ideal genotypes were identified as per Olivoto and Nardino (2020). Varimax rotation principle (Kaiser 1958) was used for estimation of final loadings (factor loadings/factors). The rescaled value for the studied traits was given as 100 for ideotype (I) construction. MGIDI value based on genotype-ideotype distance was constructed as (Olivoto and Nardino 2020):

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

where $\mathrm{MGIDI_i}$, MGIDI for the ith genotype; γ_{ij}, Score of ith genotype in the jth factor; γ_j, Score of ideotype in the jth factor.

Hence, the genotype with the lowest MGIDI nearer to the constructed ideotype, indicating that the genotype in question is having desired values for majority of traits.

The proportion of the MGIDI of the ith genotype explained by the jth factor (ω_{ij}) is used to show the strengths and weaknesses of genotypes/treatments and is computed as:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f} \sqrt{D_{ij}^2}}$$

where D_{ij}, Distance between the ith genotype and the ideotype for the jth factor. Low contributions of a factor indicate that the traits within such a factor are close to the ideotype.

Heritability in broad sense was formulated for all the traits as described by Hanson *et al*. (1956). Selection differential is the average superiority of the selected genotypes over the original population from which the genotypes were selected. It was computed by considering the selection intensity at 5%.

RESULTS AND DISCUSSION

Mean performance and estimates of variability: The data from 127 blackgram genotypes recorded on 10 quantitative traits were analyzed to estimate the variability. Univariate analysis of variance explained that all the genotypes were significantly different for all traits. Out of the 10 traits 9 recorded higher genotypic variance than the residual variance except for days to 50% flowering. Maximum variability was recorded in plant height, pods/plant and days to maturity. While test weight and pod length had least variation. These results indicate that there is enough variability for majority of traits with scope for efficient selection. Similar technique was employed for estimating variability in elephant grass (Rocha *et al*. 2018) and in strawberry (Barth *et al*. 2020) for various traits.

Selection differential, heritability and expected selection gain: Information on estimates of heritability, genetic associations, expected selection gain are essential in developing a breeding strategy (Barth *et al*. 2020). The effect of selection can be predicted by the heritability estimates in conjunction with that of expected genetic gains. MGIDI value provided selection differential and selection gain for all the traits with desired values (Table 1). Percentage of selection differential for traits with higher desired values ranged from 1.33% (branches/plant) to 145% (grain yield/plant) and for traits with desired lower values ranged from -0.62% (days to 50% flowering) to -1.88% (days to maturity). All the higher desired values are positive and lower desired values are negative indicating 100% success rate for the traits considered. There is greater scope for successful selection to realize higher actual genetic gains in the desirable direction. Similar selection differentials were obtained by Olivoto *et al*. (2021) in strawberry with 91% success rate where 20 out of 22 traits were in desired direction. In oats, desired selection differential varied from

Table 1 Selection differential, heritability and selection gain for 10 traits in blackgram

Trait/Variable	Overall genotypes mean	Selected genotypes mean	SD (%)	h^2 (%)	SG (%)
Days to 50% flowering	44.10	43.80	-0.62	40.01	-0.25
Days to maturity	82.80	81.20	-1.88	69.20	-1.30
Plant height (cm)	52.10	61.20	17.60	96.13	16.80
Branches/plant	3.24	3.29	1.33	82.21	1.08
Clusters/plant	8.08	16.90	109.00	91.31	99.20
Pods/plant	25.90	46.80	80.30	96.25	77.10
Pod length (cm)	5.03	5.21	3.54	80.23	2.82
Seeds/pod	6.24	7.40	18.60	93.12	17.30
Test weight (g)	4.34	4.42	1.79	84.24	1.51
Grain yield/plant (g)	6.16	15.10	145.00	96.27	139.00

SD, Selection differential; h^2, Heritability in broad sense; SG, Selection grain percentage.

9–11 out of 13 traits included under selection at two different locations separately (Klein *et al*. 2023).

All the traits except days to 50% flowering recorded high heritability in broad sense (>60%). The traits, clusters/plant, pods/plant and grain yield/plant had higher estimates of heritability and expected selection gain indicating the significant contribution of additive gene effects whereas, plant height and seeds/pod had high heritability estimates with moderate expected selection gain inferring the involvement of both non-additive and additive gene actions. However, remaining traits had high heritability with low genetic advance suggesting the presence of non-additive gene action. This non-additive gene effects may be dominance or epistasis. This information on possible gene actions is helpful in choosing suitable breeding strategies for improving the concerned traits. Similar complex genetic inheritances were indicated by Barth *et al*. (2020) for the traits related to yield in strawberry.

Linear relationships: Significantly positive associations with grain yield/plant in desirable directions were exhibited by clusters/plant (0.75***), pods/plant (0.59***), seeds/pod (0.59***), plant height (0.33***) and pod length (0.29***) (Fig. 1). The traits which exhibited significant positive associations with the dependent variable are to be considered simultaneously for improving the blackgram genotypes for yield. However, these yield traits had non-significant correlations with the earliness which hinders the selection process for potential genotypes with early duration. Similar robust correlations for yield-related characteristics were reported by Barth *et al*. (2022).

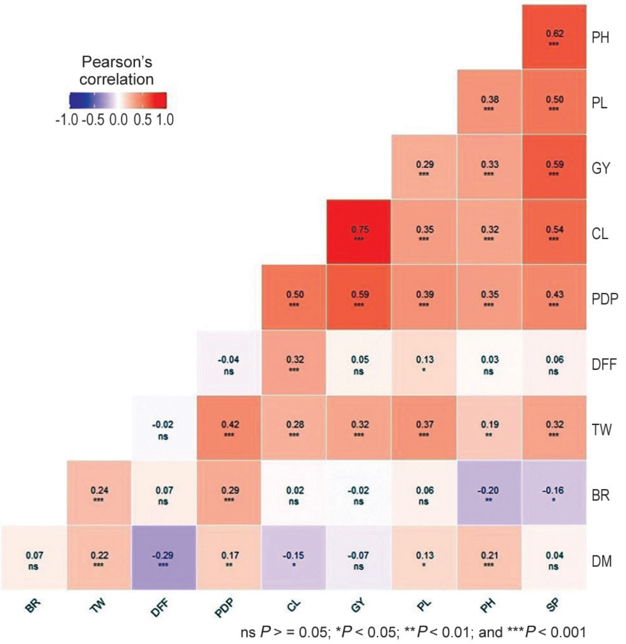

Fig. 1 Pearson's correlations for all the traits under study. DFF, Days to 50% flowering; DM, Days to maturity; PH, Plant height; BR, Branches/plant; CL, Custers/plant; PDP, Pods/plant; PL, Pod length; SP, Seeds/pod; TW, Test weight; GY, Grain yield/plant.

Factor loadings (FA) and factor delineation: Among the 10 principal components which were obtained from genetic correlation matrix, 4 components showed eigen values greater than one (Table 2) with cumulative variance of 76.40%. After varimax rotation the communality ranged from 0.589 (test weight) to 0.965 (days to 50% flowering) with an average communality of 0.764. The first factor was found to have high genetic correlations for clusters/plant, pods/plant, seeds/pod and grain yield/plant which indicates that major yield contributing factors in the present population were grouped in this factor. Branches/plant and test weight were grouped into second factor. For third factor, high correlations were obtained for days to maturity, plant height and pod length whereas, days to 50% flowering was accounted for fourth factor (Table 2). Similar experiments on wheat by Olivoto and Nordino (2020) using MGIDI were reduced 14 original traits into 5 final latent variables (factors) that explained ~87% of the original data. Similarly,

Table 2 Eigen values, factor loadings of different factors and communalities after varimax rotation

Trait/Variable	Factor 1	Factor 2	Factor 3	Factor 4	Communality	Uniqueness
Days to 50% flowering	0.07	0.03	-0.01	**0.98**	0.97	0.03
Days to maturity	-0.19	0.14	**-0.79**	-0.09	0.69	0.31
Plant height	-0.47	0.43	**0.56**	-0.08	0.73	0.27
Branches/plant	0.01	**-0.90**	0.06	-0.06	0.81	0.19
Clusters/plant	**-0.87**	-0.02	-0.03	-0.25	0.83	0.17
Pods/plant	**-0.71**	-0.40	0.28	0.13	0.75	0.25
Pod length	-0.47	-0.05	**0.60**	-0.17	0.61	0.39
Seeds/pod	**-0.76**	0.32	0.36	-0.07	0.81	0.19
Test weight	-0.44	**-0.45**	0.44	0.01	0.59	0.41
Grain yield/ plant	**-0.92**	-0.02	-0.07	0.03	0.85	0.15
Eigen values	3.85	1.53	1.23	1.02		
Variance (%)	38.50	15.30	12.40	10.20		
Cumulative variance (%)	38.50	53.80	66.20	76.40		

Values in bold indicate that the trait in that row is grouped into the factor in the corresponding column.

Olivoto *et al*. (2021) obtained 5 significant factors with eigen value more than one and accounted for 90.48% of the total variation among the studied traits. Further, they observed that various traits were grouped into different factors based on their correlations. Sixteen traits were reduced to 6 factors with nearly 73% variance explained in rice mutants (Mamun *et al*. 2022). This dimensional reduction makes it simpler to the interpretation and decision making by breeders. Because factor analysis produces orthogonal axes among final factors, it is possible to obtain genotype's scores free from multicollinearity.

Multi-trait genotype ideotype distance index: Farmers prefer productive genotypes having short duration (early duration for days to 50% flowering and days to maturity) with higher *per se* for plant height, branches/plant, clusters/plant, pods/plant, pod length, seeds/pod, test weight and grain yield/plant. Hence, in rescaling of the data set during construction of MGIDI, minimum and maximum values differed with respect to their importance in obtaining potential ideal genotypes. MGIDI for each genotype was obtained based on the genotype-ideotype distance by the utilization of the scores from factor analysis. MGIDI plot (Fig. 2) easily interprets the selection of genotypes. The lower the MGIDI value better the performance of genotype for all the traits which is nearer to the ideotype, hence such genotypes are selected. Simultaneous improvement of two or more characters influences the selection intensity. Based on the selection intensity the top most genotypes superior for all the traits will be selected. By applying 5% selection intensity the top 6 genotypes selected in order were

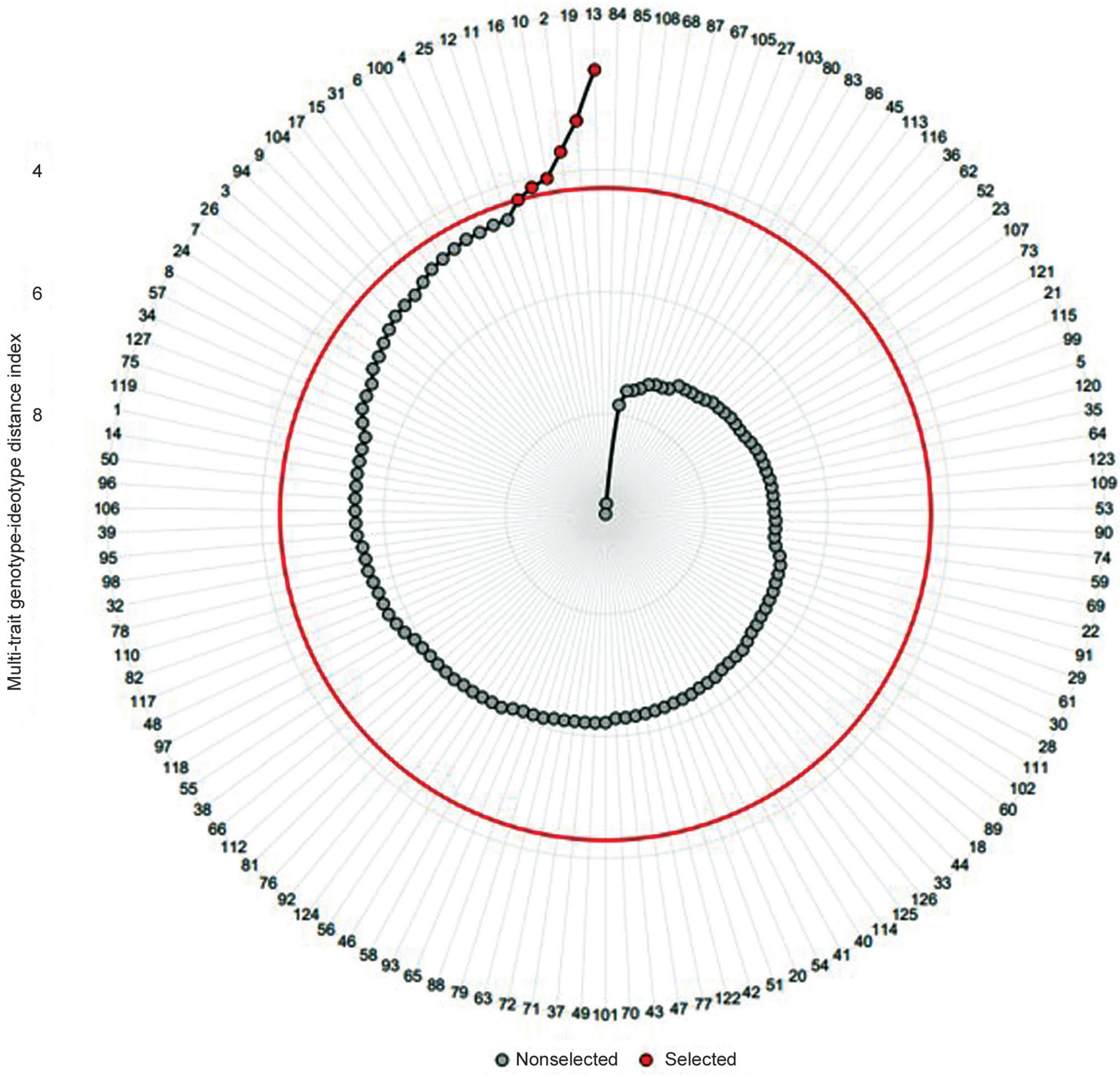

Fig. 2 Genotype ranking based on the MGIDI.
Selected genotypes at 5% selection intensity were represented in red colour dots.

Table 3 Performance of the selected 6 genotypes

Selected genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches/ plant	Clusters/ plant	Pods/ plant	Pod length (cm)	Seeds/ pod	Test weight (g)	Grain yield/ plant (g)
GAVT 12	40.50	72.00	47.90	3.40	18.30	56.90	5.40	7.90	4.96	15.41
GAVT 7	45.50	81.00	67.65	3.47	23.40	57.87	5.02	6.40	4.73	14.27
TBG 106	40.00	89.00	38.50	3.40	14.75	43.60	5.38	8.00	4.37	16.71
VBG 13-003	42.00	76.50	73.90	3.00	15.90	37.10	5.28	8.00	4.45	14.21
GBG 12	47.50	87.50	73.30	3.40	18.60	47.90	5.10	8.10	4.10	18.03
MBG 1046	45.00	77.00	68.73	3.10	15.30	42.40	5.37	6.50	4.01	14.52

GAVT 12, GAVT 7, TBG 106, VBG 13-003, GBG 12 and MBG 1046. The *per se* performance of these genotypes is presented in Table 3. Substantial selection differential was observed for the selected genotypes with respect to all the traits. The magnitude of the selection differential varied as the function of measured trait. Estimates of heritability were greater than 80% for majority of the studied traits, suggesting the success in selection of genotypes. All the traits also had desired selection gains. It is also further inferred that the selected genotypes encountered higher favourable alleles for various traits which were considered during the present study. The use of these genotypes in further breeding programmes would be beneficial in improvement of blackgram production. Similar approach was used by Barth *et al*. (2020) to select potential hybrids for fresh consumption and processing in strawberry; and by Olivoto *et al*. (2021) to identify the best treatment in strawberry. Mamun *et al*. (2022) applied 10% selection intensity to select top 10 mutants out of total 100 rice mutants considered in their study. Jorben *et al*. (2022) identified G3 as a stable chickpea line for multiple traits using MTSI.

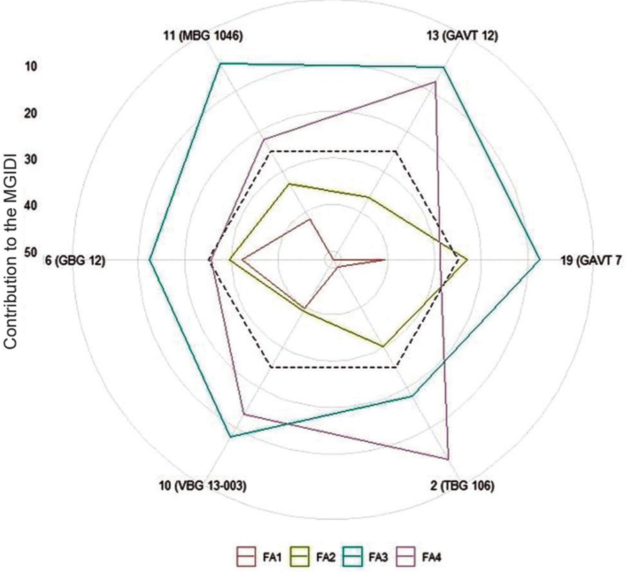

Fig. 3 Strengths and weaknesses view of selected genotypes. FA1, Factor 1; FA2, Factor 2; FA3, Factor 3; FA4, Factor 4.

Strengths and weaknesses of selected genotypes: Proportion of each of the four factor loadings (FAs) towards the MGIDI value of selected 6 genotypes (Fig. 3). In Fig. 3 dashed line shows the theoretical value of all the factors when contributed equally and factors which are placed outside the dashed line are positive strengths of the respective genotypes. The contributing factors towards the higher value of MGIDI of a genotype were closer to the center and the traits grouped under such factors were contributing less towards the respective MGIDI value of the genotype whereas, the factors that are contributing less towards the MGIDI of a genotype were plotted at the edge of the plot and the traits categorized under those factors had higher contribution and were closer to the ideotype trait value. Interestingly it was observed among the selected genotypes, that the FA1 which considered for grain yield traits contributed most, while FA3 consisting of plant stature and duration contributed least to the MGIDI. The traits which had higher contribution towards factor 3 (indicated as blue line in Fig. 3), viz. days to maturity, plant height and pod length resulted in lesser MGIDI and are strength to all the selected six genotypes. However, MBG 1046 and GAVT 12 were stronger in terms of early duration and short plant height, respectively. Similarly, factor 4 (indicated as violet line in Fig. 3) had higher performance TBG 106, GAVT 12 indicated by their early days 50% flowering. In case of FA2 which is strength for the genotype, GAVT 7 which had good performance regarding branches/plant and test weight compared to the remaining genotypes. Among all selected six genotypes, GBG 12 which had highest grain yield and high pods/plant appears to be stronger for the first factor. From this it easier to conclude that, GAVT 12 was stronger for three out of four factors. It is a high yielding variety with short stature and early flowering. Both factor 3 and factor 4 were strengths regarding the genotype GAVT 12 suggesting that this genotype had good performance regarding earliness, height of the plant and pod length. Among the four factors, factor 3 contributed maximum towards all the selected genotypes. A similar study was taken up by Benakanahalli *et al*. (2021) in guar and found productive crude protein, fibre and gum as strengths of selected genotypes. Similarly, Olivoto *et al*. (2021) reported the strengths and weaknesses of the top two treatments for various traits considered in their study. Pour-Aboughadaresh and Paczai (2021) also plotted strength and weakness plots to identify strengths of the two factors for the selected 15 genotypes.

The selection index formulated by Multi-trait Genotype Ideotype Index (MGIDI) gives one of the easy ways to identify potential cultivars in blackgram breeding programme. This technique found 6 genotypes, viz. GAVT 12, GAVT 7, TBG 106, VBG 13-003, GBG 12 and MBG 1046 as ideal genotypes among the 127 studied genotypes at 5% selection pressure with positive and negative selection differentials for the traits based on their increased or decreased magnitudes, respectively. Further, the identified genotypes can be used as parents in hybridization programmes which may result in good hybrid combinations to produce transgressive segregants in their respective F_2 and subsequent segregating generations.

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