

Using the multi-trait genotype ideotype distance index to identify optimal blackgram (*Vigna mungo*) genotypes

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ABSTRACT

To create superior varieties, the ideal parental types with the majority of the improved traits must be carefully identified. An enhanced method for choosing ideal genotypes in plant breeding was provided by the recently created genotype-ideotype distance-based selection index. In order to identify potential blackgram [*Vigna mungo* (L.) Hepper] genotypes with the majority of the improved traits, the current experiment was carried out at the research farm of Agricultural College (Acharya N. G. Ranga Agricultural University), Bapatla, Andhra Pradesh, during the rainy (kharif) seasons of 2021 and 2022. The Multi-trait Genotype Ideotype Distance Index (MGIDI) was used to analyze 127 blackgram genotypes in order to identify superior genotypes with enhanced traits. For every trait with desired values, MGIDI offered selection gain and selection differential. Ten characteristics were grouped under four factors following varimax rotation, which together accounted for roughly 76.4% of the total variance with eigen values greater than 1. Six superior genotypes (GAVT 12, GAVT 7, TBG 106, VBG 13-003, GBG 12, and MBG 1046) were found by the MGIDI index at 5% selection intensity out of the 127 blackgram genotypes that were examined. Factor 1, which includes grain yield/plant, clusters/plant, pods/plant, and seeds/pod, contributed the most to the MGIDI values, while factor 3, which includes days to maturity, plant height, and pod length, contributed the least. In any hybridization program, these chosen genotypes with superior per se performance for several traits based on the MGIDI can be used as genitors to create superior varieties, which will increase the productivity of blackgram.

Keywords: selection gain, phenotypic selection, multicollinearity, multi-trait genotype ideotype distance index, Blackgram, and factor contributions

Introduction

With a diploid chromosome number of $2n=2x=22$ and an estimated genome size of 574 Mbp, blackgram [*Vigna mungo* (L.) Hepper] is a significant short-duration, self-pollinating tropical legume crop that belongs to the Fabaceae family (Arumuganathan and Earle 1991). With 25–26% easily digested, high-quality protein, 60% carbs, 1.5% fat, minerals, amino acids, and vitamins, it is extremely nutritious (Jeberson et al. 2018). Additionally, it is fed to milch animals (Fery 2002). With an average unit production of 599 kg/ha, India produced more than 2.77 Mt of blackgram from 4.63 Mha in 2021–2022 (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

1Agricultural College (Acharya N. G. Ranga Agricultural University), Bapatla, Andhra Pradesh; 2Agricultural Research Station (Acharya N. G. Ranga Agricultural University), Vizianagaram, Andhra Pradesh. *Corresponding author email: d.ratnababu@angrau.ac.in 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

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

METHODS AND MATERIALS

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):

OUTCOMES AND TALK

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

MGIDI $\square \square \square f(\square 0.5 ij \square \square j)^2 \square 91\%$ success rate where 20 out of 22 traits were in desired direction. The intended selection difference in oats ranged from

where γ_{ij} is the score of the i th genotype in the j th factor, γ_j is the score of the ideotype in the j th factor, and MGIDI $_i$ is the MGIDI for the i th genotype.

As a result, the genotype with the lowest MGIDI is closer to the created ideotype, suggesting that the genotype in issue has the necessary values for the majority of attributes. To illustrate the advantages and disadvantages of genotypes and treatments, the percentage of the MGIDI of the i th genotype explained by the j th factor (ω_{ij}) is

calculated as follows:

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

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

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

where D_{ij} is the difference between the ideotype for the j th factor and the i th genotype. A factor's low contributions suggest that its characteristics are similar to the ideotype.

Hanson et al. (1956) developed a wide definition of heritability for every attribute. The average superiority of the chosen genotypes over the initial population from which they were drawn is known as the selection differential. It was calculated using a 5% selection intensity.

SD stands for selection difference; h^2 for wide heritability; and SG for selection grain percentage.

9–11 of the 13 features that were subject to selection at two distinct places independently (Klein et al. 2023).

With the exception of days to 50% blooming, every attribute had strong heritability (>60%). While plant height and seeds/pod had high heritability estimates with moderate expected selection gain suggesting the involvement of both non-additive and additive gene actions, 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. The other qualities, however, showed minimal genetic advancement and high heritability, indicating the existence of non-additive gene activity. These non-additive gene effects might represent epistasis or dominance. The selection of appropriate breeding techniques for enhancing the relevant characteristics is aided by this knowledge of potential gene activities. Barth et al. (2020) found similar complicated genetic inheritances for strawberry yield-related variables.

Linear relationships: Clusters/plant (0.75***), pods/plant (0.59***), seeds/pod (0.59***), plant height (0.33***), and pod length (0.29***) showed significantly positive connections with grain yield/plant in favorable directions (Fig. 1). In order to improve the blackgram genotypes for yield, the qualities that showed strong positive relationships with the dependent variable should be taken into consideration concurrently. The selection method for possible genotypes with early duration is hampered by the non-significant correlations between these yield variables and earliness. Barth et al. (2022) observed similar strong associations for yield-related parameters.

Factor delineation and factor loadings (FA): Four of the ten main components derived from the genetic correlation matrix had eigen values larger than one (Table 2), with a total variance of 76.40%. Following varimax rotation, the average communalities were 0.764, with a range of 0.589 (test weight) to 0.965 (days to 50% blooming). The first component

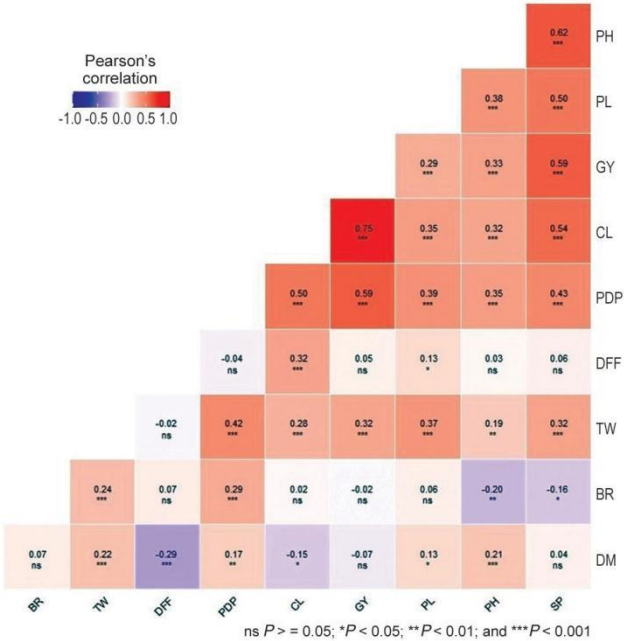


Fig. 1 Pearson's correlations for all the traits under study.
DFF stands for Days to 50% flowering; DM for Days to maturity; PH for Plant height; BR for Branches; CL for Clusters; PDP for Pods; PL for Pod length; SP for Seeds; TW for Test weight; and GY for Grain yield/plant.

was shown to have substantial genetic correlations for clusters/plant, pods/plant, seeds/pod, and grain yield/plant, suggesting that this factor aggregated the main yield-contributing components in the current population. The second aspect included test weight and branches/plant. Days to maturity, plant height, and pod length showed strong relationships for the third element, whereas days to 50% blooming accounted for the fourth factor (Table 2). In comparable wheat trials, Olivoto and Nordino (2020) used MGIDI to reduce 14 original features into 5 final latent variables (factors) that explained around 87% of the original data. Likewise, 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) identified five significant variables that accounted for 90.48% of the overall variance among the characteristics under study and had eigen values greater than one. They also noticed that, according to their connections, different features were categorized into distinct variables. In rice mutants, six parameters accounted for roughly 73% of the variation in sixteen characteristics (Mamun et al. 2022). Breeders can more easily perceive and make decisions because to this dimensional reduction. It is feasible to acquire genotype scores free from multicollinearity since factor analysis generates orthogonal axis among final factors.

Multi-trait genotype ideotype distance index: Farmers favor productive genotypes with shorter duration (early duration for days to maturity and days to 50% flowering) and higher per se for plant height, branches/plant, clusters/plant, pods/plant, pod length, seeds/pod, test weight, and grain yield/plant. Therefore, minimum and maximum values varied in terms of their significance in determining possible ideal genotypes throughout the rescaling of the data set during the building of MGIDI. Using the results from factor analysis, MGIDI for each genotype was determined based on the genotype-ideotype distance. The MGIDI map (Fig. 2) makes it simple to understand the genotype selection. These genotypes are chosen because the lower the MGIDI score, the better the genotype performs for all the characteristics that are closer to the ideotype. The selection intensity is influenced when two or more traits improve simultaneously. The best genotypes for each attribute will be chosen based on the degree of selection. The top six genotypes chosen with a 5% selection intensity were

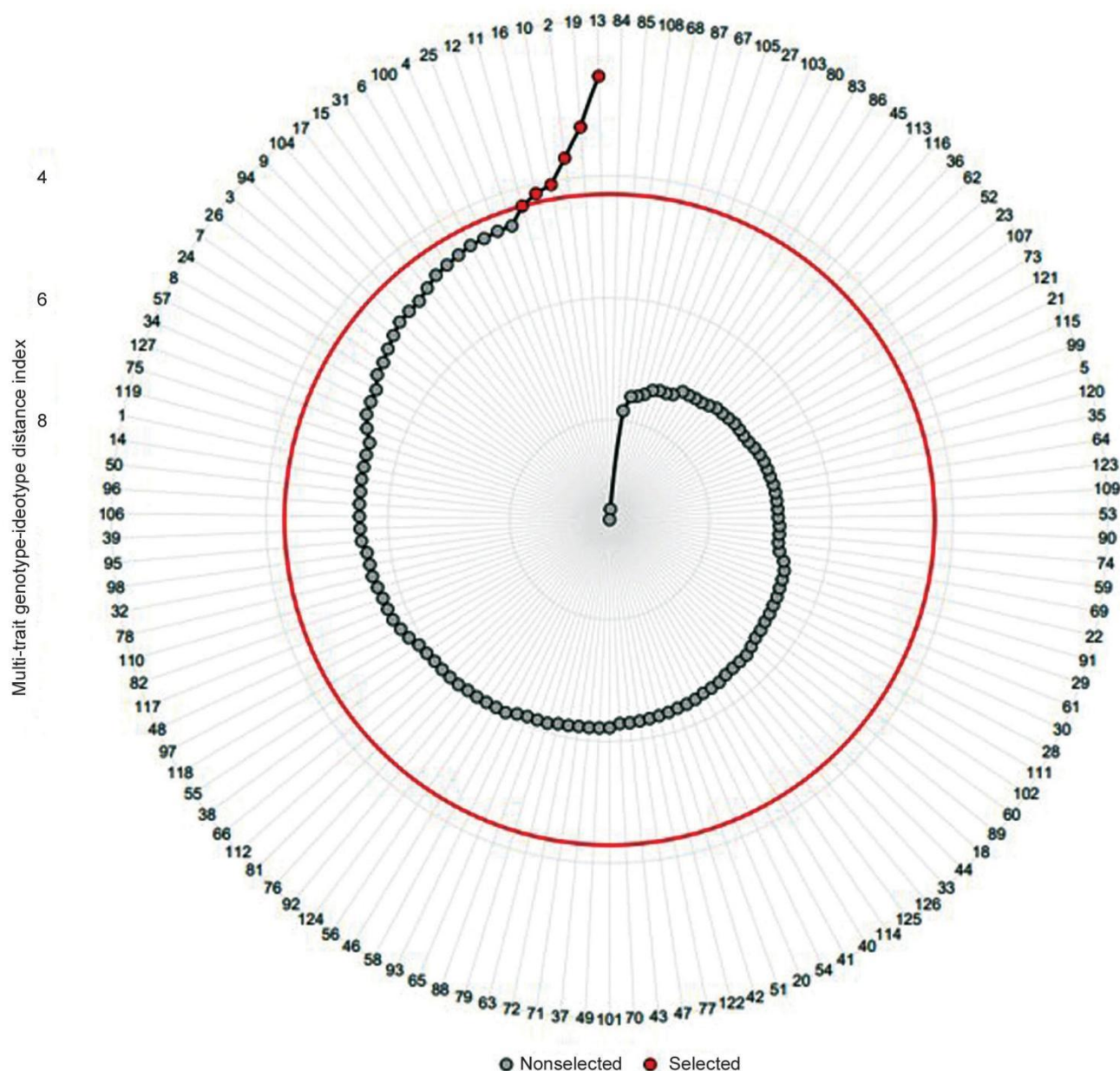


Fig. 2 Genotype ranking based on the MGIDI.
Selected genotypes at 5% selection intensity were represented in red colour dots.

Table 3 Performance of the selected 6 genotypes

Selected genotypes	Days 50% flowering	toDays maturity	toPlant 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

GBG 12, GAVT 12, GAVT 7, TBG 106, VBG 13-003, and MBG 1046. Table 3 displays these genotypes' overall performance. For all the characteristics, a significant selection difference was found for the chosen genotypes. Depending on the assessed attribute, the selection differential's size changed. For most of the variables under study, estimates of heritability were more than 80%, indicating that genotype selection was successful. Additionally, each attribute had the intended selection gains. Additionally, it is implied that the genotypes that were chosen had more advantageous alleles for the several attributes that were taken into account in this investigation. Blackgram output might be improved by using these genotypes in future breeding initiatives. Similar methods were used by Olivoto et al. (2021) to determine the optimal strawberry treatment and by Barth et al. (2020) to choose possible hybrids for fresh consumption and processing. Mamun et al. (2022) used 10% selection intensity to choose the best 10 mutants from the 100 rice mutants they looked at. Using MTSI, Jorben et al. (2022) found that G3 is a stable chickpea line for many characteristics.

Advantages and disadvantages of certain genotypes: percentage of each of the four factor loadings (FAs) in relation to the chosen six genotypes' MGIDI value (Fig. 3). The dashed line in Figure 3 represents the theoretical value of each factor when supplied equally; factors beyond the dashed line indicate positive strengths of the corresponding genotypes. The factors that contributed to a genotype's higher MGIDI value were closer to the center, and the traits grouped under those factors contributed less to the genotype's corresponding MGIDI value. In contrast, the factors that contributed less to a genotype's MGIDI were plotted at the plot's edge, and the traits grouped under those factors contributed more and were closer to the ideotype trait value. It's interesting to note that among the chosen genotypes, FA1, which took into account grain yield attributes, contributed the most to the MGIDI, while FA3, which took into account plant size and lifespan, contributed the least. Days to maturity, plant height, and pod length are the features that contributed more to factor 3 (shown as a blue line in Fig. 3) and produced lower MGIDI for all six genotypes that were chosen. But when it came to early duration and short plant, MBG 1046 and GAVT 12 were superior.

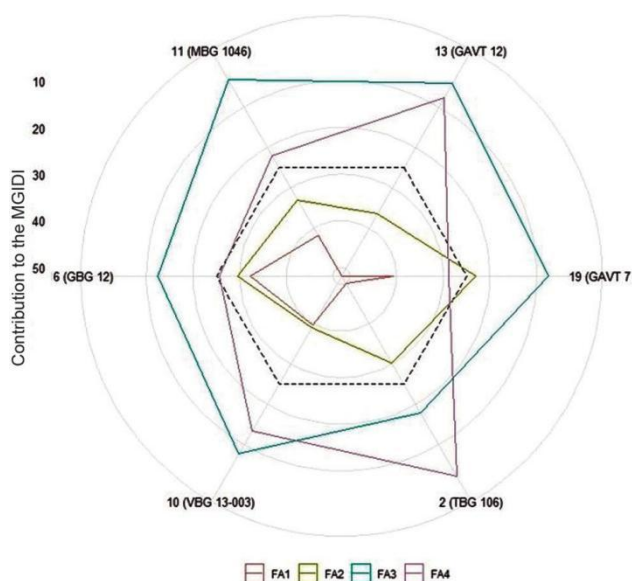


Fig. 3 Strengths and weaknesses view of selected genotypes.
FA1, Factor 1; FA2, Factor 2; FA3, Factor 3; FA4, Factor 4.

height, correspondingly. Similar to this, factor 4 (shown as the violet line in Fig. 3) performed better, as seen by TBG 106 and GAVT 12's early-day 50% blooming. In contrast to the other genotypes, GAVT 7 performed well in terms of branches/plant and test weight in the case of FA2, which is the genotype's strength. GBG 12, which had the best grain production and the most pods per plant out of the six genotypes that were chosen, seems to be stronger for the first criteria. This makes it simpler to determine that GAVT 12 was superior for three of the four variables. It is a short-statured, early-flowering cultivar with a high yield. Regarding the genotype GAVT 12, factors 3 and 4 were both strong, indicating that this genotype performed well in terms of earliness, plant height, and pod length. Factor 3 had the most contribution to all of the chosen genotypes out of the four factors. Benakanahalli et al. (2021) conducted a similar investigation in guar and discovered that some genotypes were strong in crude protein, fiber, and gum. In a similar vein, Olivoto et al. (2021) detailed the advantages and disadvantages of the top two therapies for a variety of characteristics taken into account in their research. In order to determine the strengths of the two variables for the chosen 15 genotypes, Pour-Aboughadaresh and Paczai (2021) also created strength and weakness plots.

One of the simplest methods for identifying possible cultivars in a blackgram breeding program is to use the Multi-trait Genotype Ideotype Index (MGIDI) selection index. Among the 127 genotypes examined at 5% selection pressure, this method identified six genotypes—GAVT 12, GAVT 7, TBG 106, VBG 13-003, GBG 12, and MBG 1046—as ideal genotypes with positive and negative selection differentials for the traits based on their increased or decreased magnitudes, respectively. Additionally, the genotypes that have been found may be employed as parents in hybridization programs, which might create favorable hybrid combinations that result in transgressive segregants in their respective F₂ and following segregating generations.

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