



Multi Trait Selection of Backgram Genotypes using Multi-Trait Genotype Ideotype Distance Index (MGIDI)

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ABSTRACT

The growing demand for superior genotypes has led the black gram breeders to seek auxiliary techniques on multivariate selection to obtain ideal cultivars with improved traits. The Multi trait Genotype Ideotype Distance Index (MGIDI) provides a unique, robust and easy to handle selection process and also identifies the strengths and weaknesses of the genotypes. The present experiment was carried out with 50 black gram genotypes at Agricultural College Farm, Bapatla during two *khari* seasons of 2021 and 2022 for the genetic selection of superior black gram genotypes using Multi trait Genotype Ideotype Distance Index. It provided desired values of selection differential and expected selection gain for all the traits except for plant height, indicating the potential to select superior genotypes. A total of ten traits were grouped under two factors, cumulatively explained 57.2% of total variance with a significant eigen value of more than one. The MGIDI index identified five genotypes *viz.*, LBG 884, TBG 129, TBG 141, SUG 11-37 and LBG 904 at 10% selection intensity. Among the two factors, factor 2 contributed least towards the MGIDI value of majority of the selected genotypes, while factor 1 is the higher contributor. 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.

Key Words: Factor contributions, Linear relationships, Multitrait Genotype Ideotype Distance Index, Selection gain and Transgressive Segregants.

Blackgram also known as urdbean, black matpe bean and mash is an important short duration tropical legume crop. It is a self-pollinated crop belongs to *Fabaceae* family and having diploid chromosome number of $2n=2x=22$ with an estimated genome size of 574 Mbp (Arumuganatha and Earle, 1991). This crop can be grown under different agro-climatic conditions and adapts well to different cropping systems and also grown all over the world. It is mainly cultivated in Asian countries including Pakistan, Myanmar and parts of Southern Asia. Because of its extensive cultivation throughout India it occupies a unique position in Indian subcontinent. In Andhra Pradesh it has special significance as it fits well in rice-pulse cropping system. During 2021-22, more than 2.77 million tones of black gram was produced from 4.63 million hectares in India with an average unit production of 599 kg/ha (Ministry of Agriculture, 2021-22). Even though, India is the largest producer of black gram the average productivity is less due to unavailability of suitable ideotype, lack of resistance

to biotic and abiotic stresses, lack of genetic variability and lack of new potential/stable genotypes or varieties specific to local conditions (Chauhan *et al.*, 2018). Hence there is a need to explore ideal black gram genotypes with diverse gene complexes to improve the production.

Identification of superior genotypes for any breeding programme based on the economic value of a plant (generally grain yield, which is determined by several yield related characters) is not sufficient. Most of the yield related traits are correlated because genes influencing these characters are located on the same chromosome. Hence due consideration is to be given for multiple traits to exploit correlated response of characters during selection of desired genotypes. Therefore, an efficient selection procedure which consider all the component correlated traits to obtain better genotypes with improved economic value is required. The rapid improvement in the economic value is expected from simultaneous selection applied to all the characters, which will

determine the economic value of a plant. It is possible by constructing a score or index by combining all the component characters and selection applied based on that index may result in superior genotype with improved traits. For this a widely used phenotypic selection index is Smith-Hazel index (SH index) proposed by Smith (1936) and Hazel (1943). Because of the inversion of phenotypic covariance matrix and presence of multicollinearity in SH index results in undesirable estimates of genetic gains.

To overcome the problem of multicollinearity, Olivoto and Nardino (2020) proposed a novel selection index i.e., Multi trait Genotype Ideotype Distance Index (MGIDI) for selecting genotypes based on the information of multiple traits, which overcome the defects of traditional selection index methods (Benakanahalli, 2021). MGIDI utilizes factor analysis and genotype scores free from multicollinearity (Dormann *et al.*, 2013) obtained due to production of orthogonal axes among the factors and provides high success rate in selecting traits with more selection gains (Olivoto and Nardino, 2020). Hence, the present study was carried out to identify genotypes with improved economic value and with favorable genetic gains using MGIDI.

MATERIAL AND METHODS

Experimental location

The experiment was performed at the experimental farm of Agricultural College Farm, Bapatla during two *kharif* seasons of 2021 and 2022 which resides at 15.54°N latitude, 80.47° E longitude and 5.49 m altitude.

Plant material and Experimental layout

Fifty black gram genotypes were evaluated in Randomized Complete Block Design (RCBD) in three replications. In each replication each genotype was accommodated in two rows of four meter length with 30 cm row-row spacing and 10 cm plant-plant spacing in each row. All the recommended cultural practices were taken up in raising a healthy crop.

Measurement/Determination of quantitative traits

Throughout the crop cycle and after harvesting ten traits were recorded. The traits *viz.*, plant height (cm), branches/plant, clusters/plant, pods/plant were recorded at physiological maturation stage on five

randomly selected plants per each genotype. Post harvesting data was obtained for traits *viz.*, pod length (cm), seeds/pod, test weight (g) and grain yield/plant (g). Days to 50% flowering and days to maturity were recorded on plot basis. The data 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

Multi-trait Genotype Ideotype Index (MGIDI)

MGIDI index (Olivoto and Nardino, 2020) was computed in R software version 4.3.2 (R Core Team 2023) by using *metan* package (Olivoto and Lucio, 2020) to select ideal genotypes. 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):

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

Where,

MGIDI_i is the multi-trait genotype-ideotype distance index for the i^{th} genotype; γ_{ij} is the score of the i^{th} genotype in the j^{th} factor ($i = 1, 2, \dots, g; j = 1, 2, \dots, f$), g and f are the number of genotypes and factors, respectively; and γ_j is the j^{th} score of the ideotype. The genotype with the lowest MGIDI is then closer to the ideotype and therefore have desired values for all the p traits.

Computation of strengths and weaknesses of genotypes

The proportion of the MGIDI index of the i^{th} genotype explained by the j^{th} factor (ω_{ij}) is used to show the strengths and weaknesses of genotypes and is computed as:

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

Estimation of heritability, Selection differential and Expected Selection gain

Heritability in broad sense was estimated for all the traits as the ratio of genotypic variance to the total phenotypic variance 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 is computed by considering the selection intensity at 10%. So that, out of the 50 genotypes evaluated 5 genotypes with the lowest MGIDI index were selected. Expected genetic advance was calculated based on the formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Estimates of variability and Linear relationships

The data recorded on ten quantitative traits was subjected to estimate variability. The results of univariate analysis of variance explained that all the genotypes were significantly different for all traits. Genotypic variance was higher than the residual variance for all the traits (Figure 1). The range of variation for all the traits was presented as box plots in figure 2. Plant height, pods/plant and days to maturity recorded maximum variability. While test weight and panicle length recorded least variation among the studied genotypes. The traits viz., pods/plant (0.72***), clusters/plant (0.66***), test weight (0.53***), seeds/pod (0.52***), pod length (0.46***) and branches/plant (0.43***) associated significant positively with grain yield (Figure 3). Hence these traits can be considered simultaneously for improving the yield in black gram.

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). MGIDI index provided desired selection differential (SD) and selection gain (SG) for 9 traits out of 10 studied traits with a success rate of 90% in selection of traits with desired values (Table 1). Plant

height recorded undesired selection differential (-2.09) and selection gain (-1.98). SD percentage for traits with higher values were desired was ranged from 0.39 % (test weight) to 11.0 % (pods/plant) and traits with lower values were desired was ranged from -1.15 (Days to maturity) to -2.17 (Days to 50% flowering). All the traits recorded high heritability (>70%) along with desired selection differential except for plant height. Clusters/plant, pods/plant and grain yield/plant recorded higher estimates of heritability and expected genetic advance indicating the predominance of additive gene action, while branches/plant and pod length had 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. The information on gene actions helps in selection of suitable breeding programme for improving the concerned traits.

Factor loadings and factor delineation

Out of the ten principal components, two factors were retained (with eigen value >1). The variation explained by these two factors was 57.2% (Table 2) out of the total variation. After varimax rotation the communality ranged from 0.39 (Branches/plant) to 0.81 (Grain yield/plant) with an average communality of 0.57. The ten traits were grouped into two factors: Factor 1 (FA 1) contains high correlations for seven traits viz., branches/plant, clusters/plant, pods/plant, pod length, seeds/pod, test weight and grain yield/plant, indicating that most of the yield contributing factors are grouped into the first factor. While the remaining three traits viz., days to 50% flowering, days to maturity and plant height were subsided under second factor (FA 2). The dimensional reduction of traits into factors simplifies the interpretation of the results by producing the orthogonal axes among the final factors and by eliminating the multicollinearity.

Multi-trait Genotype Ideotype Distance Index

MGIDI plot easily interprets the selection of ideal genotypes and was constructed by rescaling the data set as per minimum and maximum values of the traits with respect to their importance to the ideal genotype. By utilizing the scores from factor analysis, MGIDI for each genotype was obtained. The lower the MGIDI value better is the performance of genotype for all the traits which is nearer to the ideotype, hence such genotypes are selected. Selection intensity of 10% was applied and the top five genotypes selected were LBG 884, TBG 129, TBG 141, SUG 11-37 and LBG 904 (Figure 4).

Strengths and weaknesses of selected genotypes

The proportion of each factor towards the MGIDI index of all the genotypes and selected genotypes were represented as strengths and weaknesses of the genotypes as the factor contribution plot (Figures 5&6, respectively). The dashed line in the plot indicate the theoretical values of all the factors when contributed equally and factors which are placed outside the dashed line are positive strengths of the respective genotypes. The factors which contribute more towards the MGIDI of a genotype were close to the centre indicating the performance of the traits grouped under these factors is poor. Whereas, the factors which contribute less towards the MGIDI of a genotype were plotted at the edge of the plot and the traits categorized under those factors performed well and are close to the ideotype trait value. The traits under factor FA1 *viz.*, branches/plant, clusters/plant, pods/plant, pod length, seeds/pod, test weight and grain yield contributed more towards the MGIDI and placed towards the centre except for the genotype LBG 904 in which they became strengths for this genotype. The same genotype performed low for two traits *ie.*, days to 50% flowering and days to maturity under FA2. The traits days to 50% flowering, days to maturity and plant height under FA2 had least contribution for MGIDI of majority of the selected genotypes as their performance is good and were placed at the edge of the plot.

CONCLUSION

The multivariate index *i.e.*, Multi-trait Genotype Ideotype Index (MGIDI) efficiently

selected five superior black gram genotypes, *viz.*, LBG 884, TBG 129, TBG 141, SUG 11-37 and LBG 904 as ideal genotypes among the 50 studied genotypes at 10% selection pressure with desirable selection gains for most of the studied traits. Further, 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 transgressive segregants in turn improving the black gram productivity.

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Table 1. Selection differential, heritability and selection gain for ten traits in black gram

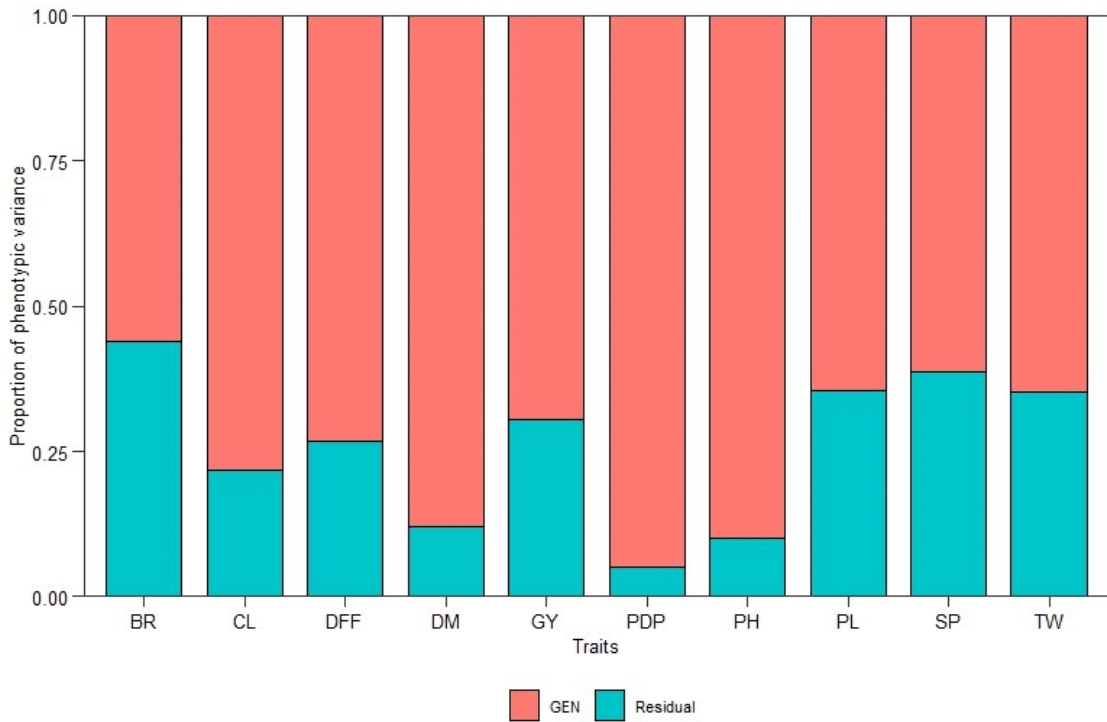
Traits/Variables	Overall genotypes Mean	Selected genotypes mean	SD	SD (%)	h^2	SG	SG (%)
Days to 50% flowering	44.40	43.50	-0.97	-2.17	0.85	-0.82	-1.84
Days to maturity	85.40	84.40	-0.98	-1.15	0.94	-0.92	-1.08
Plant height	67.30	65.90	-1.41	-2.09	0.95	-1.33	-1.98
Branches/plant	2.93	3.71	0.79	26.80	0.72	0.57	19.30
Clusters/plant	8.91	13.10	4.21	47.30	0.88	3.70	41.60
Pods/plant	29.30	40.30	11.00	37.70	0.97	10.80	36.80
Pod length	5.47	6.35	0.88	16.20	0.79	0.69	12.70
Seeds/pod	7.05	7.51	0.46	6.46	0.76	0.35	4.91
Test weight	4.47	4.87	0.39	8.81	0.79	0.31	6.93
Grain yield/plant	5.71	8.28	2.57	45.00	0.82	2.11	37.00

SD = Selection Differential; SD (%) = Selection differential percentage; h^2 = Heritability in broad sense; SG = Selection Gain; SG (%) = Selection gain percentage

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

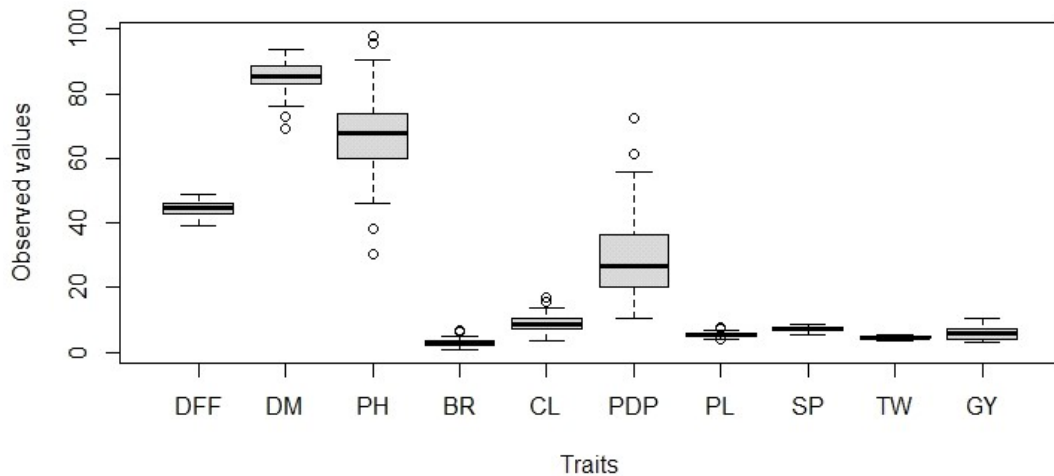
Trait/Variable	Factor 1	Factor 2	Communality	Uniquenesses
Days to 50% flowering	-0.02	-0.86	0.75	0.26
Days to maturity	0.13	-0.85	0.73	0.27
Plant height	-0.17	0.73	0.56	0.44
Branches / plant	-0.61	0.15	0.39	0.61
Clusters / plant	-0.68	-0.11	0.48	0.52
Pods / plant	-0.77	0.18	0.62	0.38
Pod length	-0.62	0.20	0.43	0.57
Seeds / pod	-0.64	0.18	0.44	0.56
Test weight	-0.71	0.03	0.51	0.49
Grain yield / plant	-0.90	-0.01	0.81	0.19
Eigen values	3.82	1.90		
Variance (%)	38.20	19.00		
Cumulative variance(%)	38.20	57.20		

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



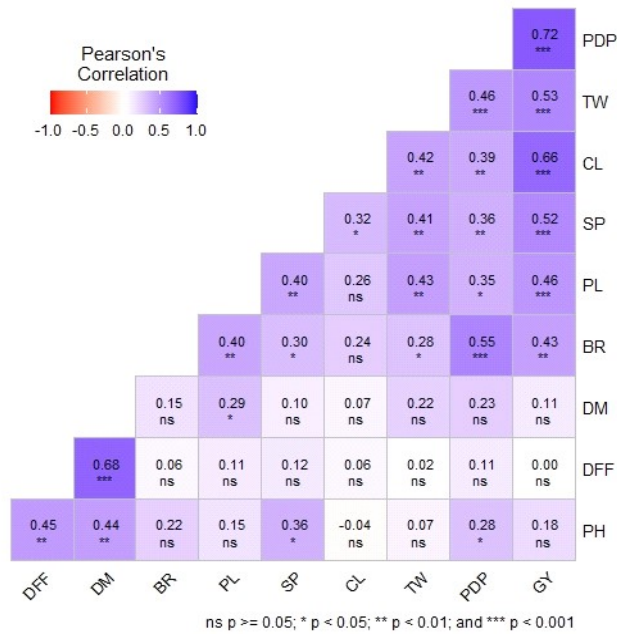
DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; BR: Branches/plant; CL: Clusters/plant; PDP: Pods/plant; PL: Pod length; SP: Seeds/pod; TW: Test weight; GY: Grain yield/plant

Figure 1. Proportion of phenotypic variance for ten traits in black gram



DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; BR: Branches/plant; CL: Clusters/plant; PDP: Pods/plant; PL: Pod length; SP: Seeds/pod; TW: Test weight; GY: Grain yield/plant

Figure 2. Box plot showing the variation for ten different characters of studied genotypes



DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; BR: Branches/plant; CL: Clusters/plant; PDP: Pods/plant; PL: Pod length; SP: Seeds/pod; TW: Test weight; GY: Grain yield/plant

Figure 3. Pearson’s correlations for all the traits under study

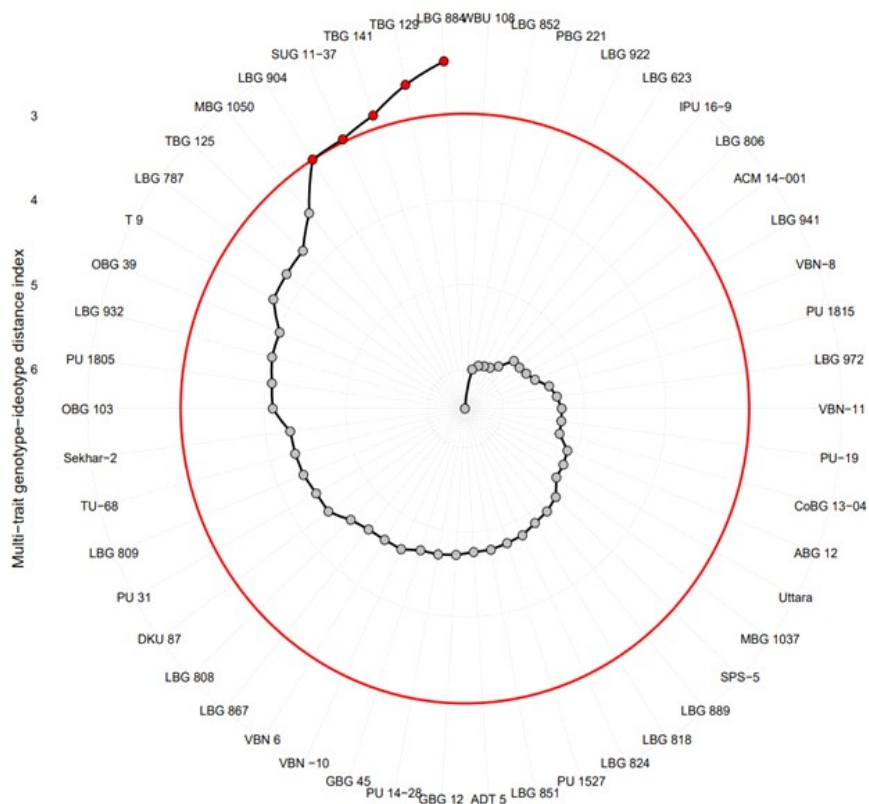


Figure 4. Genotype ranking based on the Multi-trait Genotype Ideotype Distance Index (MGIDI). Selected genotypes at 10% selection intensity were represented in red colour dots

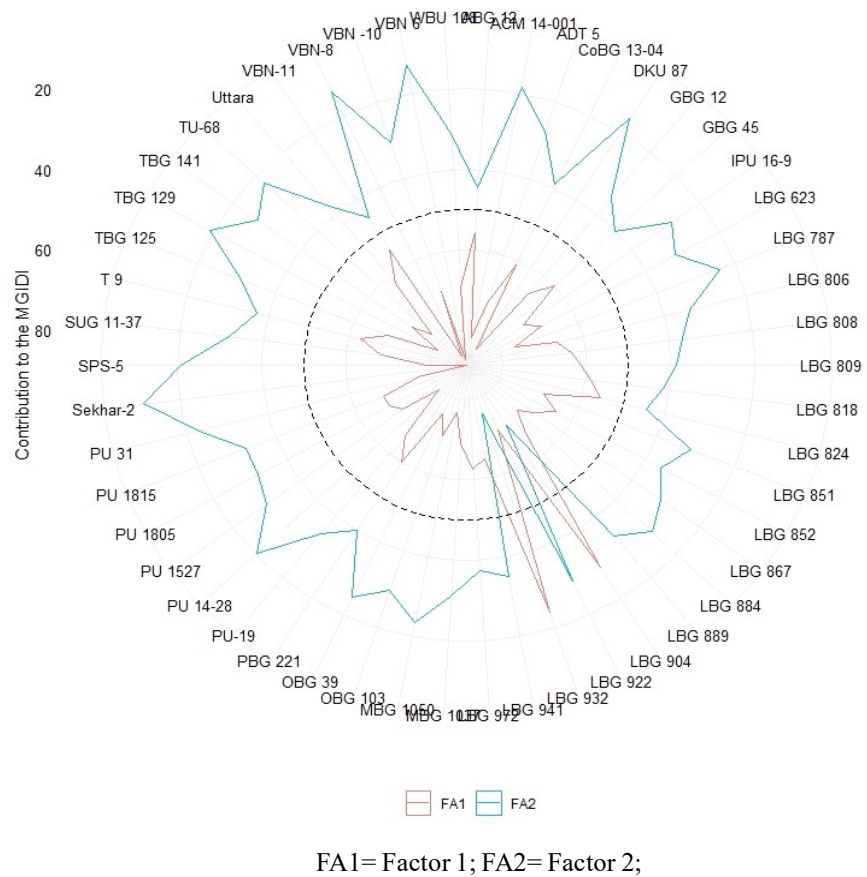


Figure 5. Strengths and weaknesses view of all the genotypes

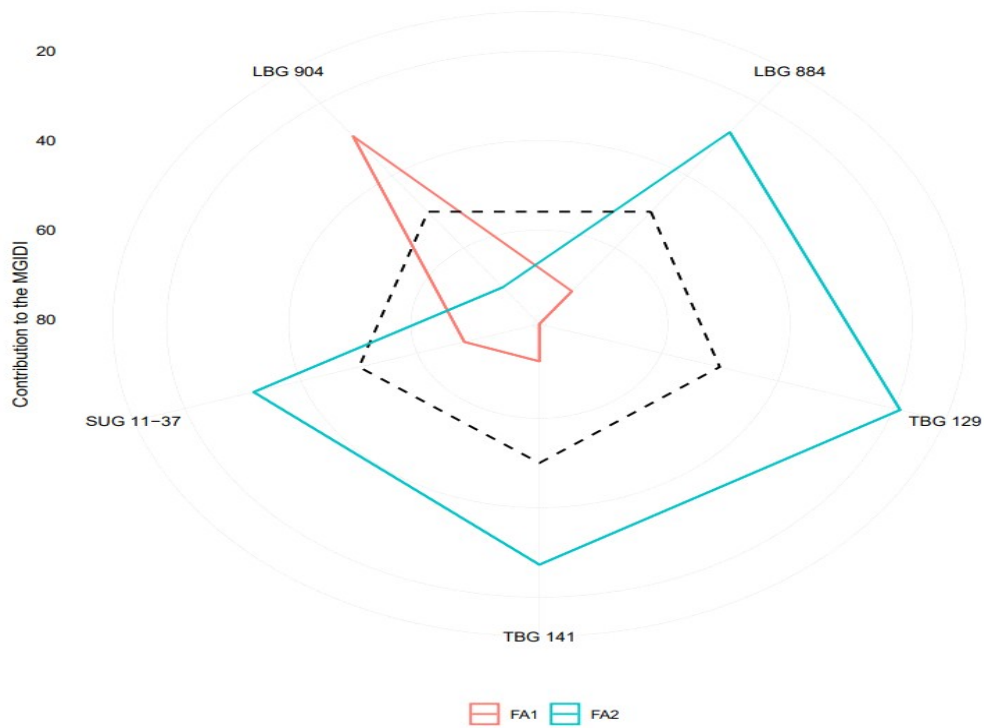


Figure 6. Strengths and weaknesses view of selected genotypes

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