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Genetic variability, trait association and MGIDI - driven ideotype selection for yield and gum content in guar (*Cyamopsis tetragonoloba* L. Taub.)

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Abstract

Cluster bean (*Cyamopsis tetragonoloba* L. Taub.) has transitioned from a vegetable crop into a high-value industrial source of galactomannan gum. Twenty-two elite gum type genotypes along with check variety MDU 1 were evaluated for seven agronomic and biochemical traits in randomized block design during *Rabi* 2023. Analysis of variance revealed highly significant genotypic differences ($P < 0.01$) for all traits. High heritability and genetic advance for single plant yield, pods per plant, and plant height confirmed additive gene action. Path analysis showed single plant yield was driven directly by pods per plant, while gum content showed negligible direct effect, indicating cumulative yield as the target trait for gum yield per unit area. Principal component analysis captured 75.25 % of total variation, discriminating pod yield from seed quality traits. Through MGIDI at 15 % selection intensity, RGR 18-1, RGR 20-15 and RGC 197 emerged as superior ideotypes, showing significant standard superiority (+44.2 % to +86.4 %) over MDU 1. By developing these guar genotypes into superior gum-type varieties, may replace the cultivation of existing vegetable-type cluster bean for gum purpose. Further, the introduction of new crop to southern districts of Tamil Nadu in the rainfed situation will ultimately help to improve the livelihood and standard of living of the farming community.

Keywords: Cluster bean, Guar gum, Heritability, MGIDI, Path analysis

INTRODUCTION

Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.], commonly known as guar is an annual self-pollinated leguminous crop (2n = 14). It is well adapted to arid and semi-arid regions of the world due to its resilient character and deep penetrating tap root system (Hymowitz and Upadhya, 1963; Boghara *et al*., 2016). Cluster bean has been traditionally grown as a vegetable, forage and a green manure crop but today has become a prime industrial cash crop globally. This transformation is due to the existence of a high valuable natural hydrocolloid galactomannan (guar gum) present in the seed endosperm (Bhatt *et al*., 2016). Guar gum is a polysaccharide made up of linear sequences of D-mannopyranose units linked by beta-D-(1→4) glycosidic bonds, with side branches of D-galactopyranose, often in a mannose to galactose ratio of around 2:1 (Mudgil *et al.,* 2014; Bhatt *et al*., 2016). It is widely used in petroleum, oil-drilling fracking, pharmaceutical, food stabilizer, cosmetics, paper and textiles industrial sectors due to its unique cold-water solubility and high viscosity-forming capabilities at low concentrations (Dhugga *et al*., 2004; Benakanahalli *et al*., 2021). India is the world's highest producer of guar and accounts for around 80% of the total guar gum production. Traditionally, north-western states such as Rajasthan have been the biggest contributors in terms of production (Bhatt *et al*., 2016). So, the increased demand in the international market and economic returns open the introduction of specific guar cultivars into places like Tamil Nadu, Karnataka and Maharashtra (Bhatt *et al*., 2016). Plant breeders should have a deep knowledge about the genetic architecture and relationships of the agronomic and biochemical variables to develop high-yielding and good industrial quality guar cultivars (Kgasudi *et al*., 2020 a). Gum yield and seed yield are complex polygenic variables that are greatly influenced by the environmental factors. Hence, due to the complex physiological and morphological interactions among the traits, selection for yield alone may sometimes be ineffective (Remzeena and Anitha, 2026).

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Previously the traditional selection indices Smith-Hazel (SH) index has been broadly utilized for multi-trait selection. However, it has multicollinearity difficulties due to the use of inadequate conditioned phenotypic and genotypic covariance matrices (Olivoto and Nardino, 2021). In response to such limitations, Olivoto and Nardino (2021) developed the Multi-Trait Genotype-Ideotype Distance Index (MGIDI), a powerful multivariate selection mechanism that represents correlation structures without covariance inversion and effectively conducts multi-trait selection based on the genotype-ideotype distance concept. Therefore, the present experiment was conducted to assess the 23 genotypes of guar in southern Tamil Nadu condition at Agriculture College and Research Institute (AC & RI), Madurai. The study was made to estimate the genetic variability parameters, character association and route effects of yield-related characteristics and also to exploit the MGIDI index towards the selection of multi-trait superior industrial guar genotypes suitable for southern Tamil Nadu.

MATERIALS AND METHODS

The experiment consists of 23 genotypes of guar (**Table 1**). The 22-elite gum-type guar genotypes were obtained from S.K.N. Agricultural University, Rajasthan and was evaluated along with the local check variety, MDU 1 (vegetable type), from AC&RI, Madurai. The experiment was carried out in Randomized Block Design with three replications during *Rabi* 2023. The row spacing was 45 cm, plant spacing was 15 cm, and the plot size was 10.5 sqm. All the recommended agronomic practices were followed for the better expression of the crop. Observations were recorded on ten randomly selected plants per plot in each replication for six quantitative traits *viz*., days to maturity, plant height (cm), number of pods per plant, number of seeds per pod hundred-seed weight (g) and single plant yield (g). Besides, biochemical estimation of guar gum content (%) was also performed for all the genotypes. The estimation of gum content in guar

Table 1. List of guar gum genotypes used in the experiment

S.No.	Genotypes	S.No.	Genotypes
1	RGC 3	12	GD 568
2	RGC 1038	13	RGR 12-1
3	GD 589	14	RGC 936
4	RGC 1055	15	RGC 1017
5	GD 588	16	RGC 1066
6	RGR 18-1	17	GD 565
7	RGC 1033	18	GD 601
8	RGC 197	19	RGC 1002
9	M 83	20	RGR 20-11
10	RGR 20-7	21	RGC 4
11	RGR 20-15	22	GD 573
Check	MDU 1 (Vegetable Type)		

was conducted at the Biochemistry Laboratory, AC&RI, Madurai. Five grams of the seeds were soaked in distilled water for 12 hours, after which the seeds were manually divided into hull, endosperm, and germ for the extraction of crude guar gum. The endosperm was dried by the oven-drying process until a stable weight was achieved and then ground to assess the crude gum production. The quantitative assessment of galactomannan was performed using standard phenol–sulfuric acid methodology established by Das *et al.* (1977) as modified by Joshi (2004). Fine seed powder (0.1 g) was autoclaved at 15 psi in 0.01 M $HgCl_2$ solution, precipitated overnight with ethanol, and centrifuged. The residue was dissolved in $HgCl_2$, treated with 2% phenol and concentrated sulfuric acid, and the absorbance of the colour complex was read at 490 nm in a spectrophotometer. Standard curves were made using galactose: mannose 1:2. The percentage of crude guar gum was calculated. The data obtained were used for the statistical analysis. The analysis of variance (ANOVA) for RBD was one as per Panse and Sukhatme (1967). The genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were assessed by the method of Burton and De Vane (1953) and were categorized into low (< 10%), moderate (10% to 20%), and high (> 20%) according to Sivasubramanian and Madhava Menon (1973). Heritability in general (h^2) was calculated by applying the formula of Lush (1949) and classified as low (< 30%), moderate (30% to 60%) and high (> 60%) based on Johnson *et al.* (1955). The genetic advance as percent of mean (GAM) was evaluated and categorized into low (< 10%), moderate (10%-20%) and high (> 20%) by Johnson *et al.* (1955). Standard superiority over the check variety MDU 1 (vegetable type) was determined for single plant yield, number of pods per plant, guar gum content. The phenotypic and genotypic correlation coefficients were estimated from variance and covariance components following the method of Singh and Chaudhury (1996). The evaluations of direct and indirect effect influences on the characteristics of dependent variable, single plant yield, were derived through path coefficient analysis, as suggested by Dewey and Lu (1959). The impacts were categorized as very low (0.00 to 0.09), low (0.10 to 0.19), moderate (0.20 to 0.29), high (0.3 to 1.0) and very high (>1) as per Lenka and Mishra (1973). Principal component cnalysis (PCA) and the correlation matrix was used for dimensionality reduction and genotypic arrangement. Principal components displaying eigenvalues greater than or equal to 1.0 were retained following Kaiser's criterion (Kaiser, 1958). Hierarchical cluster analysis was performed on standardized mean values using Ward's minimum variance method (Ward.D^2) and visualized as a genotype-by-trait heatmap. Simultaneous selection of superior genotypes across multiple characters were estimated using the Multi-Trait Genotype-Ideotype Distance Index (MGIDI). The selection intensity of 15% was fixed (3 out of 23 genotypes). Genotypic strengths and weaknesses across retained factor axes (FA1 and FA2) were profiled using radial and radar visualizations. All statistical and

multivariate analyses were conducted through R Studio using the R packages "variability" (for ANOVA, genetic variability parameters, correlations, and path analysis), "FactoMineR" and "factoextra" (for principal component analysis), "pheatmap" (for hierarchical clustering and heatmap visualization), and "metan" (for MGIDI computation and radar profiling).

RESULTS AND DISCUSSION

Highly significant genotypic differences were observed in ANOVA (**Table 2**) among the 23 guar genotypes for all the seven quantitative and biochemical traits. These attributes comprise of days to maturity, plant height, number of pods per plant, number of seeds per pod, hundred-seed weight, single plant yield and guar gum content. The mean sum of squares exhibited significance ($P < 0.01$) for all characters studied, which indicates adequate genetic heterogeneity among the evaluated germplasm lines. Such considerable genetic diversity establishes a strong foundation for straightforward phenotypic selection and targeted hybridization programs aimed to enhance productive traits. The mean performances of the traits studied are represented in **Fig. 1.** The mean for days to maturity was 100.39 days, where RGR 1033 was found to be earlier with 93 days, followed by GD 601 (95.00 days) and RGC 1038 (96.00 days). The check variety MDU1 recorded the maximum plant height (95.50 cm), followed by RGR 20-15 (88.50 cm) and RGR 18-1 (85.50 cm). The grand mean for the plant height was 64.17 cm. The genotypes RGR 18-1 (95.50 pods), RGR 20-15 (90.00 pods), and RGC 197 (89.50 pods) had high pod numbers per plant with an average of 56.9 pods per plant. The average number of seeds per pod was 7.80, while RGR 18-1 registered maximum number of seeds (9.30 seeds), followed by RGR 20-15 (8.80 seeds) and MDU 1 (8.80 seeds). However, the check variety MDU 1 (vegetable type) was found to be bold seeded with 4.80g followed by RGC 1066 (4.00 g) and M 83 (3.90 g). The average hundred-seed weight was 3.46 g. The mean guar gum content for industrial grade was 40.92 %, where RGC 1055 had maximum of 47.38 %, followed by RGC 1017 (47.03 %) and RGC 4 (45.50 %). However, the high-yielding genotypes RGR 18-1 (31.09 g), RGR 20-15 (25.34 g), and RGC 197 (24.06 g), registered moderate guar gum content.

Table 2. Analysis of variance across 23 cluster bean genotypes

Source of Variation	df	Days to maturity	Plant height	Number of pods per plant	Number of seeds per pod	Hundred seed weight	Guar gum content	Single plant yield
Replication	2	0.076	3.355	6.344	0.158	0.12	0.736	2.018
Genotype	22	47.59**	647.63**	957.99**	1.99**	0.54**	28.36**	100.53**
Error	44	2.974	9.321	15.373	0.176	0.053	0.943	2.164
Total	68							

** Significant @1%

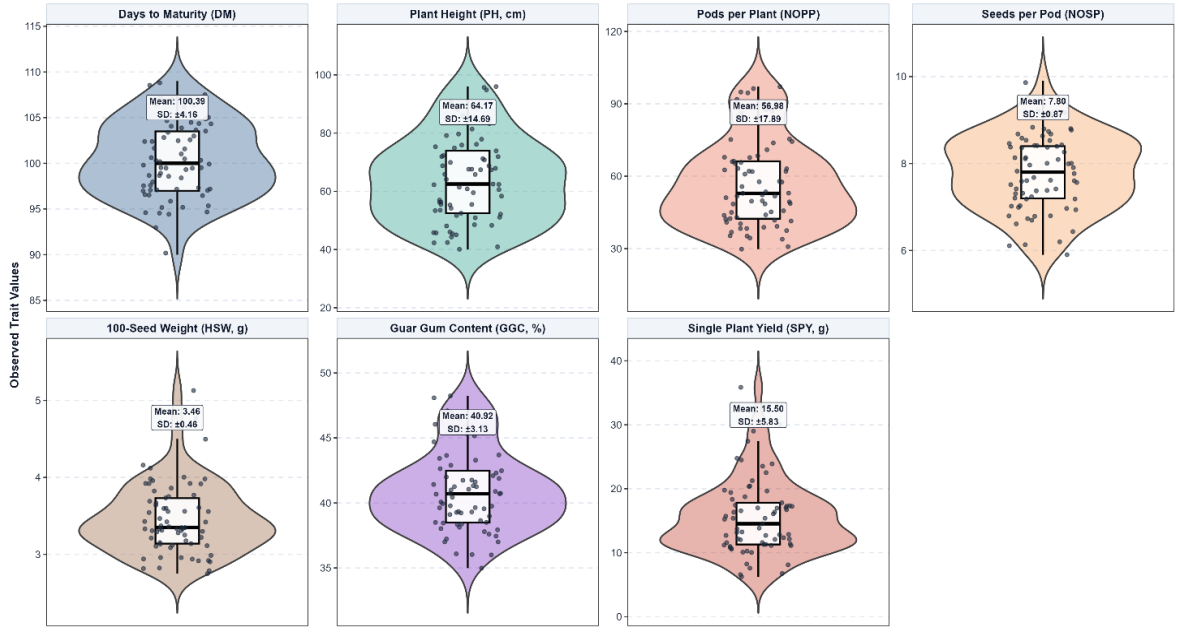


Fig. 1. Box plots of the mean values of the traits among 23 cluster bean genotypes

The genetic factors, such as mean, genotypic coefficient of variation, phenotypic coefficient of variation, broad-sense heritability, and genetic advance as a percent of mean, were estimated to determine the nature and scope of heritable variation (**Table 3**). The study revealed that PCV was found to be higher than GCV for the characters studied. Thus, the physical representation of these traits was influenced by the environmental factors however, the differences between GCV and PCV was small. The narrow differences between phenotypic and genotypic coefficients indicate that environmental variation contributes a small proportion to the total phenotypic variance and phenotypic values are the good indicators of genetic potential. Similar results were reported by Gangadhara *et al.* (2023), Manivannan and Anandakumar (2013) in guar. Single plant yield (36.95 %, 38.15 %), number of pods per plant (31.11 %, 31.86 %) and plant height (22.73 %, 23.22 %) showed high for both GCV and PCV. These high estimates of variability confirm wide genetic diversity in the population and it provides a good scope for selection. Hundred-seed weight (11.64 %, 13.40 %) and number of seeds per pod (9.97 %, 11.32 %) exhibited moderate estimates for GCV and PCV. Days to maturity (3.84 %, 4.21 %) and guar gum content (7.39 %, 7.76 %) had the lowest GCV and PCV revealed that the biometrical and quality traits were highly conserved and had a narrow range of variability among the lines studied, which is in agreement with the findings of Yeswanth *et al.* (2019) and Kgasudi *et al.* (2020 a).

Heritability estimates expose the proportion of genotypic part to the total phenotypic value, which is most powerful when combined with genetic advance as a percent of mean so as to predict the selection gain. In the present study, broad-sense heritability values were exceptionally high for all the seven traits. High heritability coupled with high genetic advance as percent of mean was observed for plant height (95.80 %, 45.83 %), number of pods per plant (95.34 %, 62.57 %), and single plant yield (93.81 %, 73.72 %). According to Johnson *et al.* (1955), this co-inheritance of high heritability and high GAM indicates the preponderance of additive gene action governing these traits, and simple directional selection based on these attributes will be highly effective for improving the specific traits. This is in accordance with the observations of Teja *et al.* (2023) and Sushmitha *et al.* (2025) for guar genotypes. However, days to maturity (83.34 %) and hundred seed weight (75.38 %) had high heritability with low to moderate genetic advance as percent of mean (7.22 % and 20.81 %, respectively). This trend indicates the effect of non-additive genetic interactions such as dominance and epistasis and developmental canalization which suggests that simple selection will not result in much genetic gain. Hence, recurrent selection and biparental mating can be used for improvement in plant height and seed weight as shown by Remzeena and Anitha (2025).

Evaluation of standard superiority over the local commercial check variety MDU 1 revealed substantial genetic gain across productive yield attributes and industrial gum content **(Fig. 2).** Wide range of economic superiority was evident with the top performance by genotypes *viz*., RGR 18-1 (+86.4 %), RGR 20-15 (+51.9 %), and RGC 197 (+44.2 %) for pronounced yield advantage over the check MDU1. This superiority in grain yield was closely underpinned by a concomitant expansion in cumulative pod biomass; RGR 18-1 (+141.8 %), RGR 20-15 (+127.8 %), and RGC 197 (+126.6 %) which was more than double the number of pods per plant compared to the check MDU 1. The check variety MDU 1 is primarily cultivated as a vegetable type but utilized and commercially exploited in southern districts for Tamil Nadu for guar purpose and seeds are being marketed for gum purpose to northern states. Guar genotypes *viz*., RGC 1055 (+23.1 %), RGC 1017 (+22.2 %), RGC 4 (+18.2 %), and RGC 3 (+16.8 %) excelled for guar gum content over the check. Especially the genotypes such as RGR 18-1 and RGR 20-15 found to be superior per seed yield advantage along with moderate guar gum content (+1.4 % and +10.8 %, respectively) over the check variety MDU1.

Single plant yield is a complex, polygenic trait that is highly influenced by many yield-contributing traits. Consequently, direct selection for yield is often inefficient, so deep understanding of genotypic and phenotypic correlation among the traits are more important **(Fig. 3).** The present study revealed that genotypic correlation coefficients were found to be higher than their phenotypic counterparts. This pattern suggests that the traits are strongly and intrinsically genetically linked and not

Table 3. Genetic variability parameters for yield-contributing traits among the cluster bean genotypes

Traits	Mean	GCV (%)	PCV (%)	Heritability (%)	GAM (%)
Days to maturity	100.39	3.84	4.21	83.34	7.22
Plant height	64.17	22.73	23.22	95.80	45.83
Number of pods per plant	56.98	31.11	31.86	95.34	62.57
Number of seeds per pod	7.80	9.97	11.32	77.47	18.07
Hundred seed weight	3.46	11.64	13.40	75.38	20.81
Guar gum content	40.92	7.39	7.76	90.65	14.49
Single plant yield	15.50	36.95	38.15	93.81	73.72



Fig. 2. Superiority percentage over check variety MDU1 for single plant yield, number of pods per plot and guar gum content

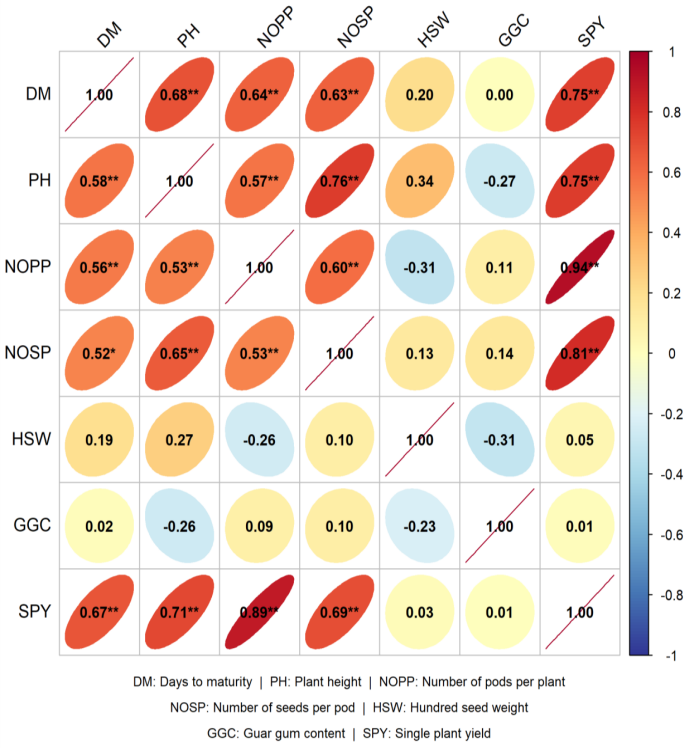


Fig. 3. Genotypic (upper diagonal) and Phenotypic (lower diagonal) correlations among 23 guar genotypes
** & * Significant @1% and 5 % level, respectively

affected by the environmental factors. Single plant yield was highly significant and positively associated with number of pods per plant (0.94**), number of seeds per pod (0.81**), plant height (0.75**) and days to maturity (0.75**). These associations suggest that selection of plants with tall stature, greater number of pods and longer vegetative duration had direct association which translate into superior yield, as demonstrated earlier by Khatoon *et al.* (2024). In contrast, the hundred-seed weight (0.051) and guar gum content (0.013) showed non-significant and negligible association with single plant yield. The guar gum content and seed yield are of immense industrial significance. During the selection process, it is important to prioritize seed yield without causing a negative pleiotropic effect that reduces gum content of the seed. This is in accordance with Gresta *et al.* (2017), who demonstrated that total gum yield is primarily determined by total seed yield rather than individual seed endosperm concentration of guar gum content.

The correlation study exposes the degree of association between the yield-related traits which is unable to partition these associations into direct and indirect effects, ultimately mask the true causal relationships. Therefore, genotypic path coefficient analysis was executed to designate single plant yield as the dependent variable **(Table 4).** Based on the categorization of direct effects suggested by Lenka and Mishra (1973), Number of pods per plant exhibited a very high positive direct effect on single plant yield (0.9841), coupled with an exceptionally high positive genotypic correlation (0.937**). So, Number of pods per plant is the major yield-determining component in guar to increase the gum yield per unit area. Further, number of seeds per pod (0.3902) and hundred seed weight (0.3603) are also showed high positive direct effect and thus priority should be given for these traits and during selection for the improvement of total gum yield.

Days to maturity and plant height also showed a significant association. Although both traits displayed high significant positive genotypic association with single plant yield (0.749** and 0.751**, respectively), their direct effects on single plant yield were negative (-0.0466 for days to maturity and -0.2233 for plant height). This contradiction is completely resolved by the indirect effects. Despite having low direct effects, both days to maturity and plant height exerted positive indirect effects on single plant yield primarily through number of pods per plant (0.6280 and 0.5630, respectively) and number of seeds per pod (0.2460 and 0.2950, respectively). This demonstrates that the tall, late maturing types not directly contribute for higher yield, but rather act as more biomass and reproductive sinks, allowing the plant to produce a greater number of productive nodes and clusters which in turn resulted with higher cumulative pod production. This causal pathway is in line with the observations reported by Boghara *et al.* (2016) among guar genotypes. The residual effect of path analysis was low (0.0528), which supports the representativeness of the selected traits in path model.

PCA was performed to condense the total multi-character phenotypic variation and to map genotypic relationships regardless of scale. The PCs with eigenvalues equal to 1.0 or greater than 1.0 were retained per Kaiser's criterion. The first two PCs (PC1 and PC2) explained 75.25 % of the total genotypic variance among the evaluated guar genotypes **(Table 5 and Fig. 4).** PC1 explained 53.65 %

Table 4. Genotypic path analysis for the 23 cluster bean genotypes

Traits	Days to maturity	Plant height	Number of pods per plant	Number of seeds per pod	Hundred seed weight	Guar gum content	Correlation for single plant yield
Days to maturity	-0.0466	-0.1519	0.6280	0.2460	0.0734	-0.0002	0.749**
Plant height	-0.0317	-0.2233	0.5630	0.2950	0.1216	0.0268	0.751**
Number of pods per plant	-0.0298	-0.1277	0.9841	0.2325	-0.1121	-0.0105	0.937**
Number of seeds per pod	-0.0294	-0.1688	0.5862	0.3902	0.0474	-0.0137	0.812**
Hundred seed weight	-0.0095	-0.0753	-0.3062	0.0513	0.3603	0.0301	0.051
Guar gum content	-0.0001	0.0613	0.1058	0.0549	-0.1111	-0.0976	0.013

Diagonal values indicate the direct effect. Residual effect: 0.0528

Table 5. Eigenvalues and variance explained by principal components among the cluster bean genotypes

PC Number	PC Axis	Eigenvalues	Variance explained (%)	Cumulative variance (%)
1	PC1	3.76	53.65	53.65
2	PC2	1.51	21.6	75.25
3	PC3	0.837	11.96	87.21
4	PC4	0.437	6.24	93.46
5	PC5	0.277	3.96	97.41

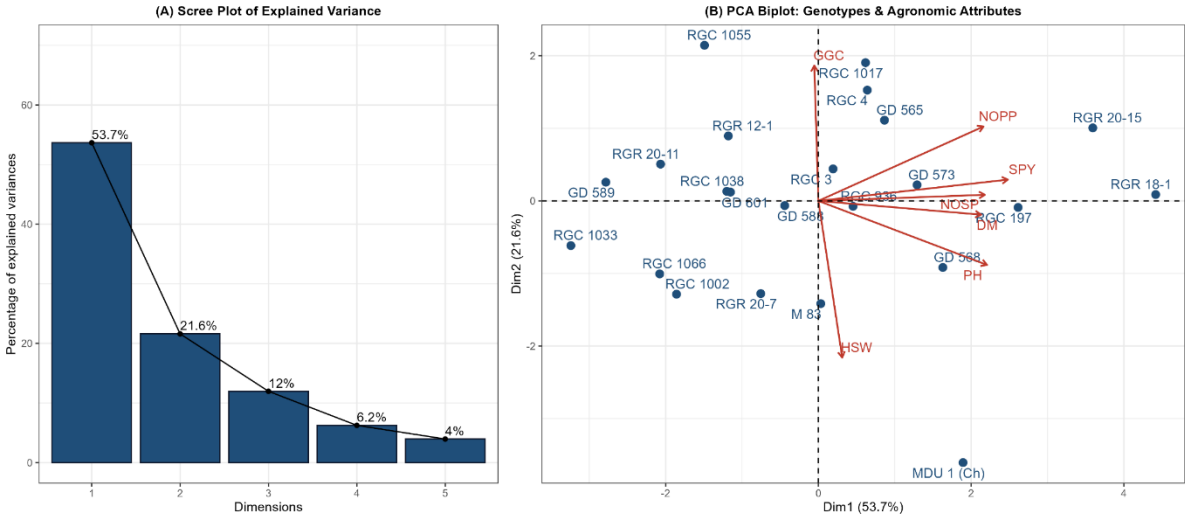


Fig. 4. Principal component analysis of the 23 guar genotypes

of variance with an eigenvalue of 3.76 and PC2 explained 21.60 % of variance with an eigenvalue of 1.51. The first principal component (PC1) had heavy loading on single plant yield, number of pods per plant and plant height as a main biomass and yield sink factor. Conversely, PC2 was highly correlated with hundred seed weight and guar gum content, comprising individual seed density and quality endosperm traits are independent to vegetative growth. This dimensional partitioning corresponds to the findings of Khatoon *et al.* (2024) and Kumar *et al.* (2024) where yield capacity traits and individual seed traits are controlled by independent orthogonal factors in guar. The Hierarchical cluster analysis was based on Ward's minimum variance method (Ward.D^2), which successfully grouped the twenty-three genotypes into divergent clusters **(Fig. 5)**. This hierarchical clustering distinguished the high pod bearing and high biomass accessions from lines with high seed weight or specific vegetative phenological profiles. This confirms that there is a substantial genetic divergence exist among the lines studied, provides an objective basis for parental selection during the hybridization programme. Generally crossing parents of highly divergent clusters optimizes the utilization of transgressive segregants and heterosis, as supported by the genetic diversity studies of Boghara *et al.* (2016) and Kgasudi *et al.* (2020 b).

Simultaneous selection of multiple desirable traits is majorly affected by genetic correlations and multicollinearity. To overcome these constraints, the Multi-Trait Genotype-Ideotype Distance Index developed by Olivoto and Nardino (2021). MGIDI considers correlation structures without the need for matrix inversion, thus avoiding antagonistic selection gains commonly seen in classical Smith-Hazel indices. Karthik and Hanamaratti (2025) have identified superior genotypes using MGIDI at 15 % selection intensity in sorghum. The MGIDI index identified three elite ideotype genotypes at a selection intensity of about 15 % (3 out of 23 genotypes): RGR 18-1, RGR 20-15 and RGC 197, by targeting yield-contributing traits and guar gum content.

Radar and factor contribution profiling (**Fig. 6**) confirmed that these selected genotypes successfully balanced the primary yield-determining component—number of pods per plant with high single plant yield and superior guar gum content without any negative trade-offs. The selected genotypes exhibited superior biomass, robust branches, high pod load, and stable biochemical quality traits. Hence, these three genotypes *viz*., RGR 18-1, RGR 20-15 and RGC 197 is recommended as outstanding parents to suit industrial and agricultural purpose and possible to integrate the superiority via future breeding programs to combine high productivity along with superior gum yield.

This study revealed the existence of sufficient genetic variability among the twenty-three guar genotypes for all the evaluated morphological, quality, and guar gum content. High broad-sense heritability coupled with high genetic advance as percent of mean for plant height, number of pods per plant and single plant yield confirmed the preponderance of additive gene action, affirming that direct selection based on these traits will be highly effective for crop improvement. Genotypic correlation and path coefficient analyses established that single plant yield is governed by cumulative pod production and seeds per pod, rather than individual seed gum content. Regarding path analysis, number of pods per plant exhibited the highest positive direct effect on yield, with a low residual effect confirming model completeness. The multi-trait selection using MGIDI index, identified genotypes (RGR 18-1, RGR 20-15 and RGC 197) having superior yield with optimum gum content, thus paving a roadmap for targeted genetic improvement in guar gum types. Hence, from this study the development and introduction of exclusive guar gum cluster bean variety may substantially replace the existing

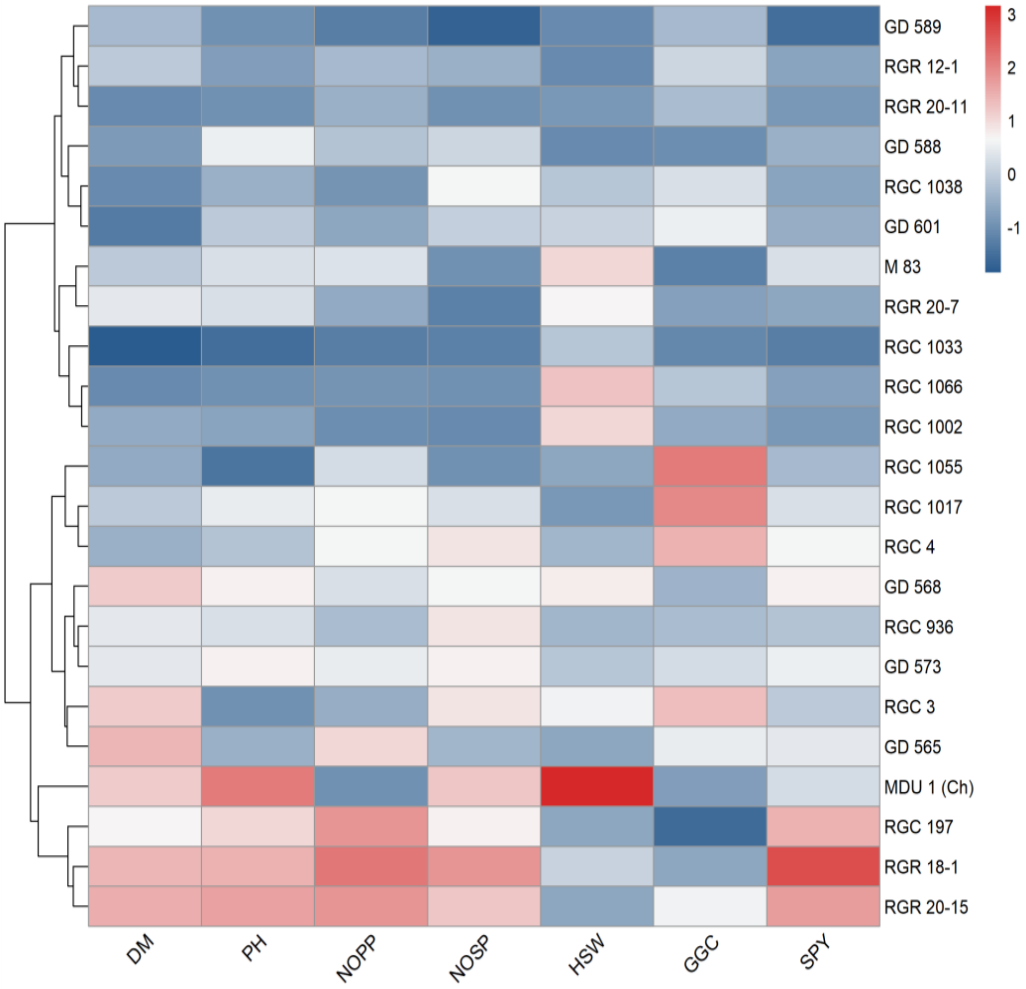


Fig. 5. Clustering of 23 guar genotypes for the traits (wards. D^2)

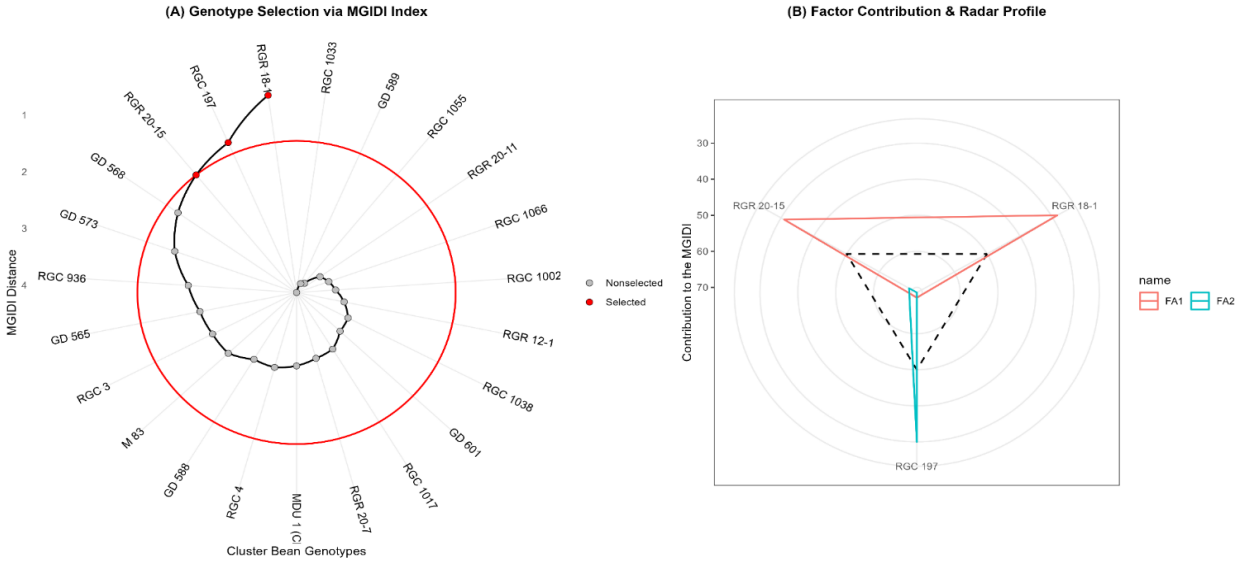


Fig. 6. MGIDI index and factor contributions among cluster bean genotypes

vegetable type cluster bean varieties being cultivated for gum purpose which ultimately improves the standard of living of the farming community in the southern districts of Tamil Nadu.

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