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Intergenerational relationship and Multi-trait Genotype-Ideotype Distance Indexing (MGIDI) in inter-varietal cross derivatives of black gram [*Vigna mungo* (L.) Hepper

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Abstract

Black gram is a highly self-pollinated short-duration crop cultivated in various cropping systems *viz.,* rainfed, intercrop and rice fallow. In the present study, hybridization was made between 2 black gram varieties *viz.,* CO 6 and VBN 11, aimed to develop the recombinants and select superior progenies through Multi-trait Genotype-Ideotype Distance Index (MGIDI) at Tamil Nadu Agricultural University, Coimbatore. The parent-offspring regression analysis was carried out in the F_3 and F_4 progenies of CO 6 × VBN 11. The significant regression and intergenerational correlation coefficients were observed for all the traits studied. The narrow sense heritability was found to be high for the number of seeds per pod. The other traits *viz.,* plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight and seed yield per plant showed moderate narrow sense heritability. The MGIDI was calculated for 62 F_4 progenies of CO 6 × VBN 11 considering nine yield component traits. In F_4 progenies, high broad sense heritability was observed for all the yield-contributing traits and high selection gain was recorded for seed yield per plant (49.77%), number of branches per plant (46.29%), number of pods per plant (37.74%) and number of pods per cluster (20.80%). Based on the MGIDI, six F_4 progenies *viz.,* P_1, P_6, P_{22}, P_{49}, P_{50} and P_{53} were selected. The selected progenies could be further evaluated and yield tested for commercial exploitation.

Keywords

black gram; ideotype; intergenerational correlation; MGIDI; narrow sense heritability; parent-offspring regression; selection gain

Introduction

Black gram (*Vigna mungo* (L.) Hepper) is a highly self-pollinated diploid crop with 22 chromosomes and a genome size of 574 Mbp (1). India is considered a primary centre of origin and Central Asia is the secondary centre of origin (2). It was domesticated in India around 3500 to 4500 years ago from its wild progenitor, *Vigna mungo* var. *silvestris* (3) and later spread to the west coast peninsular of Thailand about 2300 years ago (4). The cultivation is widespread in the countries *viz.,* Afghanistan, Bangladesh, India, Myanmar, Pakistan, Sri Lanka, Thailand and Vietnam (5). India is the largest producer (25% of global production), consumer (27% of world consumption) and importer (14%) of pulses (6). India's black gram production stands at 2.77 million tonnes from an area of 4.63 million ha, with a productivity of 599 kg/ha (7). The 100 g of black gram seeds contain 24 to 26 g of proteins, 60 g of carbohydrates and 1.3 g of fats. The notable amounts of phosphorus, potassium, iron and calcium were found in seeds along with essential amino acids and vitamins (8). It is commonly consumed as popular Indian dishes like idli, dosa and vada prepared using black gram batter (9). The versatility of black gram extends to its potential use in the food industry as functional food and nutraceutical as well as applications in the cosmetic and pharmaceutical industries (10). The continuous breeding efforts are required to develop improved cultivars and to increase productivity. The success of this hybridization-driven variability relies on the heritability of the yield component traits. High heritability ensures that the desirable traits have a greater likelihood of being transmitted to subsequent generations (11). Further, narrow sense heritability helps in understanding the inheritance of traits due to additive genetic components. It indicates the extent to which offspring resemble their parents in a specific trait or phenotype. A higher coefficient of parent-offspring regression (12) suggests a strong genetic influence, implying that the trait is more likely to be inherited from parents to offspring due to genetic factors. In addition to prioritizing the seed yield, the breeding program should adopt its correlated traits in the selection process. Correlated traits are those that exhibit some degree of association with seed yield and their inclusion in the selection process will contribute to crop improvement (13). Hence, an effective approach that simultaneously considers multiple trait improvements in a desired direction is essential. The modern approach, Multi-trait Genotype-Ideotype Distance Index (MGIDI) is a multiple trait-based index that calculates the distance between genotype and defined ideotype (14). In practical applications, MGIDI stands out for its ease of interpretation, eliminating the need for economic weights or arbitrary coefficient selection. Demonstrating superior performance, MGIDI emerges as a crucial tool for genetic and population analysis, providing breeders with a robust means to ensure long-term gains in both primary and secondary traits in plant breeding experiments. Hence, the current study involved the analysis of narrow sense heritability of yield contributing traits by parent-offspring regression analysis and the selection of superior F_4 progenies of black gram based on the MGIDI.

Materials and Methods

The present study was conducted in the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore, India. A crossing between two black gram varieties *viz.,* CO 6 (ovule parent) and VBN 11 (pollen parent) were made during summer, 2022. The true hybrids were identified (*kharif*, 2022) on the basis of pod hairiness (dominant trait) inherited from the pollen parent and the plants were harvested individually. The F_2 population derived from a single F_1 plant was evaluated during *rabi*, 2022-23 and plants were harvested individually to obtain F_3 seeds. A total of 62 F_3 and F_4 progenies were evaluated during summer, 2023 and *kharif*, 2023 respectively, in a single row of 4 m length with a spacing of 30 × 10 cm. The recommended package of practices and need-based crop protection measures were followed to maintain a good crop stand. Nine quantitative traits *viz.,* plant height (PH) (cm), number of branches per plant (NBP), number of clusters per plant (NCP), number of pods per cluster (NPC), number of pods per plant (NPP), pod length (PL) (cm), number of seeds per pod (NSP), hundred seed weight (HSW) (g) and seed yield per plant (SYP) (g) were recorded from five randomly selected plants from each progeny of F_3 and F_4 generations. The mean data of the each F_3 and F_4 progenies were used for the parent-offspring regression analysis (12). The coefficients for parent-offspring regression were computed by regressing the mean value of a trait in the F_4 (o-offspring) against the corresponding value of a trait in the F_3 (p-parent).

Intergenerational correlation coefficients (r) were determined for yield contributing traits across 2 subsequent generations (F_3 and F_4) using parent-progeny regression analysis.

$$\text{Parent - offspring regression } (b_{op}) = \frac{\text{Covariance (op)}}{\text{Variance of p}} \quad \text{(Eqn. 1)}$$

Where, b_{op} = parent-offspring regression, σ_p= standard deviation of parents, σ_o= standard deviation of offspring.

$$\text{Intergenerational correlation} \quad b_{op} \text{ x } \frac{\sigma_p}{\sigma_o} \quad \text{(Eqn. 2)}$$

The narrow sense heritability was calculated using parent-offspring regression and intergenerational correlation as follows (15).

$$\text{Narrow sense heritability } (h^2) = \frac{b_{op}}{2r_{po}} \text{ x } 100 \quad \text{(Eqn. 3)}$$

The Multi-trait Genotype-Ideotype Distance Index (MGIDI) was calculated for 62 F_4 progenies using the “metan” package (16) with ‘gamem’ and ‘mgidi’ functions in R studio (Version 4.2.1). The calculation of MGIDI of the genotypes (14) has 4 steps: (i) rescaling the traits so that all the values have a 0-100 range; (ii) factor analysis, which converts correlated traits into uncorrelated factors; (iii) ideotype planning, in which all the traits have the highest rescaled value and (iv) computation of MGIDI. The formula for MGIDI of a genotype ‘i’ is as follows:

$$\mathrm{MGIDI}_i = \sqrt{\sum_{j=1}^{f}(\gamma_{ij} - \gamma_j)^2} \quad \text{(Eqn. 4)}$$

Where, Y_{ij}= score of the i^{th} genotype in the j^{th} factor and Y_j = j^{th} score of the ideotype.

The selection gain (%) in the F_4 progenies was calculated for each trait of the progenies at 10% selection intensity using the formula,

$$\text{Selection gain (\%)} = \frac{(\overline{X}_s - \overline{X}_o) \text{ x } h^2}{\overline{X}_o} \text{ X } 100 \quad \text{(Eqn. 5)}$$

Where, $\overline{X}s$ = mean of the selected genotypes, $\overline{X}o$= mean of the original population and h^2 = heritability (bs).

Results and Discussion

Parent-offspring regression

The regression coefficient between F_3 and F_4 generation was significant for all the traits (Table 1). It was found to be high in PH (1.00), followed by HSW (0.98), NCP (0.91), PL (0.91) and SYP (0.87). It revealed the higher linear response of the traits across generations. A significant intergenerational correlation was observed for all the traits (Table 1). The highest correlation was found in HSW (0.92), followed by SYP (0.88), PL (0.87), PH (0.85) and NCP (0.82). It showed a robust relationship between F_3 and F_4 generations for all the traits. The significant regression and intergenerational correlation for yield-contributing traits were also reported in green gram (17), cowpea (18) and chickpea (19).

Narrow-sense heritability for quantitative traits was estimated using regression and intergenerational correlation. The narrow sense heritability was high for the trait NSP (87.84%) (Table 1). It is attributed to significant additive gene action and lesser influence of epistatic components in the expression of trait (20). The previous studies have reported high narrow sense heritability for NSP in chickpeas (21) and pigeon peas (22). The moderate values were observed for the other traits *viz.,* PH (59.20%), NBP (55.69%), NCP (55.41%), NPC (56.73%), NPP (55.21%), PL (52.35%), HSW (53.50%) and SYP (49.14%). The moderate heritability could be attributed to the presence of non-fixable genetic components alongside additive gene action (23, 24). Hence, postponing the selection to later generations is suggested to make the selection process more effective. In earlier reports, the above traits were highly heritable (narrow sense) in various crops *viz.,* green gram (17), chickpea (21) and cowpea (18). The higher heritability observed in previous studies suggested making the selection in the earlier generations for effective improvement of the yield component traits.

The selection in the F_4 generation is encouraged by a decrease in heterozygosity, which reduces the influence of dominance and interactions between dominant genes. This suggests that progenies could be efficiently selected from the F_4 generation, considering the strong correlation across generations and the significant heritability observed in the traits.

Table 1. Parent progeny regression analysis in F_3 and F_4 progenies of CO 6 × VBN 11

Sl. No.	Trait	b_{op}	r_{po}	ns h^2 (%)
1.	Plant height	1.00**	0.85**	59.20
2.	Number of branches per plant	0.74**	0.66**	55.69
3.	Number of clusters per plant	0.91**	0.82**	55.41
4.	Number of pods per cluster	0.53**	0.47**	56.73
5.	Number of pods per plant	0.75**	0.68**	55.21
6.	Pod length	0.91**	0.87**	52.35
7.	Number of seeds per pod	0.65**	0.37**	87.84
8.	Hundred seed weight	0.98**	0.92**	53.50
9.	Seed yield per plant	0.87**	0.88**	49.14

b_{op}: Parent offspring regression coefficient; r_{po}: Intergenerational correlation coefficient; ns h^2: Narrow sense heritability (%); **Significant at P ≤ 0.01

Multi-trait Genotype Ideotype Distance Index

The MGIDI was computed for 62 F_4 progenies derived from CO 6 × VBN 11 cross. The first 3 factors exhibited more than one eigenvalue. Factor 1 was associated with major yield-contributing traits such as NPC, NPP, PL, NSP and SYP. Factor 2 was attributed to NBP and NCP, while factor 3 was associated with PH and HSW (Table 2). The broad sense heritability in F_4 progenies was found to be high in all the traits studied (Table 2). At 10% selection intensity, mean values were increased in all traits (Table 2). Notably, the mean value of the NPP increased from 54.50 to 76.50. The mean SYP for the progenies increased from 15.99 to 24.16 g in the selected progenies with the selection differential of 8.17 g. Consequently, the predicted selection gain was notably higher for SYP (49.77%), followed by NBP (46.29%), NPP (37.74%) and NPC (20.80%) (Table 2). The high heritability and potential for selection gain are likely due to the additive nature of gene action, indicating that selection in the F_4 generation will be efficient in enhancing the traits. Therefore, the traits *viz.,* SYP, NBP, NPP and NPC are expected to be enhanced at higher levels in the next generation. A higher selection gain has been reported for NPP and SYP in soybean (25) and seed yield in lentil (26), rice bean (27) and green gram (28).

In MGIDI analysis, 6 progenies were selected (Fig. 1) with the aim of improving all 9 yield contributing traits (desired ideotype). The mean performance of the 6 selected progenies and their MGIDI are presented in Table 3. The progenies having a low MGIDI value are more desirable as they are more similar to the expected ideotype. The MGIDI was low in the progeny P_{22} (2.17) followed by P_{53} (2.49), P_1 (2.61), P_6 (2.67), P_{50} (3.05) and P_{49} (3.29). Among these, a higher SYP than the mean value (24.16 g) was observed in the progenies *viz.,* P_1 (25.85 g), P_6 (28.50 g) and P_{22} (30.20 g). In addition to seed yield per plant, P_1 demonstrated commendable performance in traits such as NBP, NCP, NPP and NSP than the overall mean value. Notably, P_6 excelled in six additional traits, including NBP, NPC, NPP, PL, NSP and HSW. Meanwhile, P_{22} stood out in PH, NBP, PL and HSW, in addition to SYP. The above progenies were selected based on their superior performance for multiple traits, including yield and its correlated characters. Considering the high heritability of these traits, the selected progenies *viz.,* P_1, P_6, P_{22}, P_{49}, P_{50} and P_{53} hold significant potential for the development of high-yielding cultivars. Selections were done based on MGIDI in rice bean (27), chickpea (29), soybean (30) and green gram (28). A substantial improvement in the yield contributing traits was observed in their studies. Hence, the MGIDI-based selection could be utilized for the simultaneous

Table 2. Various selection response parameters in F_4 progenies of CO 6 × VBN 11 by Multi-trait Genotype-Ideotype Distance Index

Sl. No.	Trait	Factor	Xo	Xs	SD	bs h^2 (%)	SG	SG (%)
1.	Plant height (cm)	FA 3	58.06	62.17	4.11	96.90	3.98	6.86
2.	Number of branches per plant	FA 2	2.56	3.83	1.27	93.30	1.18	46.29
3.	Number of clusters per plant	FA 2	21.11	23.00	1.89	96.40	1.82	8.63
4.	Number of pods per cluster	FA 1	2.84	3.50	0.66	89.50	0.59	20.80
5.	Number of pods per plant	FA 1	54.50	76.50	22.00	93.5	20.57	37.74
6.	Pod length (cm)	FA 1	4.74	4.95	0.21	97.30	0.20	4.31
7.	Number of seeds per pod	FA 1	6.32	7.00	0.68	90.00	0.61	9.68
8.	Hundred seed weight (g)	FA 3	5.26	5.51	0.25	98.30	0.25	4.67
9.	Seed yield per plant (g)	FA 1	15.99	24.16	8.17	97.40	7.96	49.77

Xo: Mean of original population; Xs: Mean of selected progenies; SD: Selection differential; bs h^2: Broad sense heritability; SG: Selection gain at 10% selection intensity

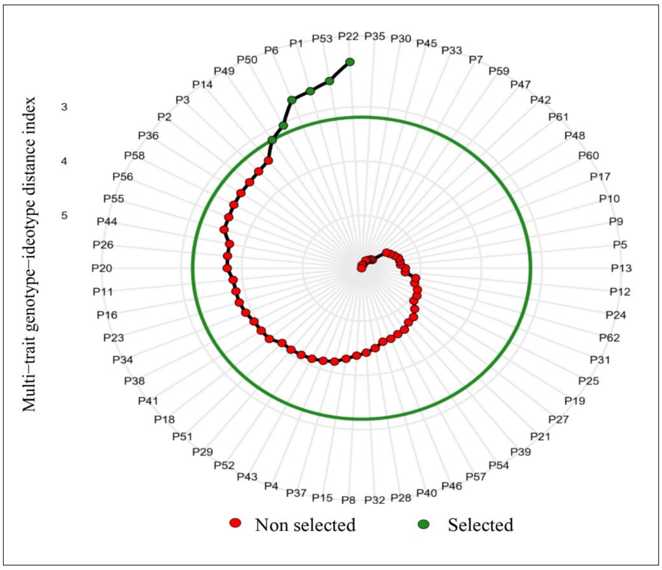

Fig. 1. Multi-trait Genotype-Ideotype Distance Indexing (MGIDI) in F_4 progenies of CO 6 × VBN 11.

improvement of the multiple traits.

Strength and weakness view

The strength and weakness view of the selected progenies was depicted in Fig. 2. The MGIDI index ranked the contributions of each factor, placing the most influential factor near the plot centre and less influential factors toward the plot edge. With respect to FA1, P_{53} and P_1 progenies had better contributions from the traits *viz.,* NPC, NPP, PL, NSP, HSW and SYP. Considering the FA2, the above progenies had a lesser contribution from the traits *viz.,* NBP and NCP. The higher contribution of PH and HSW was strong (FA_3) in the progenies P_1 and P_6.

Conclusion

The present study involved the segregating generations of inter varietal cross of black gram. The parent-offspring regression analysis in the F_3 and F_4 generations explained the strong relationship across the generations for yield component traits. It gave hope for the improvement of traits through simple selection. The MGIDI analysis of 62 F_4 progenies highlighted high heritability and substantial selection gain for key yield-contributing traits such as seed yield per plant, number of branches per plant, number of pods per plant and number of pods per cluster. Six superior F_4 progenies (P_1, P_6, P_{22}, P_{49}, P_{50} and P_{53}) were selected based on MGIDI analysis and identified as having potential for further evaluation. The study underscores the importance of considering multiple traits simultaneously for effective selection and yield improvement in black gram. The utilization of techniques like MGIDI provides a robust approach for selecting superior progenies with desirable traits, ultimately contributing to the development of high-yielding cultivars in black gram.

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Authors' contributions

SA and JP were involved in the conceptualization and design of the study. SA conducted material preparation, data collection and analysis. The initial manuscript draft was authored by SA and critically revised by JP. All authors reviewed and consented to the final manuscript.

Compliance with ethical standards

Conflict of interest: The authors declare no conflicts of interest regarding the publication of this research article.

Ethical issues: None

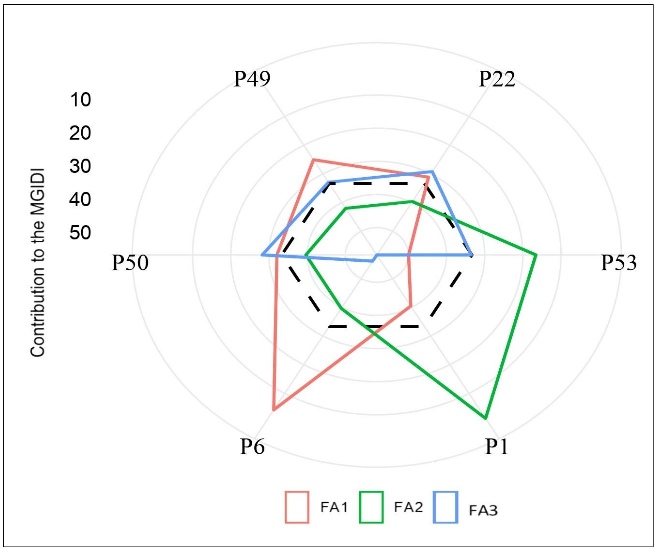

Fig. 2. Proportion of each factor on the computed Multi-trait Genotype Ideotype Distance Index of selected progenies.

Table 3. Mean performance and Multi-trait Genotype-Ideotype Distance Index of selected F_4 progenies of CO 6 × VBN 11

Sl. No.	Selected F_4 progenies	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Hundred seed weight (g)	Seed yield per plant (g)	MGIDI
1.	P1	61.00	4.00	30.00	3.00	86.00	4.70	7.33	5.10	25.85	2.61
2.	P6	48.00	5.00	19.00	4.00	90.00	5.40	7.00	5.52	28.50	2.67
3.	P22	65.00	4.00	20.00	3.00	55.00	5.40	6.33	5.73	30.20	2.17
4.	P49	59.00	3.00	21.00	4.00	73.00	4.80	7.00	5.73	21.00	3.29
5.	P50	67.00	4.00	20.00	4.00	71.00	4.60	7.00	5.44	19.00	3.05
6.	P53	73.00	3.00	28.00	3.00	84.00	4.80	7.33	5.56	20.40	2.49
	Mean	62.17	3.83	23.00	3.50	76.50	4.95	7.00	5.51	24.16	-

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