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Assessment of Genetic Parameters and Inter-relationships among Advanced Breeding Lines of Black Gram for Yield attributes

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ABSTRACT: Blackgram is the fourth most important pulse crop in India, holding a distinct place in the country's agricultural system. Blackgram production faces several constraints that hinder yield improvement and stability; to address these challenges, systematic evaluation of genetic parameters such as variability, heritability, and genetic advance is essential to identify traits with strong breeding potential. The present study was carried out during *rabi* 2021–22 at the Agricultural Research Station, Amadalavalasa, with the aim of assessing genetic variability, genotypic and phenotypic correlations, and path coefficient analysis among sixteen advanced blackgram lines for six yield-related traits, using a Randomized Complete Block Design (RCBD). Analysis of variance demonstrated significant differences among the genotypes for all traits under evaluation. High genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for days to maturity and seed yield. Days to maturity, number of branches per plant, and seed yield also showed high heritability coupled with high genetic advance as a percentage of mean, suggesting the predominance of additive gene action. Correlation studies revealed that days to maturity, number of pods per plant, and test weight were significantly and positively associated with seed yield per plant. Path coefficient analysis further indicated that days to 50% flowering, days to maturity, and number of pods per plant exerted strong positive direct effects on seed yield per plant, whereas number of branches per plant exhibited a pronounced negative direct effect. However, branches per plant and pods per plant contributed positively to yield through substantial indirect effects via days to maturity. Overall, days to maturity emerged as a key trait, as it consistently exhibited high GCV and PCV, high heritability with high genetic advance, a significant positive association with seed yield, and a strong positive direct effect. These results suggest that selection based on days to maturity would be effective for genetic improvement in blackgram, largely due to the contribution of additive gene action.

Keywords: Blackgram, Correlation, Heritability, Variability and Path Studies.

INTRODUCTION

Black gram (*Vigna mungo* L. Hepper, 2n=22) is a short-duration pulse crop belonging to the family Leguminosae, serving as an important source of dietary protein in India (Kumar *et al*., 2018). A major objective of increasing crop yields today is to meet the demands of the rapidly growing global population. With the population expanding at a rate of about 1.6–1.7% annually, nearly 95 million new consumers of agricultural products are added each year (Samghani *et al*., 2015). It is typically cultivated either as a sole crop or as a relay crop, taking advantage of residual soil moisture following rice harvest. In India, black gram occupies nearly 3.5 million hectares, with an annual production of 1.5–1.9 million tonnes and an average productivity of about 500 kg/ha (Das *et al*., 2016). Its seeds are nutritionally rich, containing 25–26% protein, 60% carbohydrates, 1.5% fat, and essential amino acids, vitamins, and minerals, owing to its high protein and lysine content, black gram plays a vital role in complementing the amino acid deficiencies of cereal-based diets (Kumari and Sangeetha 2017).

During 2019–20, India's production of black gram was estimated at 19.39 lakh tonnes, while domestic demand reached 27.5 lakh tonnes. Consequently, the country relied on imports of about 3.95 lakh tonnes, mainly from Myanmar and other sources. Exports were relatively lower, around 1.72 lakh tonnes, largely to Bangladesh, Sri Lanka, and the USA. Despite being the leading global producer, India continued to remain a net importer due to high consumption levels (Paliwal, 2020). Large tracts of rice-fallow land in India provide significant potential for expanding pulse cultivation. Nearly 11.7 million hectares of rice fallows exist, with about 20% located in southern states such as Andhra Pradesh, Tamil Nadu, and Karnataka. Broader assessments estimate over 22 million hectares across South Asia, with India contributing the majority. However, only a limited portion of this land is under pulse crops; in north coastal Andhra Pradesh, for example, just 28% of the rice-fallow area is utilized for black gram cultivation (ANGRAU, outlook 2021). The limited productivity of this crop is primarily attributed to its narrow genetic base, which restricts yield improvement. The expression and influence of any trait largely depend on the degree of genetic variability available within the breeding population (Harshit *et al*., 2021).

Current yields remain low, averaging 375–500 kg/ha. Yet, field demonstrations in Srikakulam district have shown yield gains of 14–25% when improved crop management practices were adopted. Moreover, rice–black gram relay systems have proven to be more profitable than traditional rice–rice sequences, offering an economically viable option for farmers in Andhra Pradesh (Tanveer *et al*., 2017).

Despite its importance, black gram productivity is constrained by several factors, including cultivation in marginal and rainfed soils, narrow genetic variability, photoperiod sensitivity, indeterminate growth habit, pod shattering, and susceptibility to insect pests and diseases (Gowda *et al*., 2015). Enhancing yield potential depends largely on the magnitude of genetic variability present in yield-associated traits and their heritable nature (Adhikari et al., 2018). Past studies in India using morphological traits, agronomic evaluations, and molecular markers (RAPD, ISSR, SSR) have demonstrated substantial diversity for yield and its components, often accompanied by moderate-to-high heritability and considerable genetic advance for key traits—highlighting opportunities for genetic improvement (Ramesh *et al.*, 2020).

Correlation analyses provide insights into the association between yield and its contributing characters, thereby identifying traits that can serve as effective selection criteria (Bhandari *et al*., 2017). Since direct selection for seed yield alone may not always be efficient, path coefficient analysis is widely employed to partition direct and indirect effects, offering a clearer understanding of trait interrelationships (Fischer and Rebetzke 2018). Considering this background, the present investigation focuses on assessing genetic variability, correlation, and path analysis to enhance the efficiency of black gram breeding programmes.

MATERIALS AND METHODS

The present study was carried out at the Agricultural Research Station, Amadalavalasa, during *rabi* 2021–2022. Sixteen advanced lines of black gram were obtained from different research stations under Acharya N. G. Ranga Agricultural University.

The experiment was conducted using a Randomized Complete Block Design (RCBD) with three replications, following the recommended package of agronomic practices. Each entry was sown in eight rows of four meters length, maintaining an inter-row spacing of 30 cm and intra-row spacing of 10 cm.

Data were recorded on six traits: days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, test weight (g), and seed yield (kg/ha). Observations were taken from five randomly selected plants per entry. The data were analyzed statistically using the standard analysis of variance procedure (Panse and Sukhatme 1978; Jyothsna *et al*., 2016a; Jyothsna *et al*., 2016b). Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated as per Burton (1952). Broad-sense heritability was calculated following Allard (1960) and expressed in percentage. Genetic advance as per cent of mean (GAM) was computed and classified according to Johnson *et al.* (1955). Genotypic and phenotypic correlation coefficients were derived using the method suggested by Singh and Choudhary (1985). Path coefficient analysis to assess direct and indirect contributions of yield components to seed yield was carried out based on Wright (1921), as outlined by Dewey and Lu (1959).

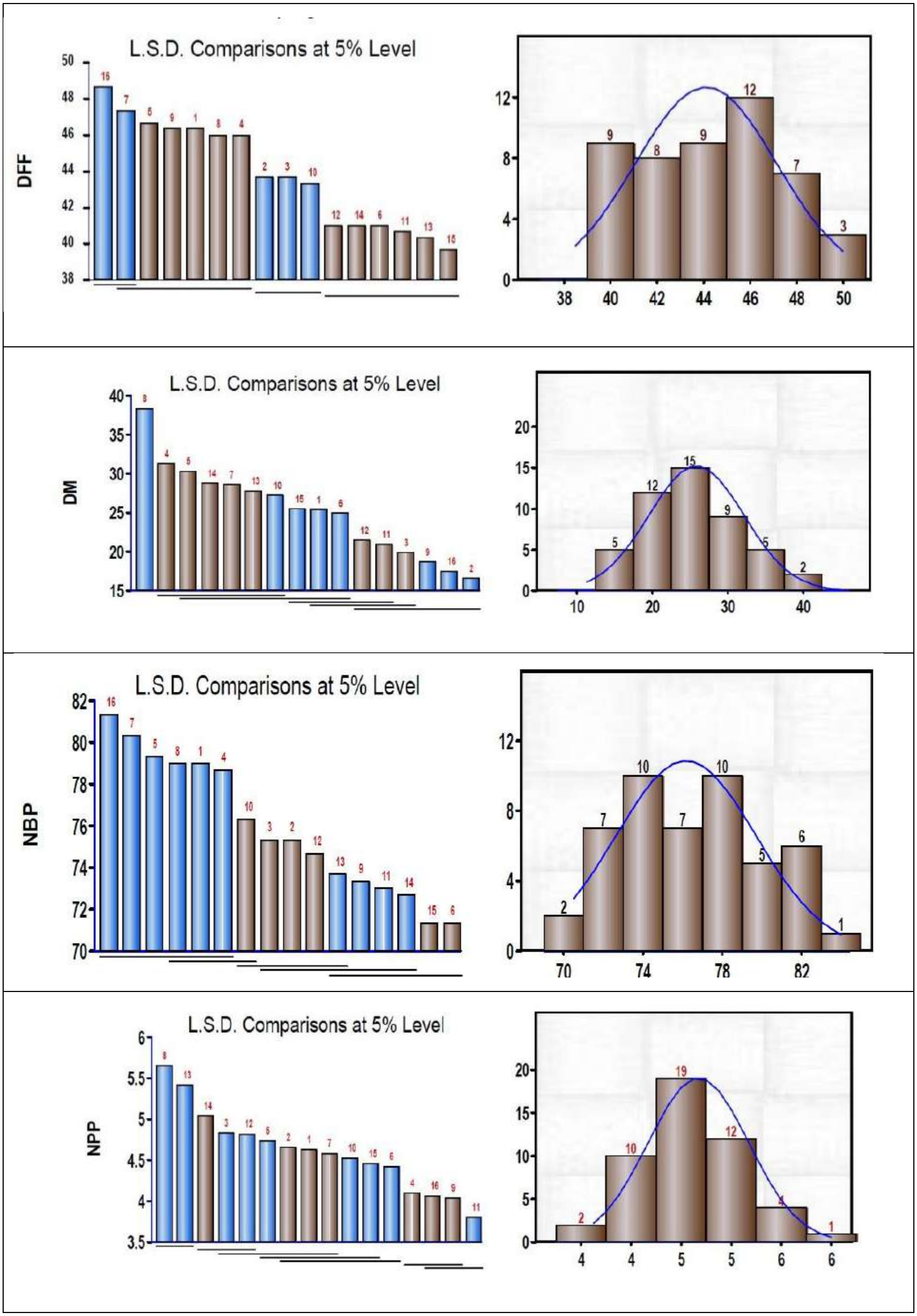
RESULTS AND DISCUSSIONS

A. Assessment of Variability and Genetic Parameters

Evaluation of variability and selection parameters forms the basis of any crop improvement programme. Genetic variability provides the essential raw material for modifying genotypes and ensures a broader base for effective selection. In the present study, the analysis of variance revealed significant to highly significant differences among the genotypes for all six traits under consideration (Fig. 1).

Genetic Parameters. Variability was assessed using the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). For most traits, PCV values were slightly higher than their corresponding GCV values, reflecting a limited role of environmental influence in trait expression (Table 1). Similar results were earlier reported by Hadimani *et al*. (2015) and Blessy *et al*. (2018).

High GCV estimates were recorded for days to maturity (21.81) and seed yield (28.86), while moderate values were observed for test weight (16.79) and number of pods per plant (10.45). Low GCV values were associated with number of branches per plant (4.12) and days to 50% flowering (6.54). Similarly, high PCV values were noted for days to maturity (25.40), test weight (31.01), and seed yield (30.91); moderate values for number of pods per plant (11.07); and low values for days to 50% flowering (7.02) and number of branches per plant (4.74).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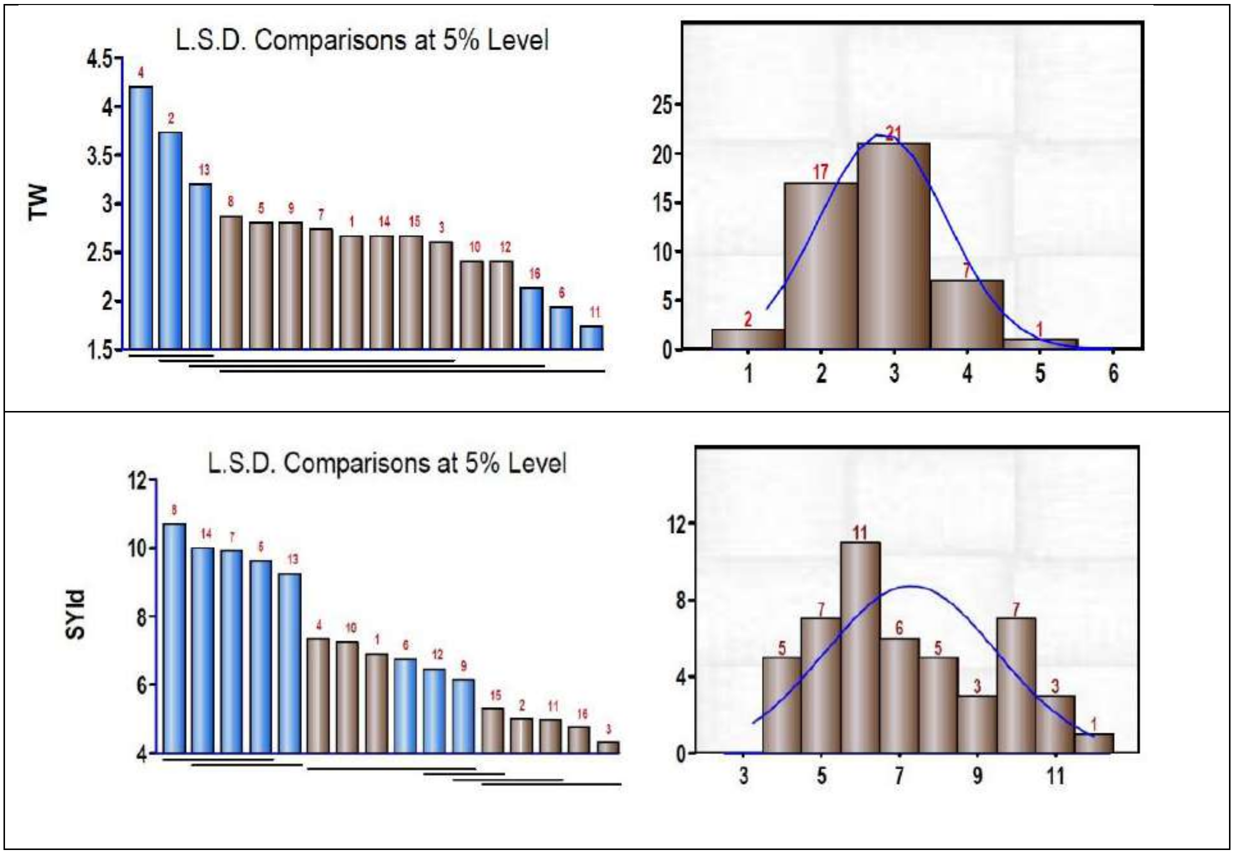


Fig. 1. The Fisher's Least Significant Difference (LSD) test and distribution of breeding material.

Table 1: Genetics Parameters of the advanced breeding lines of Black Gram.

	Days to 50 % Flowering	**Days to Maturity**	**Number of branches per plant**	**Number of pods per plant**	**Test weight**	**Seed yield**
Var Environmental	1.27	10.79	3.18	0.03	0.50	0.63
ECV	2.57	13.03	2.35	3.65	26.07	11.07
Var Genotypical	8.21	30.22	9.76	0.23	0.21	4.28
GCV	6.54	21.81	4.12	10.45	16.79	28.86
Var Phenotypical	9.49	41.01	12.94	0.26	0.71	4.91
PCV	7.02	25.40	4.74	11.07	31.01	30.91
h^2 (Broad Sense)	86.60	73.70	75.40	89.10	29.30	87.20
Genetic Advancement 5%	5.49	9.72	5.59	0.94	0.51	3.98
Genetic Advancement 1%	7.04	12.46	7.16	1.20	0.65	5.10
Gen.Adv as % of Mean 5%	12.53	38.56	7.36	20.31	18.72	55.51
Gen.Adv as % of Mean 1%	16.05	49.42	9.44	26.03	24.00	71.13
General Mean	43.85	25.21	75.92	4.61	2.72	7.17
Exp Mean next Generation	49.35	34.93	81.51	5.55	3.23	11.15

The high estimates of GCV and PCV for days to maturity and seed yield suggest their utility as selection criteria, in agreement with earlier findings (Gowsalya *et al.*, 2016 and Hemalatha *et al*., 2017). Test weight, on the other hand, showed moderate GCV but high PCV, indicating strong environmental influence also observed by Chakraborthy *et al*. (2010). Number of pods per plant exhibited moderate GCV and PCV values, as also noted by Hadimani *et al.* (2015). In contrast, both days to 50% flowering and number of branches per plant exhibited low GCV and PCV similar to Sunanya *et al*. (2017).

Heritability and Genetic Advance. Selection efficiency depends not only on variability but also on heritability estimates. Since heritability and genetic advance (GAM) are complementary, their joint consideration provides a better prediction of selection response (Johnson *et al*., 1955).

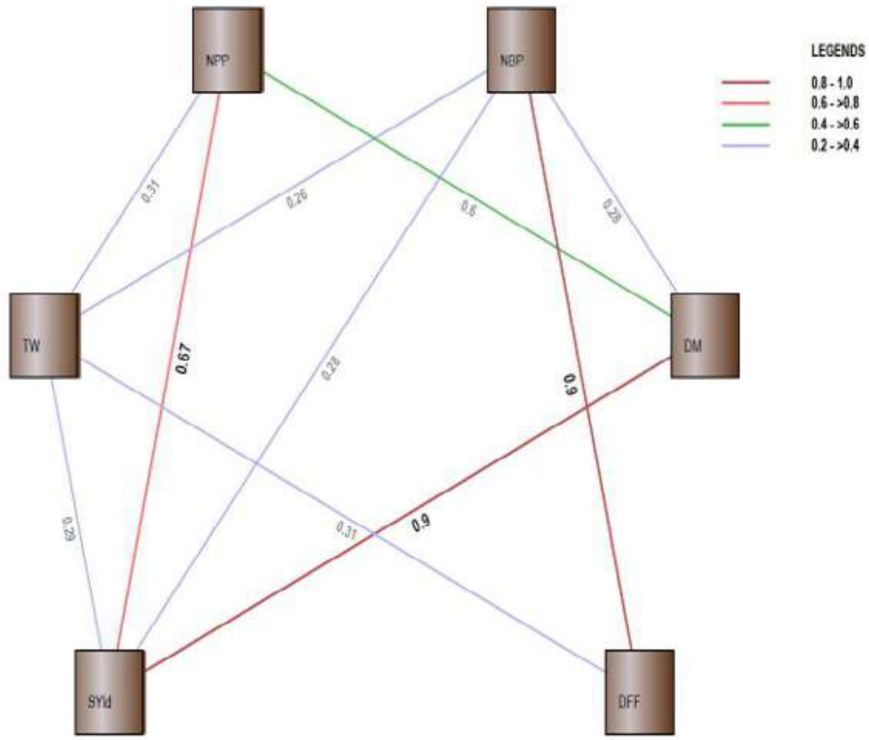
In this study, high heritability estimates were observed for days to 50% flowering (86.60), days to maturity (73.70), number of branches per plant (75.40), number of pods per plant (89.10), and seed yield (87.20), while test weight exhibited low heritability (29.30). High GAM values were recorded for days to maturity (38.56), number of pods per plant (20.31), and seed yield (55.51). Moderate GAM was observed for days to 50% flowering (12.53) and test weight (18.72), whereas number of branches per plant showed a low GAM (7.36). High heritability combined with high GAM for days to maturity, number of pods per plant and seed yield indicates the predominance of additive genetic variance, suggesting these traits are reliable for selection and genetic improvement (Sathya *et al*., 2018). Conversely, days to 50% flowering showed high heritability with moderate GAM (Bandi *et al*., 2018), test weight showed low heritability with moderate GAM (Chakraborthy *et al*., 2010) and number of branches per plant showed high heritability but low GAM.

Genotypic Correlations. Correlation analysis (Table 2) revealed that genotypic correlations were generally higher than phenotypic ones, indicating the predominance of genetic variance in trait expression. Seed yield exhibited significant positive associations with days to maturity (0.90*), number of pods per plant (0.67*), and test weight (0.29*). These results corroborate the findings of Sridhar et al. (2020) for days to maturity, Reddy et al. (2020) for number of pods per plant and Chauhan *et al*. (2018) for test weight. Among inter-trait associations, number of branches per plant showed a strong positive correlation with days to 50% flowering (0.90*), while number of pods per plant correlated significantly with days to maturity (0.60*) similar to Reddy *et al*. (2020). Test weight showed positive correlations with several traits, including days to 50% flowering (0.31*), number of branches per plant (0.26*), and number of pods per plant (0.31*). Similar patterns were observed by Bandi *et al.* (2018) for days to 50% Mathivathana *et al*. (2015) for number of branches per plant and number of pods per plant.

Path Coefficient Analysis. While correlation measures the degree of association, it does not partition direct and indirect effects. Since seed yield is influenced by multiple interrelated traits, path analysis provides a better understanding by separating these effects (Kumar *et al*., 2017). In this study, the residual effect was estimated at 0.343, indicating that the causal factors explained 65.70% of the variability in seed yield (Table 2, Fig. 2).

Table 2: Correlation and Path Studies of the advanced breeding lines of Black Gram.

	Correlation Analysis					
	Days to 50 % Flowering	Days to Maturity	Number of branches per plant	Number of pods per plant	Test weight	Seed yield
Days to 50 % Flowering	1.00					0.15
Days to Maturity	0.09	1.00				0.90*
Number of branches per plant	0.90*	0.28	1.00			0.28
Number of pods per plant	-0.18	0.60*	0.03	1.00		0.67*
Test weight	0.31*	0.19	0.26*	0.31*	1.00	0.29*
	Path Analysis					
	Days to 50 % Flowering	Days to Maturity	Number of branches per plant	Number of pods per plant	Test weight	Seed yield
Days to 50 % Flowering	**0.50**	0.05	0.45	-0.09	0.16	0.15
Days to Maturity	0.07	**0.79**	0.23	0.47	0.15	0.90
Number of branches per plant	-0.36	-0.11	**-0.40**	-0.01	-0.10	0.28
Number of pods per plant	-0.05	0.18	0.01	**0.30**	0.10	0.67
Test weight	0.00	0.00	0.00	0.00	**-0.01**	0.29



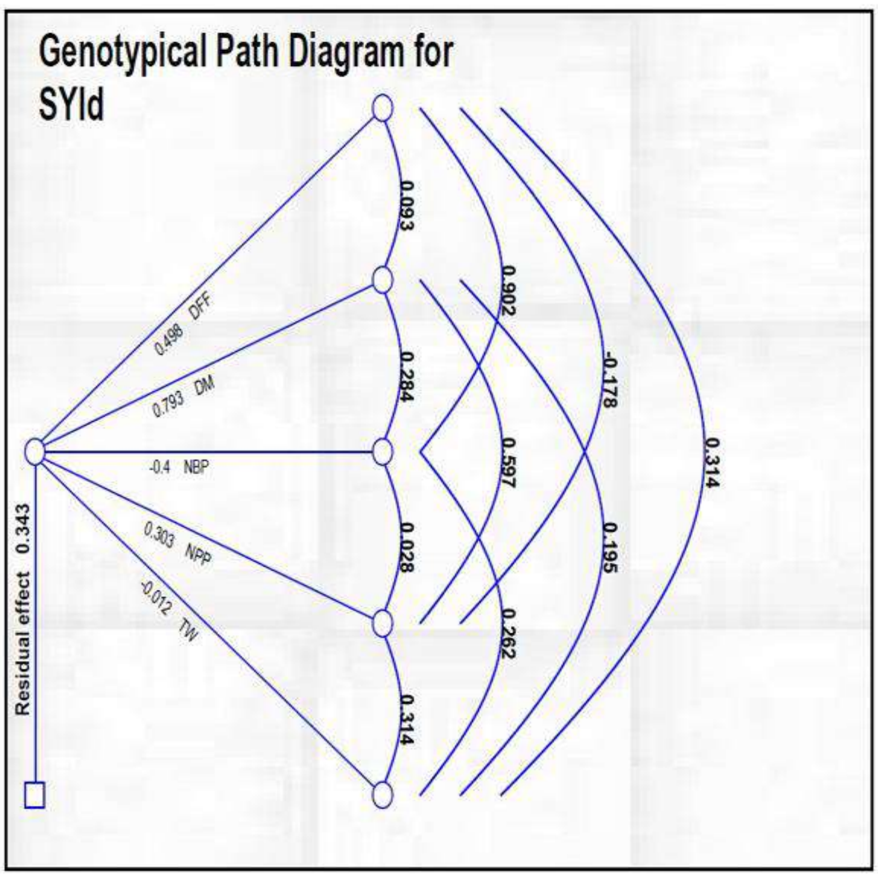


Fig. 2. Correlation and Path analysis of the advanced breeding lines of Black Gram.

The path coefficient analysis revealed that days to 50% flowering (0.50), days to maturity (0.79) and number of pods per plant (0.30) exerted high positive direct effects on seed yield. Similar findings were noted by Rajasekar et al. (2017) for days to 50% flowering and days to maturity and Sathya et al. (2018) for number of pods per plant. In contrast, number of branches per plant (-0.40) showed a strong negative direct effect similar to Arya *et al*. (2017). For days to maturity, the correlation coefficient with seed yield (0.90) was largely attributable to its direct effect (0.79), suggesting that direct selection based on this trait would be highly effective. Overall, traits with strong positive direct effects should be prioritized in selection strategies for improving seed yield in black gram.

CONCLUSIONS

The present study revealed that phenotypic variances were consistently higher than genotypic variances, indicating a considerable influence of environmental factors on trait expression. Traits with high heritability coupled with high genetic advance suggest the predominance of additive gene action, thereby ensuring greater effectiveness of selection in subsequent generations. Among all morphological and yield attributes, seed yield emerged as the most important trait. Improvement in seed yield of mungbean can be achieved by selecting component traits such as days to maturity, number of pods per plant, and test weight, which exhibited positive direct effects on yield. Among the sixteen advanced lines evaluated during *rabi* 2020–21, the entries PBG 276 (10.70 q/ha), GBG 92 (10.01 q/ha), and PBG 275 (9.92 q/ha) recorded significantly higher yields compared to the check variety LBG 787 (7.26 q/ha). These results highlight the potential of these genotypes for future breeding programmes aimed at yield improvement in black gram.

FUTURE SCOPE

Black gram generally records low yields as it is often cultivated in marginal lands with limited irrigation, poor nutrient management, and inadequate pest control. In addition, access to quality seeds of improved varieties is limited, compelling farmers to rely on locally available materials that are inconsistent in performance and highly susceptible to diseases. Considering these constraints, there is considerable potential to enhance productivity by creating and exploiting genetic variability and selecting key yield-contributing traits. Future research on genetic parameters and association studies in blackgram should therefore emphasize the integration of genomic approaches with conventional variability assessments to improve selection efficiency.

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Conflict of interest: The authors declare that they have no conflict of interest

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