



HERITABILITY, GENETIC GAIN, AND PATH COEFFICIENT ANALYSES IN BLACK GRAM AT POONCH RAWALAKOT, AZAD JAMMU AND KASHMIR

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SUMMARY

Black gram (*Vigna mungo*) is a principal pulse crop worldwide. The research aimed to screen the genetic diversity among 10 black gram genotypes using biometrical tools, such as, genotypic and phenotypic correlation, path coefficient analysis, and heritability and genetic gain. The highest genotypic and phenotypic variability resulted from pods per plant, plant height, primary branches, and seeds per pod. The study recorded very low estimated heritability for all the studied traits. The correlation coefficient indicated that seed yield per plant showed a positive and significant correlation with pods per plant and pod length, indicating that further use of these characteristics can improve the black gram yield. Path coefficient analysis revealed a positive and direct effect on seed yield per plant with plant height, days to 50% flowering, primary branches, branch length, pod per plant, and seeds per pod. These traits proved relevant for the direct selection criteria and future breeding programs. The investigation results can be very helpful in selecting the black gram's suitable genotypes with appropriate yield for cultivation in rainfed conditions of Poonch Rawalakot, Azad Jammu and Kashmir, Pakistan.

Keywords: Black gram (*Vigna mungo* L.), genotypic and phenotypic coefficient of variability, heritability, genetic gain, path coefficient analysis

Key findings: Based on the mean performance, the genotype NARC Mash-3, followed by Arooj-11, Lr. Sialkot and Lr-Samahni proved superior as these genotypes showed maximum seed yield under agro-climatic conditions of Rawalakot, Azad Jammu and Kashmirs.

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INTRODUCTION

Black gram is a commonly cultivated pulse (Nag *et al.*, 2006). This crop, widely known as “mash,” is self-pollinating with a $2n = 2 \times$ chromosome number of 22. Agro-ecologically, black gram originated from India (Mehra *et al.*, 2016). India is the biggest producer of black gram, sharing 70% of the global production on 5.0 million ha with an annual yield of 3.8 million t (Singh *et al.*, 2014; Kaewwongwal *et al.*, 2015). It is an essential source of protein (25%–28%), carbohydrates (62%–65%), fiber (3.5%–4.5%), oil (0.5%–1.5%), and amino acids like lysine, and vitamins viz., thiamine, niacin, riboflavin, including iron and phosphorus (Sohel *et al.*, 2016; Usharani and Kumar, 2016; Jegadeesan *et al.*, 2021). Black gram also plays a vital role in soil fertility and matches well in different cropping systems, i.e., dry farming and intercropping (Kaewwongwal *et al.*, 2015).

The cultivated black gram belongs to the family Leguminosae, and its chromosome number is 24. It is a day-neutral warm-season crop grown semi-arid to low land and sub-tropics. The mash bean or black gram can be a cash crop, mixed crop, and consecutive crop in residual humid conditions after rice planting and later during rice harvest under semi-watered and arid situations (Parveen *et al.*, 2011). The yield of black gram in Pakistan increased compared with the previous year (GOP, 2021). Black gram was cultivated on 11,000 ha in Pakistan during 2020–2021 with a production record of 7,000 t. The production of black gram increased by 7.7% compared with last year’s yield (Pakistan Bureau of Statistics, 2021).

The study of inheritance is crucial for developing fruitful characters by assessing genetic diversity. It includes components of variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic gain that help choose an effective breeding program for a crop. Genotypic and phenotypic associations of yield constituents and path analysis are beneficial for crop development programs and selecting the desired kinds. Heritability and genetic gain help to prompt selection criteria for developing high-yielding varieties of black gram (Rao *et al.*, 2006; Singh *et al.*, 2007). The association and path analysis information are significant for a fruitful pooling of qualitative characters. Moreover, correlation study among different yield-related traits provides important knowledge for yield constituents that help plant breeders in

selection (Robinson *et al.*, 1951; Hegde *et al.*, 2018).

Path analysis helps to find out yield components and impacts yield. Therefore, the investigation started to measure the genetic variability, association, and path coefficient evaluations of economically significant plant features and to identify the characteristics that donate to seed yield in pulses. Previously, numerous efforts assessed the degree of variability for yield and its component traits in black gram (Konda *et al.*, 2009).

In Pakistan yield of black gram is low despite their high nutritional and economic value. However, black gram cultivation existed about three decades ago in Poonch, Azad Jammu and Kashmir. Later, due to a lack of interest, its cultivation declined in Poonch, Azad Jammu and Kashmir. This research aimed to search for diverse genotypes suitable for the area for general cultivation and selection to initiate a breeding program. The study assessed the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic gain correlation coefficients, and path coefficients to define selection criteria for evolving the high-yielding genotypes of black gram. This estimates the contribution of components on yield and their association in black-gram genotypes suitable for selection and utilization for varietal improvement, recommendation of high yielding genotypes ideal for cultivation under Rawalakot conditions, and further use in hybridization programs.

MATERIALS AND METHODS

The study conducted the research in the field and the laboratory of the Department of Plant Breeding and Molecular Genetics, University of Poonch Rawalakot, Azad Kashmir, Pakistan. It obtained seeds of five black-gram genotypes from the Plant Genetic Resources Institute (PGRI), NARC Islamabad, Ayub Agricultural Research Institute Faisalabad, and Barani Agricultural Research Institute, Chakwal, Pakistan, and five landraces from different districts of Samhani, Bhimber, Mirpur, Lahore, and Sialkot, Pakistan (Table 1). These genotypes were grown in a well-prepared field under a randomized complete block design with three replications to determine the genetic diversity. The experiment prepared five rows per entry and employed uniform agronomic practices for all the genotypes by applying the fertilizer at a recommended concentration of 12.5 kg N, 25 kg P_2O_5 , and 12.5 kg of K_2O per

Table 1. List of genotypes and landraces of black gram utilized in the study.

Genotypes	Landraces
Mash-97	Lr. Bhimber
Arooj-11	Lr. Samhani
Chakwal-2000	Lr. Mirpur
NARC mash-2	Lr. Sialkot
NARC mash-3	Lr. Lahore

ha, respectively (Raju, 2019). Row length was kept at 1.2 m, while distances between rows and plants were maintained at 30 and 10 cm, respectively (Qayyum *et al.*, 2019).

Morpho-physiological traits

Recorded data on plant height (cm), days to 50% flowering, days to 50% pod setting, primary branches/plant, branch length (cm), pods/plant, pod length (cm), seed/pod, days to maturity, 100-seed weight (g), and seed yield/plant (g) were analyzed for the phenotypic and genotypic variations among the genotypes and landraces of the black gram using various biometrical techniques.

Statistical analysis

Data were computed to estimate genotypic and phenotypic coefficients of association among characters (Snedecor, 1956). Path coefficient study was calculated following Dewey and Lu (1959). Assessment of heritability (h^2) and genetic gain (G) at 5% selection intensity ($K = 2.06$) was calculated by the method reported by Allard (1960) using the following biometrical equations:

$$\sigma^2_g = \frac{MS_2 - MS_1}{r}$$

$$\sigma^2_p = \frac{MS_2}{r}$$

$$\sigma^2_e = \frac{MS_1}{e}$$

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

$$\Delta G = K\sqrt{\sigma^2_p} \times h^2$$

Where,

MS_2 = Genotype mean square

h^2 = Heritability

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

MS_1 = Error means square

G = Genetic gain

RESULTS

Genetic variability, heritability, and genetic gain in black gram genotypes

The phenotypic coefficient of variability (PCV) was greater than the genotypic coefficient of variability (GCV), and the variance clearly showed that environmental aspects had influenced the variation (Table 2). Higher values of phenotypic and genotypic coefficient of variability got detected for the pod/plant surveyed by plant height, primary divisions, and seed per pod. In contrast, lower values for the phenotypic and genotypic coefficient of variability got noted in days to 50% flowering, days to 50% pod setting, and days to 90% ripening. Moderate values for the phenotypic and genotypic coefficient of variability got also noted for branch length and seed yield/plant. Higher values of the GCV and PCV indicated that maximum variability exists, with better scope for improvement through selection. The study observed high values of ECV at seed per pod (9.916), followed by plant height (6.356) and primary branches (5.704), whereas minimum values for ECV were detected for days to 50% flowering (1.416) and days to 50% pod setting (1.136). Moderate values of ECV got recorded in branch length (3.722), pod per plant (2.913), and pod length (2.882). Higher values of ECV revealed that these characters are under the effect of the environment.

Heritability estimates revealed the maximum values for pod/plant (0.99) days to the 90% ripening (0.99), days to 50% pod setting (0.98) monitored by branch length (0.97), primary branches (0.96), seed yield per plant (0.94), pod length (0.95), seed/pod (0.93), and hundred-seed weight (0.81). Genetic gain

values were higher for days to 90% maturity (27.66), days to 50% maturity (23.98), and plant height (23.94). Values of genetic gain were lower for hundred seed weight (0.81), pod size (0.80), primary branches (1.82), seed yield per plant (1.05), branch length (2.00), and seed per pod (1.35).

Table 2. Genetic variability, heritability, and genetic gain in black gram genotypes for various traits.

Parameters	GCV	PCV	ECV	Heritability	Genetic gain
PH	32.05	32.674	6.356	0.962	23.9474
DF50%	4.653	4.864	1.416	0.915	5.4055
D50PS	10.106	10.169	1.136	0.988	23.9899
PB	31.455	31.968	5.704	0.968	1.8217
BL	22.587	22.891	3.722	0.974	2.0052
P/P	56.23	56.306	2.913	0.997	7.8633
PL	12.932	13.249	2.882	0.953	0.8066
SPP	36.759	38.073	9.916	0.932	1.3531
D90%M	10.552	10.587	0.854	0.993	27.6632
100SW	13.29	14.711	6.308	0.816	0.8199
SYPP	25.9	26.66	6.32	0.944	1.0569

GCV= Genotypic coefficient of variability, PCV= Phenotypic coefficient of variability, ECV= Environmental coefficient of variability, PH=Plant height, DF 50%=Days to 50% flowering, D50PS=Days to 50% Pod setting, PB=Primary branches, BL=Branch length, P/P=Pod to pod ratio, PL=Pod length, SPP=Seed per pod, D90%M=Days to 90% maturity, 100SW=100-seed weight, SYPP=Seed yield per plant

Correlation studies

Correlation coefficients indicate the association between traits in terms of the type and degree of association between various characteristics under study. Since selection might not be fruitful if one selects complex polygenic traits directly, one can improve complex traits indirectly by selecting clean characteristics that are positively correlated (Chitrakha *et al.*, 2018; Gandahi *et al.*, 2020). Coefficients for phenotypic and genotypic correlation project in Table 3. The correlation studies show various traits in positive and significant interrelationships. Therefore, selection procedures may utilize these traits to develop high-yielding mash genotypes under Rawalakot AJK conditions.

Plant height

Plant height displayed a helpful and significant correlation with days to 50% flowering (0.78*), branch length (0.89*), and days to 90% ripening (0.22*) at the genotypic level. Plant height shows a significant negative correlation with main branches (-0.28*), pods per plant (-0.32*), seeds per pod (-0.57*), and seed yield per plant (-0.23*) on the genotypic level. Plant height positively

correlates with pod size (0.07) and 100-seed weight (0.11). Plant height showed a highly significant and helpful connection with days to 50% flowering (0.74**) and branch size (0.86**) at the phenotypic level. The plant height exhibited a negative but highly significant correlation with seeds per pod (-0.55**) at the phenotypic level, indicating that plant height had no significant relation with seeds per pod. Plant height also exhibited positive but significant non-association with days to 50% pod setting (0.28), pod size (0.06), days to 90% ripening (0.22), and 100-seed weight (0.05) on the phenotypic level. Similarly, plant height showed a negative and non-significant association with main twigs (-0.27), pod/plant (-0.32), and seed yield/plant (-0.22) at the phenotypic level.

Days to 50% flowering

Days to 50% flowering showed positive and significant association with days to 50% pod setting (0.37*), branch length (0.69*), and days to 90% maturity (0.42*) on the genotypic level. Days to 50% flowering showed harmful and significant association with pod/plant (-0.34*), seed/pod (-0.23*), and seed yield/plant (-0.52*) at the genotypic level. Days to 50% flowering showed positive and

Table 3. Estimation of genotypic and phenotypic correlation coefficient in black gram genotypes.

Parameter	Correlation coefficient	PH	D50F	D50PS	PB	BL	P/P	P L	SPP	D90%M	100SW	SYPP
PH	G	1	0.78*	0.28*	-0.28*	0.89*	-0.32*	0.07	-0.57*	0.22*	0.11	-0.23*
	P	1	0.74**	0.28	-0.27	0.86**	-0.32	0.06	-0.55**	0.22	0.05	-0.22
D50F	G		1	0.37*	0.13	0.69*	-0.34*	0	-0.23*	0.42*	0.04	-0.52*
	P		1	0.35	0.14	0.67**	-0.32	-0.01	-0.21	0.40*	0.01	-0.49**
D50PS	G			1	0.31*	0.39*	0.12*	0.68*	-0.41*	0.62*	0.77*	-0.36*
	P			1	0.29	0.38*	0.12	0.65**	-0.39*	0.61**	0.69**	-0.34
PB	G				1	-0.26*	0.21*	0.33	0.75*	0.29*	0.09	-0.26
	P				1	-0.24	0.21	0.32	0.72**	0.28	0.07	-0.25
BL	G					1	-0.61*	0.07	-0.59*	0.47*	0.19	-0.64*
	P					1	-0.59**	0.07	-0.56**	0.46*	0.17	-0.61**
P/P	G						1	0.59*	0.28*	-0.43*	0.27*	0.72*
	P						1	0.58**	0.27	-0.43	0.25	0.69**
PL	G							1	-0.05	-0.04	0.69*	0.12
	P							1	-0.04	-0.04	0.63**	0.09
SPP	G								1	-0.21*	-0.34	0
	P								1	-0.19	-0.26	0
D90%M	G									1	0.24*	-0.77*
	P									1	0.23	-0.75**
100SW	G										1	-0.18
	P										1	-0.17
SYPP	G											1
	P											1

G= Genotypic correlation coefficient, P= Phenotypic correlation coefficient, GCV= Genotypic coefficient of variability, PCV= Phenotypic coefficient of variability, ECV= Environmental coefficient of variability, PH=Plant height, DF 50%=Days to 50% flowering, D50PS=Days to 50% pod setting, PB=Primary branches, BL=Branch length, P/P=Pod to pod ratio, PL=Pod length, SPP=Seed per pod, D90%M=Days to 90% maturity, 100SW=100-seed weight, SYPP=Seed yield per plant

significant results with main branches (0.13) and 100-seed weight (0.04) at the genotypic level. Days to 50% flowering exhibited harmful and non-significant outcomes with pod size (-0.00) at the genotypic level. Days to 50% flowering displayed supportive and highly significant results with branch length (0.67**) on the phenotypic level. Days to 50% flowering exhibited positive and relevant results with days to 90% ripening (0.40*) at the phenotypic level. Days to 50% flowering revealed effective and non-significant results with days to 50% pod setting (0.35), main branches (0.14), and 100-seed weight (0.01) at the phenotypic level. Days to 50% flowering exhibited harmful and highly significant results with seed yield per plant (-0.49**) at the phenotypic level. Days to 50% flowering showed toxic and non-significant results with pod/plant (-0.32), pod length (-0.01), and seed per pod (-0.21) at the phenotypic level.

Days to 50% pod setting

Days to 50% pod setting showed significant positive results with primary branches (0.31*), branch length (0.39*), pod/plant (0.12*), pod size (0.68*), days to 90% ripening (0.62*), and 100-seed weight (0.77*) on the genotypic

level. Days to 50% pod setting showed positive and significant results with seed per pod (-0.41*) and seed yield per plant (-0.36*) at the genotypic level. Days to 50% pod exhibited useful and highly significant results with pod size (0.65**), days to 50% ripening (0.61**), and 100-seed weight (0.69**) at the phenotypic level. Days to 50% pod seeding showed positive and significant results with branch size (0.38*) on the phenotypic level. Days to 50% pod setting presented harmful effects with primary twigs (0.29) and pod/plant (0.12) on the phenotypic level. Days to 50% pod setting displayed harmful but major results with seed/pod (-0.39*) at the phenotypic level. Days to 50% pod setting displayed harmful and non-significant results with seed yield/plant (-0.34).

Primary branches

Primary branches exhibited beneficial and significant results with pod/plant (0.21*), seed/pod (0.75*), and days to 90% maturity (0.29*) at the genotypic level. Primary branches showed positive but non-significant results with pod size (0.33) and 100-seed weight (0.09) on the genotypic level. Primary branches showed negative and non-significant

results with seed yield/plant (-0.26) at the genotypic level. Primary branches showed advantageous and highly significant effects with seed/pod (0.72**) at the phenotypic level. Primary branches showed effective and non-significant results with pod per plant (0.21), pod size (0.32), and days to 90% maturity (0.07) at the phenotypic level. Primary branches exhibited harmful and non-significant results with branch size (-0.24) and seed yield/plant (-0.25) at the phenotypic level.

Branch length

Branch length displayed a helpful and significant association with days to 90% ripening (0.47*) at the genotypic level. Branch length revealed a harmful and substantial connection with pod distance (-0.61*), seed/pod (-0.59*), and seed yield/plant (-0.64*) at the genotypic level. Branch size displayed a positive and non-significant connection with pod size (0.07) and 100-seed weight (0.19) on the genotypic level. Branch size exposed a positive and significant relationship with days to 90% ripening (0.46*) at the phenotypic level. Branch length presented a harmful and highly expressive association with pod/plant (-0.59**), seed/pod (-0.56**), and seed yield per plant (-0.61**) in the phenotypic stage. Branch length exposed positive and non-significant connection with pod size (0.07) and 100-seed weight (0.17) at the phenotypic level.

Pod per plant

Pods per plant displayed positive and significant results in pod length (0.59*), seed/pod (0.28*), 100-seed weight (0.27*), and seed yield/plant (0.72*) at the genotypic level. Pod/plant presented negative and significant results with days to 90% ripening (-0.43*) at the genotypic level. Pod per plant exposed helpful and highly relevant connection to pod size (0.58**) and seed yield/plant (0.69**) in the phenotypic stage. Pod/plant displayed helpful and non-significant association through seed/pod (0.27) and 100-seed weight (0.25) at the phenotypic stage. Pod/plant presented a harmful and non-significant association with days to 90% ripening (0.43) on the phenotypic level.

Pod length

Pod length displayed a helpful and significant association with 100-seed weight (0.69*) at the genotypic level. It showed a supportive and non-significant association with the seed yield/plant (0.12) and a negative and non-significant connection at seed/pod (-0.05) and days to 90% ripening (-0.04) at the genotypic level. Pod length exposed positive and highly significant results with 100-seed weight (0.63**) in the phenotypic stage. Pod size presented a helpful and significant association with seed yield/plant (0.09). It exhibited harmful and non-significant results with seed/pod (-0.04) and days to 90% maturity (-0.04) at the phenotypic level.

Seeds per pod

Seeds per pod exhibited a negative and significant connection with days to 90% maturity (0.21) on the genotypic level. It presented a harmful and non-significant association with 100-seed weight (-0.34) and seed yield/plant (-0.00) on a genotypic level. Seed per pod showed a negative and significant connection with seed yield/plant (0.00) on the phenotypic level. Days to 90% ripening (-0.19) and 100-seed weight (-0.26) exposed negative and nonsignificant associations in the phenotypic stage.

Days to 90% maturity

Days to 90% ripening exhibited a positive and significant association with 100-seed weight (0.24*) and a negative and noteworthy relationship with seed yield/plant (-0.77*) on the genotypic level. Days to 90% ripening displayed a negative and highly significant connection with seed yield/plant (-0.75**) and a positive and non-significant relationship with 100-seed weight (0.23) on the phenotypic level.

100-seed weight

A hundred-seed weight displayed a negative and non-significant connection with seed yield/plant (-0.18) at the genotypic level and uncovered a contrasting and non-significant association with seed yield/plant (-0.17) at the phenotypic level.

Path coefficient analysis

The path coefficient analysis investigated both the direct and indirect effects to get a clear insight into the yield components on grain yield (Table 4). Seed yield/plant showed a direct and positive effect on plant height (0.80), days to 50% pod setting (2.13), main branches (0.34), branch length (0.31), pods/ plant (0.94), and seeds/pod (0.10). Negative and direct outcome at seed yield/plant was affected by days to 50% flowering (-1.19), pod length (-1.71), days to 90% ripening (-1.50), and 100-seed weight (-0.62).

The 100-seed weight showed a positive and indirect effect on plant height (0.08), days to 50% pod setting (1.64), primary twigs (0.03), branch size (0.06), pods/plant (0.25), whereas 100-seed weight had a negative and indirect effect on days to 50% flowering (-0.04), pod length (-1.19), seed/pod (-0.03), and days to 90% maturity (-0.36). Days to 90% maturity have a positive and indirect influence on plant length (0.18), days to 50% pod setting (1.31), primary branches (0.10), branch length (0.15), and pod length (0.07). Days to 90% maturity have a negative and indirect effect on days to 50% flowering (-0.50), pod/plant (-0.40), seed/pod (-0.02), and 100-seed weight (-0.15).

Seeds/pod have positive and indirect influence on days to 50% flowering (0.26), primary branches (0.25), pod/plant (0.26), pod size (0.08), days to 90% ripening (0.31), and 100-seed weight (0.21). Seed/pod has a negative and indirect effect on branch size (-0.18), plant height (-0.46), and days to 50%

pod setting. Pod length exerted positive and indirect effect on plant height (0.05), days to 50% flowering (0.00), days to 50% pod setting (1.45), primary branches (0.11), branch length (0.02), pod/plant (0.55), and days to 90% maturity (0.06). Pod/plant has negative and unplanned effects on 100-seed weight (-0.43) and seed/pod (-0.00).

An indirect effect of pod/plant existed on days to 50% flowering, days to 50% pod setting (0.26), primary branches (0.07), seed/pod (0.03), and days to 90% maturity (0.64). Pod/plant has negative and indirect effect on 100-seed weight (-0.17), branch size (-0.19), plant height (-0.26), and (-1.01). Branch size positively and indirectly affects plant height (0.72) and days to 50% pod setting (0.82). Branch length gave a negative and indirect effect on primary branches (-0.08), seed/pod (-0.06), pod length (-0.11), 100-seed weight (-0.12), pod/plant (-0.57), and days to 50% flowering (-0.82).

Primary branches have a positive and indirect effect on days to 50% flowering (0.65), pod/plant (0.20), and seed/pod (0.08). Primary branches have a negative and indirect result on 100-seed weight (-0.05), branch distance (-0.08), days to 50% flowering (-0.15), days to 90% maturity (-0.44), plant height (-0.22), and pod length (-0.57). Days to 50% pod setting indicated indirect effect on plant length (0.22), primary branches (0.10), branch size (0.12), and pod/plant (0.11). Days to 50% pod setting has a negative and indirect effect on days to 50% flowering (-0.43), 100-seed weight (-0.48), days to 90% maturity (-0.92), and plant height (-1.17).

Table 4. Direct and indirect effect of seed yield per plant in black gram genotypes.

Traits	PH	D50F	D50PS	P B	BL	P/P	PL	SPP	D90M	100SW	Gen. Cor
PH	0.8099	-0.9328	0.5948	-0.0954	0.2827	-0.3036	-0.1176	-0.0624	-0.3358	-0.0695	-0.2295
D50F	0.6330	-1.1935	0.7784	0.0442	0.2199	-0.3209	0.0061	-0.0247	-0.6382	-0.0255	-0.5212
D50PS	0.2259	-0.4356	2.1327	0.1044	0.1232	0.1170	-1.1726	-0.0443	-0.9267	-0.4849	-0.3609
PB	-0.2263	-0.1547	0.6523	0.3413	-0.0827	0.2027	-0.5751	0.0816	-0.4447	-0.0562	-0.2619
BL	0.7213	-0.8266	0.8275	-0.0889	0.3175	-0.5718	-0.1150	-0.0641	-0.7136	-0.1244	-0.6381
P/P	-0.2606	0.4060	0.2645	0.0733	-0.1924	0.9433	-1.0178	0.0304	0.6429	-0.1712	0.7183*
P L	0.0555	0.0042	1.4577	0.1144	0.0213	0.5596	-1.7155	-0.0052	0.0620	-0.4372	0.1169*
SPP	-0.4630	0.2698	-0.8642	0.2550	-0.1862	0.2624	0.0816	0.1092	0.3184	0.2141	-0.0030
D90M	0.1808	-0.5062	1.3136	0.1009	0.1506	-0.4031	0.0707	-0.0231	-1.5046	-0.1507	-0.7712
100SW	0.0895	-0.0483	1.6443	0.0305	0.0628	0.2569	-1.1927	-0.0372	-0.3605	-0.6289	-0.1836

PH=Plant Height, DF 50%=Days to 50% Flowering, D50PS=Days to 50% Pod Setting, PB=Primary Branches, BL=Branch Length, P/P=Pod to Pod ratio, PL=Pod Length, SPP=Seed per Pod, D90M=Days to 90% Maturity, 100SW=100-seed Weight, SYPP=Seed Yield per Plant

Days to 50% flowering showed indirect influence on plant height (0.63), days to 50% pod setting (0.77), primary branches (0.04), branch length (0.21), and pod size (0.00). Days to 50% flowering gave a negative and indirect effect on 100-seed weight (-0.02), seed/pod (0.02), pod/plant (-0.32), and days to 90% maturity (-0.63). Plant height exhibited positive and indirect outcomes on the days to 50% pod setting (0.59) and branch size (0.28). Plant height had a negative and indirect effect on 100-seed weight (-0.06), seed/pod (-0.06), pod/plant (-0.30), days to 90% ripening (-0.33), and days to 50% flowering (-0.93).

DISCUSSION

Genotypic variation proves vital to assess the performance of various genotypes under a specific environmental condition. The results showed a considerable variation among blackgram genotypes concerning their means. Higher PCV and GCV determined the magnitude of traits' variation (Ashfaq *et al.*, 2014). However, the coefficient of variation indicated that PCV was higher than GCV, which showed the environment's influence on these traits. Studies noted higher PCV than GCV observations in other pulses, such as lablab beans (Adnan *et al.*, 2021) and mungbean (Ahmad *et al.*, 2012).

The findings seem comparable with the previous results by Priyanka *et al.* (2016) and Hemalatha *et al.* (2017). They pointed out that the traits showing higher values of heritability and genetic gain were principally under the control of additive genes. Therefore, the collection of such as these would be very effective for grain yield improvement by their simple selection. The reasonably high values of heritability and low genetic gain for characters pointed out the existence of the non-additive gene action, thus, confirming the role of the environment in the expression of such traits. Therefore, those characteristics that manifested higher estimations of genetic gain needs more preference in designing a selection strategy. The selection based on these characteristics would prove helpful in improving gain by mere selection. Hence, an effective advancement results by adopting an appropriate selection process. According to Degefa *et al.* (2014), days to 50% flowering in mungbean genotypes showed a low genotypic coefficient of variability, which indicated that environmental effects are more than genetic ones. Low heritability indicated that traits are under high ecological impacts.

The research results also agree with the findings of Kumar *et al.* (2015) that the environmental or abiotic effects highly influence these concerned characteristics as compared with the genetic one; therefore, mere phenotypic selection shows unrewarding on genotypic effect. Days to 90% ripening and days to 50% maturity showed higher values of genetic gain; hence, one can infer that all these characteristics might have additive gene effects. This trait proves essential in future selection for improved traits in various genotypes. According to Arulbalachandran *et al.* (2010), heritability plays a significant part in determining the suitability for the selection of atmosphere. The parameters which show higher counts for heritability and genetic gain could be selected directly or manipulated according to requirements, thus, attaining progress through further selection procedures. However, heritability estimates presented in the study are single season-based estimated data, so one can expect a bias unless a negligible genotype-by-environment interaction in non-crossover types existed. However, it is hardly correct for the quantitative traits of agronomical significance (Priyanka *et al.*, 2016). Therefore, researchers suggested validating further the heritability estimates acquired. Hence, future studies need replication on multiple localities, representing some targeted environments or microclimates for three to four years.

Correlation analysis determines the relationship among two or more independent variables (Ahmad *et al.*, 2012; Naseer *et al.*, 2015). Plant breeding and genetics correlation analysis estimate the importance of different characters (Ahmad *et al.*, 2012). Further research proved that positive and significant correlations between plant traits could help select desirable traits in breeding programs (Naseer *et al.*, 2015). The plant height showed a positive and significant correlation with days to 50% flowering, days to 50% pod setting, branch length, pod length, days to 90% plant maturity, and 100-seed weight at phenotypic and genotypic levels. However, this trait negatively correlated with primary branches, pods per plant, seeds per plant, and seed yield per plant. Hence, the study asserts that plant height is negatively associated with yield-related traits.

Previous studies reported a negative association of plant height with yield in mungbean (Ahmad *et al.*, 2012; Javed *et al.*, 2014), wheat (Ashfaq *et al.*, 2014), and rice (Naseer *et al.*, 2015). Seeds per pod showed a negative correlation with 100-seed weight,

indicating that the number of seeds per pod reduces the seed weight. Javed *et al.* (2014) also reported a similar result in mungbean. According to results of this study, 100-seed weight displayed a negative and non-significant association with yield per plant at both phenotypic and genotypic levels, which contrasted with previous research. Such type variation might be due to environmental factors. Correlation coefficient estimates represent the nature and extent of association between given pairs of traits (Adnan *et al.*, 2021). However, a path coefficient study involves an effective biometrical technique designed to determine the inter-relationship of various components, including their interaction's direct and indirect effects on yield (Joshna *et al.*, 2021). The study's results for plant height with pod per plant agree with the past studies, which reported for 100-seed weight and days to development, suggesting that the traits with positive and significant correlation could be used for designing selection criteria in future breeding programs to increase the grain yield (Santha *et al.*, 1999; Nagarjuna *et al.*, 2001). Similar findings have also been previously reported in wheat (Kumar *et al.*, 2013).

According to Punia *et al.* (2014), the non-significant correlation between plant height and 100-seed weight proposed that tall and broad-seeded genotypes were not much desired for attaining the enhanced seed yield in the mash. These results indicate that the environments affect such traits more in black-gram genotypes than in genetic effects. Results also matched past investigations, which revealed that days to 50% pod setting had a positive and significant correlation with plant height, number of branches, and pod length at the genotypic level (Joshna *et al.*, 2021). So these traits could be utilized for further selection criteria for breeding high-yielding black gram genotypes. According to Punia *et al.* (2014), branches per plant did not show any positive or significant correlation with other traits at the genotypic and phenotypic levels. It indicates that environmental factors might have imposed such variation and association among these traits of agronomic importance. However, this study confirmed the report by Devi *et al.* (2021), who presented a positive correlation at the genotypic level with pod/plant and seed/pod. Therefore, in performing selection, preference must be given to such traits only after path analysis in replicating this research on different locations for three to four years to get fruitful results in improving yield in black gram. Chauhan *et al.*

(2007) previously conducted a similar study and found that seed yield per plant showed a strong positive link with the number of pods per plant, number of seeds per pod, plant height, and number of primary branches per plant.

According to Joshna *et al.* (2021), pods per plant showed a positive and highly significant correlation with number of seeds per pods, seed index, and harvest index at the genotypic level. Thus these traits may directly contribute to yield; hence, they could be used as a selection criterion. Other studies investigated that pod length does not show any positive and significant correlation with any other trait at the genotypic level. Still, at the phenotypic level, it showed a positive and highly significant correlation with biological yield (Joshna *et al.*, 2021). Therefore, after rigorous evaluation of available genotypes under given variable climatic conditions, pod length and size must be detected before selecting and hybridizing black gram.

Mehra *et al.* (2016) also reported that seeds per pod were insignificant in connection with seed yield per plant. Hence, the suggestion that seeds per pod need not be selected as a parameter for selecting and developing high-yielding genotypes in black gram. Usha and Sakharama (1981) have presented similar results on the black gram. Similarly, Mehra *et al.* (2016) previously observed a highly positive correlation between seeds per plant and days to maturity, so it could be an effective parameter for selecting high-yielding genotypes of mash beans.

The correlation coefficients define only the connection between the yield and other yield-crediting traits; however, it cannot show the direct and indirect effects of different traits on yield. It is because the positively correlated characters are linked to other component traits and do not put impact themselves. Hence, to get an insight into yield's direct and indirect association with other characteristics, path coefficient analysis is required and must be considered by breeders (Baisakh *et al.*, 2014; Devi *et al.*, 2021).

Path coefficient analysis supports the assessment of each variable's impact on the resultant variable directly and indirectly by partitioning the genetic correlation coefficients (Ashfaq *et al.*, 2014; Sridhar *et al.*, 2020; Adnan *et al.*, 2021). Previously, Chauhan *et al.* (2007) performed path analysis and identified the number of pods per plant, followed by number of seeds per pod, and 100-seed weight were the chief direct contributing

characteristics toward the phenotypic expression of seed yield per plant.

Similarly, a study of lablab beans also recorded a negative correlation of seed yield with yield-related traits (Adnan *et al.*, 2021). Since such traits are more physiological, the days to flowering and days to ripening are much affected by environmental factors such as daylight and temperature, so they may not be essential when setting selection criteria in legumes. The study findings strongly coincide with Singh *et al.* (2009), who recorded that the days to maturity had a high level of positive effects on seed yield through pods/plant and days to 50% flowering; however, they showed indirect effects via clusters per plant and plant height in mung bean. Such negative and positive indirect impacts by the yield components on seed yield through one or other traits reveals a complex pattern where conciliation is necessary to achieve an equilibrium of various yield components for finding an ideotype to enhance higher seed yield.

The study findings further confirm the earlier reports by Reni *et al.* (2013) and Saran *et al.* (2020); hence, selection for the traits viz., the number of pods per plant, the number of seeds per pod, seed weight per plant, and pod size had a high positive effect. Direct effect on seed yield per plant would be rewarding in improving the black-gram seed yield. Same findings for pod length, pod per plant, branch size, days to 50% pod setting, days to 50% flowering, and interaction with other traits studied here got reported by Das (1978), Rai *et al.* (2006), Malik *et al.* (2008), and Ahmad *et al.* (2012). The plant height negatively and indirectly affected seed yield. Veeranjanyulu *et al.* (2007) found the same results in their research. They indicated no effect of the plant height on the seed yield in black gram and may be disregarded in setting selection criteria for yield improvement programs.

CONCLUSIONS

Phenotypic and genotypic association, path coefficient study, heritability, and genetic gain got observed. Results showed the traits' PCV was higher than GCV. Further variability at genotypic and phenotypic levels was highest in pod per plant, plant height, primary branches, and seeds per pod. Heritability was low for all characters. The correlation constant indicated that seed yield per plant showed a positive and significant association with pods per plant and

pod length suggesting that these parameters can be utilized for breeding purposes to enhance the production of black gram. Seeds per pod were negatively associated with 100-seed weight, hence, the conclusion that higher seeds per pod negatively affected the seed weight. Path coefficient analysis discovered positive and non-stop effects on seed yield per plant with plant height, days to 50% flowering, primary branches, branch length, pods per plant, and seeds per pod. NARC Mash 3, followed by Arooj-11, Lr. Sialkot, and Lr-Samahni were found superior since these genotypes gave maximum seed yield under agro-climatic conditions of Rawalakot, Azad Jammu and Kashmir. Hence, based on the findings, the pre-breeding lines exhibiting enhanced mean values for yield assigning traits need further research in the breeding programs to develop high-yielding varieties of black gram.

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