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Morphological characterization and evaluation of Himalayan landraces of blackgram (*Vigna mungo* (L.) from North-Western plain zone for yield and its component traits

Alka Soharu*, R.K. Mittal, V.K. Sood and Navdeep Kaur
Department of Genetics and Plant Breeding, College of Agriculture,
CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062, India.

*Corresponding author; alkasoharu5@gmail.com

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Abstract

Blackgram is not only a rich source of protein, vitamins and minerals especially in the vegetarian diet but is also utilized as fodder. In any breeding and varietal development programme variability is the prime requirement to acquire favorable gene combinations in segregating generations. Keeping this in view, 23 black gram landraces were evaluated during *kharif* 2021 at two distinct locations *viz.*, KVK Berthin (Location-1) and Palampur (Location-2) using Randomized Block Design (RBD) in two replications to determine the extent of morphological variation among landraces by using 18 DUS parameters as well as genetic variability. The data was recorded for 11 polygenic characters *viz.*, days to 50% flowering, days to 75% maturity, plant height, branches per plant, biological yield per plant, harvest index, seeds per pod, pods per plant, pod length, 100-seed weight and yield per plant. On the basis of DUS characterization, these genotypes were classified into distinct groups for nine trait and may be used as reference genotypes and grouping in hybridization programs for the production of improved varieties. The analysis of variance revealed significant variations for all yield and its component traits evaluated in each environment as well as the pooled environment. In the current investigation, values of PCV were observed to be higher than GCV for all of the traits under consideration, albeit with a very minor difference, demonstrating that GCV and PCV have a tight correlation and less influence of environment on the traits under investigation. As a conclusion, attributes with a great degree of variability; a meaningful selection based on phenotype would not be misleading. High heritability was found to be associated with higher genetic advance for biological yield per plant and harvest index, demonstrating the dominance of additive gene action, thus, referring advantages selection of these traits.

Key words: Blackgram, Genetic variability, GCV, PCV, Heritability, Genetic advance

Black gram (2n=2x=22) is an essential short-term legume crop cultivated over a broad spectrum of agro-ecological conditions and cropping patterns following wide range of agricultural techniques. The crop is especially popular because of its compatibility with multiple cropping schemes as well as the ability to grow both in arid and humid environments. It is a significant grain legume crop in Asian countries, extensively grown on shallow lands with little input during *kharif* and *rabi* seasons. It forms an important source of protein, vitamins, minerals, whilst the exploitation of plant components as fodder. Black gram, like any other pulse crops, enriches soil nitrogen content, which aids in soil fertility reclamation. Traditionally, cultivation of black gram was restricted to Southern Asia including adjoining nations such as India, Afghanistan, Pakistan, Myanmar and Bangladesh. The blackgram production worldwide is estimated to be around 8.5 million tonnes (Anonymous 2018a). In India it is cultivated over an area of 4.49 million hectare with the production of 2.93 million tonnes (Anonymous 2017), while in Himachal Pradesh it is grown over an area of 12 thousand hectare with the production of 9.4 thousand tonnes (Anonymous 2018b).

In North-Western Himalayan climatic circumstances, black gram is quite well adapted in rice-pulse as well as maize-pulse cropping pattern, particularly to preserve soil fertility. Notwithstanding its prominence, there is indeed a significant disparity between current and possible productivity, which is primarily attributed toward its exposure to environmental perturbations as well as the lack of significant high yielding and robust cultivars. Especially compared to other pulse crops black gram productivity is quite poor. Utilization of landraces and breeding lines is critical for the development of improved varieties *via* hybridization. The comprehensive collection of black gram genes favoring high production became eliminated due to the dominant function of biological evolution, as well as the genetic base of today's population stays poor due to the lack of genetic variation primarily owing to its self-pollinated nature. Manipulating variability in legumes has been extensively utilized as a promising means to increase the variability. The preponderance and accessibility of variation in the genotypes of specific species of plants is indeed the fundamental basis for a successful crop improvement project (Soharu & Pandey 2019). As a consequence, the present study was undertaken to evaluate genetic variability, heritability, and genetic progress in order to identify superior genotypes for prospective use in breeding strategies.

Materials and Methods

Plant material and field experiments

Twenty-one landraces were characterized using the blackgram descriptors from PPV & FRA, New Delhi. During the vegetative and reproductive stages, 19 DUS parameters were measured. For genetic variability experimental material consisted of twenty-three genotypes comprising of twenty land races obtained from multiple black gram cultivated areas as well as CSK HPKV, Himachal Pradesh, India and three check varieties *viz*., Him Mash-1, HPBU-111, & Palampur-93 (Table 1). Field studies were undertaken at two unique sites: KVK, Berthin (Location-1) and

Table 1. List of blackgram genotypes used in investigation

Sr. No.	Genotype	Place	District	Latitude /Longitude
1	G1	Chamba1	Chamba	32.5 ° N /76.1 ° E
2	G2	Renuka	Sirmour	30.6° N/ 77.4° E
3	G3	Nagrota Suriyan	Kangra	32.0° N/ 76.0° E
4	G4	Shillai	Sirmour	30.6° N/ 77.7° E
5	G5	Village Mainzha	Kangra	32.1° N/ 76.5° E
6	G6	Kullu1	Kullu	31.9° N /77.1° E
7	G7	Kullu2	Kullu	31.8° N /77.1° E
8	G8	Chamba2	Chamba	32.5 ° N /76.1 ° E
9	G9	Barot-valley	Mandi	32.0° N/ 76.8° E
10	G10	Kullu-local	Kullu	31.9° N /77.1° E
11	G11	Haripur	Kullu	32.1° N/ 77.1° E
12	G12	Village Thalla	Chamba	35.5° N /76.1° E
13	G13	Village Deoki	Chamba	32.4° N /76.4° E
14	G14	Gatiyala Di Dhar	Chamba	32.4° N /76.0° E
15	G15	Village Sodi	Chamba	32.4° N /76.5° E
16	G17	Nagrota Bagwan	Kangra	32.1° N/ 76.3° E
17	G18	Karsog	Mandi	31.3° N/ 77.2° E
18	G19	Bharmour-1	Chamba	32.4° N /76.5° E
19	G20	Sadar	Bilaspur	31.3° N/ 76.6° E
20	G21	Bharmour-2	Chamba	32.4° N /76.5° E
21	Him Mash-1	Pure line selection from local material of Himachal Pradesh by CSKHPKV, Palampur		
22	Palampur-93	Pure line selection from local material of Himachal Pradesh by CSKHPKV, Palampur		
23	HPBU-111	Pure line selection from local material of Himachal Pradesh by CSKHPKV, Palampur		

CSKHPKV, Palampur (Location-2) during *kharif* 2021. The experimental material was laid out at each location in two replications as per Randomized Block Design in paired rows with 10cm × 30cm spacing. The crop was raised following standard operational package and approaches. Data were recorded for 11 polygenic characters on five randomly selected plants from each plot for yield and its component traits *viz*., plant height (cm), branches per plant, pods per plant, pod length (cm), biological yield (g), harvest index (%), 100-seed weight (g), yield per plant (g), seeds per pod, however observations were recorded on plot basis for days to 50% flowering and days to 75% maturity.

Statistical analysis

The significance of the characteristic traits under study has been assessed against error sum of squares by employing analysis of variance (ANOVA) for single environment. To establish the homogeneity of error variance over the environments, Bartlett's test of homogeneity was utilized. So when error variance was confirmed to be heterogeneous within environment, as confirmed by Bartlett's test, the transformation of data involves dividing each observation of each environment by the square root of Mean Square Error (MSE) of that environment. Therefore, further analyses were performed as phenotypic and genotypic coefficients of variation using Burton's approach (1952) and heritability in a broad sense and genetic advance as a percent of means by Johonson *et al*. (1955).

Results and Discussion

Indigenous landraces are major source of important genes for genetic diversity. Genetic variability of landraces and gene pools can improve agricultural production efficiency in a variety of cropping conditions, and more diversified farming systems are usually more resilient to the effects of stress. As a consequence, evaluating a local collection of blackgram genes is a suitable technique in identifying genes that are uncommon or absent in cultivars. A total of 23 blackgram genotypes were evaluated for 18 DUS characteristics (Table 2 and 3) out of which they enough range of variation for nine traits (Table 3). Two genotypes *viz*., E1 and E2 showed

Table 2. Details of morphological characterization of blackgram genotypes and their proportional distribution based on DUS parameters

Characteristics	Descriptor state	Proportion of genotypes (%)
Anthocyanin	Present	100
Growth habit	Erect	10
	Semi-erect	90
	Spreading	0
Plant habit	Determinate	100
	Inderterminate	0
Twining habit	Viny	0
	Non-viny	100
Stem color	Purple	81
	Green with purple	19
Stem pubescence	Present	100
	Absent	0
Shape of terminal leaf	Ovate	95
	Lanceilate	0
	Cuneate	5
Leaf color	Light green	48
	Green	43
	Dark Green	9
Petiole color	Green with purple splashes	57
	Purple	43
Vein color	Green	24
	Purple	76
Leaf Pubescence	Present	100
	Absent	0
Length of peduncle	<15cm short	100
	15-20 cm medium	0
	>20cm long	0
Mature pod color	Brown	55
	Black	45
Pubescence on pod	Present	100
	Absent	0
Seed color	Greenish Brown	52
	Black	48
	Mottled	0
Seed coat luster	Shiny	0
	Dull	100
Seed shape	Globose	0
	Oval	100
	Drum	0
Seed size	<3.5 g small	24
	3.5-4.5g mediun	71
	>4.5g large	5

Table 3. Morphological characteristics of blackgram genotypes

Genotypes	Growth habit	Stem color	Shape of terminal leaf	Leaf color	Petiole color	Vein color	Mature pod color	Seed color	Seed size
G1	Erect	Purple	Ovate	Green	Greenish with purple	Purple	Black	Black	Medium
G2	Erect	Purple	Ovate	Dark-green	Purple	Purple	Black	Black	Small
G3	Semi-erect	Purple	Ovate	Green	Purple	Purple	Brown	Black	Medium
G4	Semi-erect	Purple	Ovate	Green	Greenish with purple	Purple	Brown	Black	Medium
G5	Semi-erect	Purple	Ovate	Green	Greenish with purple	Green	Brown	Greenish-brown	Medium
G6	Semi-erect	Purple	Ovate	Light-green	Purple	Purple	Brown	Greenish-brown	Medium
G7	Semi-erect	Purple	Ovate	Green	Purple	Green	Brown	Black	Medium
G8	Semi-erect	Purple	Ovate	Light-green	Purple	Green	Brown	Greenish-brown	Medium
G9	Semi-erect	Purple	Ovate	Green	Purple	Purple	Black	Black	Medium
G10	Semi-erect	Purple	Ovate	Light green	Greenish with purple	Green	Black	Black	Medium
G11	Semi-erect	Green with purple	Ovate	Green	Greenish with purple	Purple	Brown	Black	Medium
G12	Semi-erect	Green with purple	Ovate	Light-green	Greenish with purple	Purple	Black	Greenish-brown	Medium
G13	Semi-erect	Green with purple	Ovate	Light-green	Greenish with purple	Purple	Brown	Greenish-brown	Small
G14	Semi-erect	Green with purple	Ovate	Light-green	Greenish with purple	Purple	Brown	Greenish-brown	Medium
G15	Semi-erect	Purple	Ovate	Light-green	Greenish with purple	Purple	Brown	Black	Small
G16	Semi-erect	Purple	Ovate	Light-green	Greenish with purple	Purple	Black	Black	Medium
G17	Semi-erect	Purple	Cuneate	Dark-green	Purple	Green	Black	Black	Medium
G18	Semi-erect	Purple	Ovate	Green	Purple	Purple	Black	Greenish-brown	Medium
G19	Semi-erect	Purple	Ovate	Green	Purple	Purple	Brown	Greenish-brown	Small
G20	Semi-erect	Purple	Ovate	Light-green	Greenish with purple	Purple	Black	Greenish-brown	Large
G21	Semi-erect	Purple	Ovate	Light-green	Greenish with purple	Purple	Brown	Greenish-brown	Small

erect type of growth habit, while rest of the accessions had semi-erect type of growth habit. Among the 23 genotypes four namely G11, G12, G13 and G14 exhibited green with purple splashes type of stem color, which was distinct to the rest of the accessions as they contained purple colored stem. Only one accession *i.e.* G17 had cuneate type of terminal leaf shape, whereas rest of the genotypes bears ovate type of terminal leaves. The green color generally leads to more accumulation of photosynthates, the dark green color of the foliage is attributed to the high chlorophyll content in the leaves, which corresponds to higher yield. The polymorphism in leaf color was recognized from light-green to dark-green with nine genotypes (G1, G3, G4, G5, G7, G9, G11, G18 and G19) demonstrated green colored leaves and the two (G2 and G17) had dark green color, whereas the remaining 10 had light green colored leaves. The variance in petiole color was reported as greenish-purple and purple, with nine genotypes *viz*., G2, G3, G6, G7, G8, G9, G17, G18 and G19 possessed purple colored petiole. Among all genotypes, 16 had purple vein color in the leaves, meanwhile the remaining five (G5, G7, G8, G10 and G17) displayed green vein color. The diversity in mature pod color varied from black to brown, in which nine (G1, G2, G9, G10, G12, G16, G17, G18 and G20) genotypes pertained black pod color and the rest 12 genotypes exhibited brown color of mature pod. Customers prefer appealing seed colors as they offer a premium market price, a comprehensive examination of the genotypes for seed color intensity demonstrated that 11 genotypes *i.e.* G1, G2, G3, G4, G7, G9, G10, G11, G15, G16 and G17 had black colored seeds and the remaining 10 had greenish-brown seeds. Bold sized seeds are mostly preferred by the buyers, so the variation in seed size was determined as small, medium and large, where five genotypes (G2 G13, G15, G19 and G21) exhibited small sized seeds, 15 had medium sized seeds and only one genotype (G20) proclaimed large/bold sized seeds. The morphological DUS descriptors could be advantageously leveraged for variety identification and grouping in hybridization programs for the production of improved varieties. Katiyar *et al*. (2010) classified 46 black gram varieties into distinct categories for each attribute based on 21 descriptors that might be used as standard varieties. Singh *et al*. (2018) grouped 56 farmer's varieties by using 21 DUS and nine agronomic parameters.

Analysis of variance

The analysis of variance for yield and yield attributing traits were analyzed and presented in Table 4, which provided an in - depth assessment of variation for traits under study for two distinct environments, L1(Berthin) and L2 (Palampur). Single environment analysis showed that the overall sum of

Table 4. Analysis of variance of blackgram genotypes evaluated for grain yield and quality characteristics at KVK, Berthin and CSKHPKV, Palampur in 2021

S.No.	Characters	Location		Source	
			Replication	Genotype	Error
			[1]	[22]	[22]
1	Days to 50 % flowering	L1	9.587**	3.765*	1.587
		L2	8.696**	18.773**	1.105
2	Days to 75% maturity	L1	13.587*	74.800**	0.314
		L2	22.261**	3.583**	1.215
3	Plant height	L1	18.283	631.223**	59.101
		L2	661.195**	116.321**	39.674
4	Branches per plant	L1	0.087	1.775**	0.023
		L2	0.005	0.387*	0.179
5	Biological yield per plant	L1	37.088*	615.589**	6.657
		L2	144.752*	49.702*	18.804
6	Harvest index	L1	10.809	150.201**	3.149
		L2	11.699	148.650**	3.180
7	Seeds per pod	L1	1.722*	0.493*	0.235
		L2	0.003	0.598*	0.285
8	Pods per plant	L1	1.722*	0.493*	0.235
		L2	0.003	0.598*	0.285
9	Pod length	L1	0.183	0.101*	0.046
		L2	0.658**	0.084*	0.040
10	100-seed weight	L1	0.031	0.223**	0.023
		L2	0.056	0.345**	0.018
11	Yield per plant	L1	0.183	5.027**	0.059
		L2	1.035	2.004**	0.557

*Significant at 0.05 level of probability; ** Significant at 0.01 level of probability, Environment = L1(Berthin),L2 (Palampur) squares due to genotypes was significant for all the attributes. Significant variances between genotypes in both the environments exhibited a wide range of variation and genetic variability among the genotypes investigated. Similar studies with positive outcomes were previously reported by Kumar *et al*. (2014), Singh *et al*. (2014) and Ozukum and Sharma (2017) for days to 50% flowering, days to maturity, plant height, number of primary branches, seed yield, seeds per cluster and number of pods per plant.

The Bartlett's test confirmed that the error variance was homogeneous for all of the variables examined except for branches per plant and biological yield per plant; hence, data were transformed for further investigation. The pooled analysis (Table 5) revealed significant differences between environments for days to 50% flowering, days to 75% maturity, plant height, and biological yield per plant, as well as for all the 23 genotypes under investigation. With the exception of harvest index, seeds per pod and pods per plant, the genotypes × environment interaction were significant in all genotypes. Kumar and Peera (2012) ended up finding indiscernible results for days to 50% flowering, number of pods per plant, clusters per plant, plant height and seed yield per plant, however, Rita *et al*. (2016) reported significant variance due to genotypes for traits like plant height, clusters per plant, pods per plant, 100-seed weight and yield per plant.

Genetic variability parameters

A quantitative character's appropriateness as a putative selection method is predominantly influenced by the strength of the genetic parameters it adopts. Table 6 illustrates the estimations of factors such as

Table 5. Combined analysis of variance for different characters over the environments in black gram genotypes

S.No.	**Characters**	**Source of variation**			
		Environ. (A) (1)	**Genotype (B) (22)**	**A × B (22)**	**Pooled Error (44)**
1	Days to 50 % flowering	585.043*	40.704**	37.862**	0.951
2	Days to 75% maturity	329.087*	10.382**	11.973**	1.16
3	Plant height	52,886.491**	401.334**	346.210**	49.388
4	Branches per plant***	1,434.64	56.156**	31.987**	1.35
5	Biological yield per plant***	1,571.221**	51.066**	44.224**	0.992
6	Harvest index	0.083	298.8**	0.052	3.165
7	Seeds per pod	0.156	0.653**	0.437	0.26
8	Pods per plant	0.156	0.653**	0.437	0.26
9	Pod length	1.725	0.095*	0.090*	0.043
10	100-seed weight	0.23	0.326**	0.241**	0.021
11	Yield per plant	3.367	3.981**	3.050**	0.308

*Significant at 0.05 level of probability; ** Significant at 0.01 level of probability

***Transformed data since the variances are not homogeneous phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability % (h^2) and genetic advance as a percentage of mean (GA %) from selection.

In the current investigation, the values of PCV were observed to be higher than GCV for all of the traits under consideration, albeit with a very minor difference, demonstrating that GCV and PCV have a tight correlation. As a conclusion, even though having a higher PCV than GCV, the expression of characters

Table 6. Estimates of parameters of variability for yield and its component traits in black gram genotypes

Traits	Location	Mean ± S.E(m)	Range	PCV (%)	GCV (%)	Heritability h^2bs (%)	GA as % of mean
Days to 50 % flowering	Berthin (L1)	44±0.89	40-49	3.24	1.42	19.25	1.28
	Palampur (L2)	49±0.39	41-56	12.58	12.54	99.37	25.75
	Pooled	47±0.4	42-53	6.87	6.76	96.95	13.72
Days to 75% maturity	Berthin (L1)	81±0.78	78-85	1.81	1.28	49.95	1.86
	Palampur (L2)	77.0±0.74	72.5-83.5	4.09	3.86	88.88	5.77
	Pooled	78±0.5	76-82	1.96	1.95	83.82	3.68
Plant height (cm)	Berthin (L1)	80.5±5.43	43-112	23.07	21.00	82.88	39.38
	Palampur (L2)	32.6±4.45	20.2-47.2	27.10	19.00	49.13	27.43
	Pooled	56.0±3.9	39.9-62.8	13.72	6.03	19.30	5.46
Branches per plant	Berthin (L1)	4.1±0.10	2.4- 6.6	23.11	22.80	97.41	46.36
	Palampur (L2)	5.1±0.29	3.7-6.3	10.94	6.64	36.77	8.29
	Pooled	5 ±1.8	4-6	16.24	16.01	97.26	32.53
Biological yield per plant (g)	Berthin (L1)	31.6±1.82	7.6- 71.6	55.97	55.35	97.79	112.75
	Palampur (L2)	17.7±3.06	12.1-29.9	33.81	22.70	45.10	31.41
	Pooled	24.7 ±1.9	12.7-46.2	44.53	43.50	95.43	87.54
Harvest index (%)	Berthin (L1)	17.5±1.25	7.0- 47.1	61.23	59.95	95.85	120.90
	Palampur (L2)	31.4 ± 5.17	17.5-62.8	34.68	25.73	55.04	39.32
	Pooled	22.9 ±1.3	12.1-40.8	61.22	59.95	95.89	120.94
Seeds per pod	Berthin (L1)	5.5±0.34	4.3- 6.5	10.93	6.50	35.38	7.97
	Palampur (L2)	5.763±0.37	4.5-6.8	11.86	7.06	35.42	8.66
	Pooled	6 ±0.3	4-6	8.97	5.06	31.09	5.75
Pods per plant	Berthin (L1)	24.4±3.17	14.9- 37.6	27.05	19.78	53.47	29.79
	Palampur (L2)	18.6±2.80	11.7-26.6	26.69	16.10	36.37	20.00
	Pooled	22 ±2.3	13-29	21.03	14.75	49.16	21.30
Pod length (cm)	Berthin (L1)	4.6±0.15	4.1- 5.1	5.96	3.63	37.12	4.56
	Palampur (L2)	4.8±0.14	4.3-5.2	5.16	3.06	35.12	3.73
	Pooled	4.7 ±0.1	4.5-5.2	4.15	2.07	24.80	2.12
100-seed weight (g)	Berthin (L1)	3.6±0.11	3.1- 4.2	9.62	8.69	81.52	16.16
	Palampur (L2)	3.7±0.09	3.1-4.6	11.39	10.81	89.88	21.10
	Pooled	3.7 ±0.2	1.2-6.3	7.87	7.30	86.01	13.95
Yield per plant (g)	Berthin (L1)	3.7±0.17	1.2- 6.2	42.67	42.17	97.67	85.86
	Palampur (L2)	31.4 ± 5.17	17.5-62.8	27.46	20.64	56.51	31.97
	Pooled	3.9 ±0.3	2.4-6.1	26.42	24.33	84.83	46.16

is less influenced by the environment owing to their near proximity. This demonstrates that attributes with a great degree of variability; a meaningful selection based on phenotype would not be misleading. The pooled investigation depicted higher values of PCV and GCV for harvest index (61.22%, 59.95%) followed by biological yield per plant than seed yield per plant (44.53%, 43.49%). On the other hand, moderate estimates for PCV and GCV were recorded for traits like number of pods per plant (21.03%, 14.75%) and yield per plant (26.42%, 24.33%). Similar findings were obtained previously for plant height, seed yield, and pods per plant by Singh *et al.* (2014). Panigrahi *et al.* (2014) and Kumar *et al.* (2015) wherein they observed strong GCV for seed yield per plant, seeds per plant, and pods per plant.

Heritability examines the level of resemblance between parents and their offspring. The coefficient of variation somehow doesn't encompass the entire range of heritable variation. Whenever heritability and genetic advance are investigated concurrently, variation can be established with more reliability. In the present investigation, heritability (h^2 in %) varied from 19.30 % for plant height to 97.26 % for branches per plant. The amplitude of heritability was reported to be higher for variables such as days to 50% flowering, days to 75% maturity, branches per plant, biological yield per plant, harvest index, 100-seed weight and yield per plant while low for plant height, seeds per pod and pods per plant and pod length. Various researchers have documented high heritability percentages in 100-seed weight and seed yield per plant (Yadav and Dahiya 2000; Panda *et al.* 2017), and number of branches per plant (Kumar *et al.* 2000).

Genetic advance (GA) under screening refers to the transmission of traits in genotypic value for the succeeding population contrasted to the base population throughout each round of selection at certain selection intensity. In forecasting the effectiveness of selection, heritability estimates coupled with genetic gain would be more informative than heritability estimates alone. The pooled statistics on genetic advance for various traits, represented as a percentage of the mean, had spectrum from 2.12 % for pod length to 120.93 % for harvest index. Biological yield per plant and harvest index pertained higher values of genetic advance as percent of mean; branches per plant and yield per plant claimed moderate; whilst days to 50% flowering, days to 75% maturity, plant height, seeds per pod, pods per plant, pod length and 100-seed weight had lower genetic advance as percent of mean. This could imply that these traits were less affected by the environment and were predominantly dependent as persistent attributes on higher potential genotypes, which could aid in individual plant selection and breeding program effectiveness. Hozayn *et al.* (2013) also found similar results to biological yield per plant, similarly Mayank and Lal (2021) for harvest index in mungbean.

The confluence of medium or high coupled with high genetic advance validates the significance of additive gene action in effective screening of the relevant traits. Therefore in investigation, high heritability combined with significant genetic advance in attributes such as biological yield per plant and harvest index demonstrates the function of additive gene action. This could imply that these traits were less affected by the environment and were predominantly dependent as persistent attributes on higher potential genotypes, which could aid in individual plant selection and breeding program effectiveness. Traits like branches per plant and grain yield per plant pertained higher magnitude of heritability coupled with moderate genetic advance also indicates the preponderance of additive gene action leads to effective selection. However, the remaining traits exhibited high heritability and low genetic advance, demonstrating the impact of non-additive gene interactions.

Conclusion

Based on the aforementioned characterization presented here, these genotypes were classified into distinct groups for nine trait and may be used as reference genotypes and grouping in hybridization programs for the production of improved varieties. The aggregated study demonstrated significant differences across environments for days to 50% flowering, days to 75% maturity, plant height and biological yield per plant, as well as for all 23 genotypes. The genotypes × environment interaction was significant in all genotypes excluding harvest index, seeds per pod and pods per plant. This variability highlighted that the genotypes had a significant potential for selection in future breeding projects. Genotypic coefficient of variation and Phenotypic coefficient of variation had a close relationship, revealing that the environment had less impact on the investigated traits. High heritability associated with significant genetic advance in traits such as biological yield per plant and harvest index this demonstrated the preponderance of additive gene action.

Conflict of interest: The authors declare that there is no conflict in this manuscript.

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