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Phenotyping of elite Black gram (*Vigna mungo* (L)) germplasm accessions under Bastar plateau for yield and adaptability

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Abstract

The research was conducted on Black gram (*Vigna mungo* (L)) genotypes during the *Kharif* season of 2022 at the New Upland Research Cum Instructional Farm, Lamker, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, IGKV, Raipur (Chhattisgarh), in randomized block design. The research focused on studying the qualitative and quantitative traits of black gram in order to characterize and evaluate the variability among 44 elite genotypes of black gram. The analysis of variance showed highly significant differences among the 44 genotypes for each trait. The variability analysis revealed that for the parameters plant height (cm), number of pods per plant and terminal leaflet width high estimates of GCV and PCV were observed, showing the importance of selection for improving output. (Indicating the genetic improvement of the traits through selection). The high heritability along with high genetic advance as percent of mean was recorded on the characters plant height, number of branches per plant, number of pods per plant, terminal leaflet length, terminal leaflet width, number of pods per cluster and seed yield. The wide range of these traits indicated the presence of sufficient variability in breeding population and also indicated better scope for improvement for mutant lines of above characters. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values showed a lot of variability exists among phenotypic as well as genotypic level and better chance for improvement is possible by selection. High heritability shows that the character is governed by additive gene action for the improvement of this character selection would be rewarding.

Keywords: Phenotyping, analysis of variance and genetic variability

1. Introduction

Black gram (*Vigna mungo* L.), also referred to as urd bean or mash, is a domesticated variety of the wild legume *Vigna mungo* var. *silvestris*. With a $2n=2x=22$ chromosome, it is a member of the leguminosae family. An Indian origin for black gram is reportedly claimed. It matured primarily during the warm or rainy seasons. Around 70% of the world's urd bean production originates in India, where the crop is grown in a variety of climates. It is raised using a variety of agricultural techniques under varied agro-ecological conditions and cropping patterns (Gupta *et al.*, 2001) [18]. Among Pulses, it is the least studied crop, and no worldwide CGIAR center includes it as one of its mandates. (Anonymous, 1976) [1]. It provides a significant contribution from its adaptation to rapid growth and low water needs. It is used in a variety of ways, with plant parts being used as fodder and seeds being consumed as a source of protein, vitamins, and minerals. In the everyday meals of the majority of Asian people, it provides a significant source of affordable vegetable protein, iron, calcium, vitamins, and vital amino acids. It is a significant pulse crop, but because of its limited genetic variety, it has been unable to produce higher yields. A self-pollinating crop, black gram also produces blossom drops (Arul balachandran *et al.*, 2010) [4]. Due to the integrated structure of plants, where the majority of characteristics are inherited and controlled by a significant number of cumulative, duplicate, and dominant genes, choosing genotypes based on yield is challenging. More than 70% of the world's black gram is currently produced in India, which leads the industry. Myanmar and Pakistan come after India. The biggest producers of black gram in India during *Kharif* are the states of Tamil Nadu 2.74 lakh ha (6.78lakh acres), Andhra Pradesh 2.55 lakh ha (6.30 lakh acres), Odisha 2 lakh ha (4.96 lakh acres), Telangana 0.178 lakh ha (0.44lakh acres), Chhattisgarh 0.14 lakh ha (0.35 lakh acres), and West Bengal 0.182 lakh ha (0.95 lakh acres). Black gram production of India is 2.68 million tonnes (Anonymous, 2023) [1].

The breeding technique for urd beans includes creating genetic material, choosing the best genotypes from the genetic diversity needed to create better variations. The knowledge of certain genetic parameters is also essential for proper understanding and their manipulation in any crop improvement program. Seed yield is the result of the expression and association of several plant growth components.

2. Materials and Methods

The experiment was carried out at New Upland Research cum Instructional Farm, SG College of Agriculture and Research Station, Jagdalpur, IGKV, Raipur, Chhattisgarh during *Kharif* 2022 – 23. The experiment was laid out in Randomized Block Design with two replications. Experimental material for the present investigation was collected from different morphological and productive attributes of Chhattisgarh. Each genotype was planted in four rows of 4 length \times 1.20 m width having 30 \times 10 cm spacing between rows and plants. The following observations were recorded as per the descriptor of IBPGR and PPV & FRA Rome. On basis of both qualitative and quantitative characteristics in Visual observations were recorded. The average values were computed as treatment mean under each replication. Phenotypic and genotypic variability were calculated as per method proposed by Burton and Devane (1953) [11]. Heritability estimates in cultivated plants were as suggested by (Hanson *et al*, 1956). Genetic advance was worked out by using the formula suggested by Robinson *et al*, (1949) [49].

3. Results and Discussion

3.1 Qualitative traits

All the genotypes were screened for various qualitative traits such as seed colour, seed vigour, stem colour, leaf pubescence, pod pubescence and Terminal leaflet shape. With respect to seed colour, genotypes were categorised as light green (1), green brown (5), brown (13) and black (25). Stem colour character was easily distinguished in the field. Maximum 23 genotypes showed green stem colour, while 14 genotypes showed green with purple splashes, 3 genotypes showed purple, and 1 showed purple with green splashes. Leaf pubescence commonly known as leaf hairs all genotypes have pubescence on leaf surface in 43 genotype leaf pubescence were present while leaf pubescence was absent in 1 genotype. Pod pubescences this trait protects for the pod borers attack mostly all genotypes have pubescence. Pod pubescence was present in 42 genotypes and absent in 2 genotypes. Terminal leaflet shape was categorized in ovate shape, lanceolate shape and cuneate shape. Maximum 24 genotypes were showed cuneate shape terminal leaflet and 13 genotypes showed ovate shape leaflet while 7 genotypes showed lanceolate shape leaflet.

3.2 Quantitative traits

Under this study, 12 quantitative characters were evaluated among 44 genotypes of blackgram. The analysis of variance revealed highly significant differences among the genotypes for all the characters under study. The following discussion covers the findings for each character. The days to 50% flowering varied from 34 to 56 days, with an average of 38 days. Late flowering was observed in genotypes TRU-258 (56 days) followed by UTD-2 and UTK-1 (42 days), while early flowering was recorded in genotypes ULB-1 (34 days) and

UL-1 (34 days). The days to maturity ranged from 87 days to 97 days, with an average value of 92 days. Early maturity was observed in genotypes TRU-55 (87 days) followed by TRU-1, UGM-1 and UTK-3 (89 days), while late maturity was observed in genotype TRU-258 (97 days). The plant height ranged from 30.90 cm to 110.90 cm and average mean was 54.46 cm. The genotypes UBSR (110.90 cm) and UTK-3 (110.50 cm) had the tallest plants, whereas ULB-1 (30.90), TRU-236 and UTK-2 (33.70 cm) had the shortest plant height. The minimum number of branches per plant was exhibited by TRU-236 (1.75), whereas UTRS (3.55) possessed the highest number of branches per plant. The mean performance was 2.56. The terminal leaflet length ranged from 6.50 cm to 11.85 cm. The average mean value was 9.25 cm. The genotype TRU-339 (11.85 cm) followed by UBS (11.35) had the maximum length, whereas TRU-258 (6.50) followed by UGM-2 (6.60) had the minimum terminal leaflet length. The terminal leaflet width was varied from 2.05 cm to 5.40 cm. The average mean value was 3.55 cm. The genotype ULB-2 (5.40 cm) followed by UTK-1 (5.35 cm) had recorded maximum width whereas genotypes RU 03-22-4 (2.05) followed by IU 08-2 (2.20) had the minimum terminal leaflet width. Observations of this trait spanned from 6.50 to 33.50, with an overall average of 19.96. A minimum mean value of 6.50 was observed for genotype UTD-2, and a maximum was found for genotype TRU-258. The increase in number of pods in the plant will increase the yield. The mean value for this trait was 2.91 and ranged from 2.0 to 4.0. The highest number of pods was observed for genotypes IU 08-2 (4.0), TRU-18 (4.0), and UTP-3 (4.0), while the lowest was observed for genotypes TRU-236 (2.0), UGM-2 (2.0), UTD-1 (2.0), UTK-2 (2.0), ULB-2 (2.0), and ULB-3 (2.0). The variability among the genotypes for trait pod length was observed to be significant. The range found in pod length was 4.30 cm (IU 02-4) to 5.75 cm (UTP-3), with an average pod length of 4.97 cm. The total number of seeds per pod was ranged from 6.00 to 8.55 with mean value of 6.99. The genotypes TRU-18 and UGM-2 (8.50) had recorded highest number of seeds per pod whereas, the lowest number of seeds per pod was recorded on genotype RU 03-22-4 (6.0). The average weight of 100 seed was 4.45, varying from 3.71 to 5.31g. Among all the genotypes, genotype KU 96-3 (ch) (5.31) and TRU-8 (5.01) had higher 100 seed weight, whereas genotypes UGM-1 (3.71) and TRU-258 (3.72) had the lowest 100 seed weight. The yield per plant ranged from 258 g to 739 g, with an average value of 480 g. The genotype UBSR (739 g) had the highest yield per plant followed by UGM-2 (669 g), while the lowest yield was recorded on genotype ULB-1 (258 g). The variability was determined by calculating the mean, coefficient of variation (genotypes and phenotypic), heritability (in the broad sense), and genetic advance. The magnitude of the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits. A high genotypic and phenotypic coefficient of variation was recorded for plant height (cm) (32.90, 33.10), followed by the number of pods per plant (25.70, 26.46), and terminal leaflet width (24.09, 25.75), respectively. The estimates of GCV and PCV were moderate for seed yield (kg/plot) (16.04, 17.49), followed by number of branches per plant (13.99, 16.97), number of pods per cluster (14.07, 16.33), and terminal leaflet length (12.27, 12.90), respectively. While the low GCV and PCV were on traits days to 50% flowering (7.03, 8.21), followed by days to

maturity (1.70, 2.39), pod length (cm) (4.70,6.94), number of seeds per pod (4.84, 8.91), and 100 seed weight (4.73, 8.74). Priyanka S., *et al.* (2016) [41], Hemalatha *et al.* (2017) [22], Ozukum and Sharma (2017) [33], Tank *et al.* (2018) [65], and Deekshith *et al.* (2022) [12] reported similar results. The estimates of the heritability for 12 quantitative characters ranged from 29.30% to 98.82%. The highest heritability (broad sense) was observed for the traits plant height (98.82%) followed by number of pods per plant (94.37), terminal leaflet length (90.34), terminal leaflet width (87.51), seed yield (84.18), number of pods per cluster (74.24), days to flowering (73.24), and number of branches per plant (67.97). Days to maturity (50.22%) and pod length (45.72%) were found to have moderate heritability (broad sense), while low heritability was observed for traits such as number of seeds per pod (29.57) and 100 seed weight (29.30). The high heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of branches per plant, number of pods per plant, terminal leaflet length, terminal leaflet width, number of pods per cluster and seed yield indicating the less influence of environmental variance in the inheritance of trait, which can be further improved by

means of simple selection. High heritability and high genetic advance may be attributed by additive gene action (Khan, 1990) and simple selection could be applied for genetic improvement. Similar result were observed by Priyanka S., *et al.* (2016) [41], Hemalatha *et al.* (2017) [22], Ozukum and Sharma (2017) [33], Tank *et al.* (2018) [65] and Deekshith *et al.* (2022) [12].

For 12 quantitative characters, genetic advance as a percentage of the mean was recorded. The estimates of genetic advancement are shown in Table 4.3. The strongest influence of genetic advance was reported for the attributes *viz.* plant height (67.38%), followed by the number of pods per plant (51.44), terminal leaflet length (87.51), and number of branches per plant (23.76). Whereas, moderate values of genetic advances were measured for the trait days to 50% flowering (12.39%). The attributes of pod length showed the least amount of genetic progress (6.54%), followed by number of seeds per pod (5.43%), 100 seed weight (5.28%), and days to maturity (2.48%). Similar findings were reported by Priyanka S., *et al.* (2016) [41] Tank *et al.* (2018) [65] Hemalatha *et al.* (2017) [22] Deekshith *et al.*, (2022) [12] and Ozukum and Sharma (2017) [33].

Table 1: Analysis of variance (ANOVA) for twelve quantitative traits in forty four black gram genotypes

SV	df	DF	DM	PH	NBPP	NPPP	PL	TLL	TLW	NPPC	NSPP	SW	SY
Repl	1	5.011	0.102	1.613	0.019	4.350	0.117	1.180	0.055	0.004	0.410	0.530	0.002
Treat	43	23.663**	9.777**	967.202**	0.445**	80.523**	0.228**	4.001**	2.301**	0.560**	0.616**	0.240**	0.019**
Error	43	2.570	2.428	3.839	0.060	1.570	0.065	0.138	0.105	0.058	0.273	0.107	0.001

*, ** significant at 5% and 1% level, respectively

DF-Days to 50% Flowering, DM-Days to Maturity, PH-Plant Height (cm), NBPP-No. of Branches/Plant, NPPP-No. of Pods/Plant, PL-Pods Length (cm), TLL-Terminal leaflet Length (cm), TLW-Terminal leaflet width (cm), NPPC-No. of pods/cluster, NSPP- No. of Seed/Pod. SW-100 Seed Weight (g), SY-Seed Yield (kg/Plot)

Table 2: Mean performance of 44 black gram genotypes under natural conditions

S.no	Genotypes	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	No. of Branches/Plant	No. of Pods/Plant	Pods Length (cm)	Terminal leaflet Length (cm)	Terminal leaflet width (cm)	No. of pods/cluster	No. of Seed/Pod	100 Seed Weight (g)	Seed Yield (kg/Plot)
1	IU 02-4	39.50	94.50	43.20	3.00	26.00	4.30	9.55	2.80	3.00	7.00	4.22	0.504
2	IU 05-2	38.50	93.50	39.60	2.00	26.50	5.05	10.20	2.45	3.55	7.00	4.86	0.492
3	IU 08-2	37.50	93.00	41.70	2.10	18.50	4.95	10.55	2.20	4.00	7.25	4.72	0.450
4	IU 02-6	37.00	89.50	39.60	2.10	26.00	4.85	9.30	2.25	3.00	6.75	4.66	0.433
5	IU 02-1-3	38.00	90.50	38.10	2.90	20.50	5.05	10.10	3.50	2.55	7.50	4.58	0.441
6	RU 03-22-4	36.50	93.50	52.80	3.00	26.50	4.65	10.10	2.05	3.00	6.00	4.46	0.436
7	RU 03-52	37.00	91.50	45.30	2.20	27.50	5.05	10.90	2.75	3.00	7.50	4.42	0.376
8	IU 2021-1	34.50	89.00	47.50	2.10	28.50	5.35	10.25	2.95	3.00	7.50	4.19	0.487
9	IU 2021-2	38.00	91.00	46.50	2.10	21.50	4.65	10.45	2.85	3.00	6.50	4.77	0.429
10	IU 2021-3	38.50	92.50	42.70	3.00	26.00	4.80	10.05	2.70	3.50	6.50	4.23	0.486
11	TRU-62	35.50	91.50	43.60	2.50	22.00	4.70	9.50	2.35	3.50	7.00	4.21	0.373
12	TRU-24	38.00	89.00	53.30	2.00	26.50	5.05	9.15	2.60	3.50	7.00	4.81	0.353
13	TRU-8	38.00	93.50	36.20	1.90	22.00	4.70	10.30	3.45	3.50	7.00	5.01	0.361
14	TRU-339	36.50	92.50	45.80	1.90	28.00	4.80	11.85	3.35	3.00	7.00	4.48	0.475
15	TRU-134	39.00	93.50	46.20	2.90	21.50	5.20	10.75	3.20	3.00	7.50	4.63	0.493
16	TRU-258	55.50	96.50	46.90	3.00	33.50	4.40	6.50	3.75	3.00	6.50	3.72	0.581
17	TRU-55	40.00	87.00	40.80	2.00	25.00	4.65	10.35	3.05	2.50	7.00	4.03	0.453
18	TRU-1	38.00	88.50	37.80	2.20	21.50	4.70	9.50	2.90	2.50	6.50	4.17	0.370
19	TRU-236	38.00	89.00	33.70	1.75	22.50	4.55	10.25	2.65	2.00	6.50	4.27	0.415
20	TRU-431	36.50	94.50	50.20	2.90	24.50	4.95	8.00	2.40	3.00	7.00	3.97	0.579
21	TRU-1-11	35.50	94.50	43.60	1.90	23.00	4.50	8.30	2.60	3.00	6.50	4.31	0.504
22	TRU-18	40.00	92.50	56.30	2.80	32.00	5.40	8.55	2.40	4.00	8.50	4.55	0.524
23	KU 96-3 (ch)	38.50	93.50	39.80	2.90	18.50	4.90	8.70	2.90	3.00	7.00	5.31	0.558
24	Indira Urd Pratham	37.50	89.00	39.10	1.90	22.50	4.80	10.45	2.75	2.50	7.00	4.73	0.459
25	UGM-1	36.00	88.50	63.65	2.90	15.95	4.85	6.65	4.40	3.00	6.80	3.71	0.487

26	UGM-2	41.00	93.50	81.80	2.95	13.15	5.55	6.60	4.30	2.00	8.50	4.70	0.669
27	UTD-1	36.50	91.50	44.55	2.05	13.15	5.15	10.55	3.40	2.00	6.45	4.01	0.348
28	UTD-2	42.00	93.50	91.50	2.80	6.50	5.25	7.05	4.10	3.00	7.45	4.64	0.582
29	UTRS	40.50	94.00	99.20	3.55	22.65	5.45	7.55	4.90	3.00	6.70	4.55	0.659
30	UTK-1	42.00	94.00	95.95	3.00	20.45	5.40	7.45	5.35	3.00	6.50	4.57	0.640
31	UTK-2	35.00	89.00	33.70	2.85	17.60	4.75	9.35	2.70	2.00	7.50	4.41	0.416
32	UTK-3	34.50	88.50	110.50	3.50	18.32	5.25	7.85	5.20	3.00	7.50	4.01	0.562
33	UTP-1	36.50	93.00	95.00	3.00	11.50	5.20	6.85	5.15	3.00	7.50	4.43	0.502
34	UTP-2	35.00	93.00	58.60	3.00	17.50	5.00	9.30	4.90	2.50	6.50	4.55	0.466
35	UTP-3	34.50	93.00	38.50	2.50	12.50	5.75	8.85	2.90	4.00	6.00	4.05	0.448
36	UBK	38.50	94.00	92.20	2.20	15.50	4.95	10.15	5.00	3.50	6.50	4.60	0.562
37	UBSR	39.50	93.50	110.90	2.75	12.45	5.60	6.85	4.90	2.75	7.50	4.45	0.739
38	ULB-1	33.50	92.50	30.90	2.10	13.45	4.40	9.45	3.35	2.50	6.50	4.12	0.258
39	ULB-2	35.50	94.00	55.10	2.80	10.45	5.00	9.15	5.40	2.00	7.50	4.86	0.365
40	ULB-3	35.00	93.50	39.70	2.85	10.60	4.90	10.00	5.20	2.00	6.50	4.10	0.404
41	UL-1	34.00	92.50	61.40	2.90	15.10	5.35	7.70	5.25	2.80	7.50	4.99	0.449
42	UL-2	36.00	94.50	57.00	2.50	12.30	5.25	9.95	5.25	2.75	6.50	4.89	0.620
43	ULK	36.50	93.50	50.10	2.50	14.80	5.05	10.85	3.80	3.00	7.50	4.63	0.438
44	UBS	37.00	94.50	35.70	2.80	13.80	4.70	11.35	4.00	2.50	6.50	4.42	0.489
	Mean	37.74	92.22	54.46	2.56	19.96	4.97	9.25	3.55	2.91	6.99	4.45	0.480
	Min	33.50	87.00	30.90	1.75	6.50	4.30	6.50	2.05	2.00	6.00	3.71	0.258
	Max	55.50	96.50	110.90	3.55	33.50	5.75	11.85	5.40	4.00	8.50	5.31	0.739
	SE(d)	1.60	1.56	1.96	0.25	1.25	0.25	0.37	0.32	0.24	0.52	0.33	0.033
	C.D.	3.24	3.15	3.97	0.50	2.54	0.52	0.75	0.65	0.49	1.06	0.66	0.067
	C.V.	4.25	1.69	3.60	9.61	6.28	5.12	4.01	9.10	8.29	7.48	7.35	6.947

Table 3: Variability parameters for twelve quantitative characters in 44 black gram genotypes

Genotypes	Mean	Min	Max	GCV (%)	PCV (%)	Heritability (%)	GA	GA% mean
Days to 50% Flowering	37.74	33.50	55.50	7.03	8.21	73.24	4.67	12.39
Days to Maturity	92.22	87.00	96.50	1.70	2.39	50.22	2.28	2.48
Plant Height (cm)	54.46	30.90	110.90	32.90	33.10	98.82	36.70	67.38
No. of Branches/Plant	2.56	1.75	3.55	13.99	16.97	67.97	0.61	23.76
No. of Pods/Plant	19.96	6.50	33.50	25.70	26.46	94.37	10.27	51.44
Pods Length (cm)	4.97	4.30	5.75	4.70	6.94	45.72	0.33	6.54
Terminal leaflet Length (cm)	9.25	6.50	11.85	12.27	12.90	90.34	2.22	24.02
Terminal leaflet width (cm)	3.55	2.05	5.40	24.09	25.75	87.51	1.65	46.42
No. of pods/cluster	2.91	2.00	4.00	14.07	16.33	74.24	0.73	24.97
No. of Seed/Pod	6.99	6.00	8.50	4.84	8.91	29.57	0.38	5.43
100 Seed Weight (g)	4.45	3.71	5.31	4.73	8.74	29.30	0.24	5.28
Seed Yield (kg/Plot)	0.48	0.26	0.74	16.04	17.49	84.18	0.15	30.32

Table 4: Number of genotypes and their frequency (%) in different categories for different characters

S.N.	Traits	Category	Noofgeno types	Frequency %
1.	Seed colour	Light Green	1	2.27
		Green Brown	5	11.36
		Brown	13	29.54
		Black	25	56.81
2	Stem colour	Green	23	52.27
		Green with Purple Flash	14	31.81
		Purple	3	6.81
		Purple with Green Flash	1	2.27
3	Leaf pubescence	Present	43	97.72
		Absent	1	2.27
4	Pod pubescence	Present	42	95.45
		Absent	2	4.54
5	Terminal leaflet	Ovate	13	29.54
		Lanceolate	7	15.90
		Cuneate	24	54.54

4. Conclusion

According to the findings of the experiment, it is indicated that the wide range of these traits indicated the presence of sufficient variability in breeding population and also indicated better scope for improvement for mutant lines of above

characters. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values showed a lot of variability exists among phenotypic as well as genotypic level and better chance for improvement is possible by selection. High heritability shows that the character is

governed by additive gene action for the improvement of this character selection would be rewarding.

5. Acknowledgements

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