Genetic Variability and Character Association Studies on Blackgram (*Vigna mungo* (L.) Hepper) for Seed Yield, Maturity and Resistance to Yellow Mosaic Virus

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Original Research Article

ABSTRACT

Analysis of variance showed highly significant differences among 20 genotypes of blackgram for 12 characters studied. High GCV and PCV was recorded for number of pods per plant followed by number of clusters, number of primary branches, seed yield per plant. High heritability coupled with high genetic advance as percent of mean was observed for number of clusters per plant, number of primary branches, harvest index, number of pods per plant, seed index, plant height, seed yield per plant and biological yield. Seed yield per plant showed positive and significant correlation at both genotypic and phenotypic levels with harvest index followed by pod length, days to maturity and biological yield. High positive direct effect on seed yield per plant was exhibited by harvest index followed by biological yield, seed index, number of pods per plant and number of primary branches per plant at genotypic level. At phenotypic level high positive direct effect on seed yield per plant was exhibited by harvest index, biological yield, number of pods per plant and days to 50% flowering. Hence, selection based on these traits would be effective in increasing the seed yield. Twenty genotypes were screened against YMV out of which only PU-31 showed resistant reaction. Fifteen genotypes showed moderately resistant reaction. Two of them showed moderately susceptible reaction and the other two genotypes showed susceptible reaction towards YMV.

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1. INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) known as urdbean, udand dal or urad in India is a short duration, self-pollinating, diploid (2n=2x=22) grain legume crop belonging to the family Leguminosae with a small genome size of 574Mbp [1] and assumes considerable importance from the point of food and nutritional security in the world.

Being a drought resistant crop, it is suitable for dry land farming and predominantly used as an intercrop with other crops. It is one of the most important food legume crop Indian sub-continent, particularly in south Asia. Almost 90% of the world's urad-bean comes from Asia. The availability of pulse grain in India is 36 g/day/capita as against the minimum requirement of 80 g/day/capita [2] and hence enhancing production of pulses is needed to meet the protein caloric balance in the diet.

The major constraints in blackgram genetic improvement are lack of exploitable genetic variability, absence of suitable ideotype for different cropping systems, poor harvest index and susceptibility to biotic and abiotic stresses and non-availability of quality seeds of improved varieties. Success of yield improvement largely depends upon the magnitude and nature of genetic variability present in yield contributing traits [3]. The systematic collection of blackgram has displayed inadequate variability for biotic and abiotic genes. It is possible that genes for high productivity could have been lost due to overriding role of natural selection [4] and the genetic base of the present-day collection remains poor [5] due to lack of variability owing to its autogamaous nature. The creation of variability is difficult through hybridization due to its high self-pollination and flower droop [6].

The development of a suitable plant breeding program is dependent on the presence of genetic variability. Study of inheritance of various quantitative traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficient of variability, heritability and genetic advance as percent of mean is a prerequisite for a plant breeder in conducting effective breeding programme. Estimation of genetic variability in conjunction with heritability and genetic advance gives an idea of the possible improvement of the character through selection.

Seed yield is the result of the expression and association of several plant growth components. Association analysis measures the mutual relationship between various plant characters and determines component characters on which selection can be based on improvement in the economically important characters [7]. Estimation of correlation coefficient enables to eliminate the characters with little or no importance during selection. Path coefficient analysis suggested by [8] proves helpful in partitioning the correlation coefficient into its direct and indirect effects. If the correlation is due to direct effect, it reflects a true and perfect relationship and such characters can be directly subjected to selection for improving yield.

The productivity of urdbean remains low due to biotic (mungbean yellow mosaic virus, powdery mildew and cercospora leaf spot) and abiotic stresses (drought, heat and preharvest sprouting). Yellow mosaic virus is one of the most prevalent and destructive viral pathogens in blackgram. It causes severe yield loss and a reduction in seed quality. YMV appear in the form of small irregular yellow specks and spots along the veins, which enlarge until leaves become completely yellow. The chemical management of the vector is not cost-effective since numerous sprays of insecticides are required to control whitefly. It remains unsuccessful in developing YMV resistant mungbean varities through conventional breeding methods due to rapid explosion of new isolates of yellow mosaic virus and also the complexity of mechanism in controlling YMV resistance. Identifying resistant donors is a very complicated task due to the lack of reliable screening protocol for assessing the resistance/susceptibility of exsisting varieties.

The present aim of the experiment is to identify high yielding blackgram genotypes for good quality traits and to establish relationship between quantitative traits with seed yield.

2. MATERIALS AND METHODS

The experimental material comprised of 20 blackgram genotypes which were raised in a Randomized Block Design with three replications at Field Experimentation Centre of Department of Plant Breeding, Prayagraj, U.P during *Kharif-*2021 (Fig. 1). The site of the experiment is

located at 25.57° N latitude, 81.56" N and 98 meters above the sea level. This region has a subtropical climate with the extreme of summer and winter. The temperature falls to as low as 1°C-2°C during the winter season especially in the month of December and January. The mercury rises to 46°C-48°C during summer. The average rainfall in this area is around 1013.4 mm annually with maximum concentration from July to September with few showers and drizzles in winter also. The soil type of the experimental site was sandy loam, low in organic carbon, nitrogen, phosphorus and potash. Experimental materials were obtained from Department of Genetics and Plant Breeding, SHUATS, Nani, Prayagraj, U.P. In each replication, genotypes were sown in a single row of four meters length with spacing of 30x10 cm. the package of practices recommended in the crop production guide was followed. Twelve quantitative traits *viz.,* plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, biological yield (g), harvest index (%), seed index (g), seed yield per plant (g) were recorded for five randomly selected plants in each of the accession per replication. Days to 50% flowering, days to maturity, screening of blackgram genotypes against YMV was recorded on plot basis. The statistical analysis and variance due to different sources was worked out according to Panse and Sukhatme [9]. Phenotypic and genotypic coefficient of variation were calculated based on the method advocated by Burton [10]. Heritability and genetic advance as percent of mean were estimated as per formula given by Johnson et al. The phenotypic and genotypic correlation coefficient were calculated from phenotypic and genotypic variances and covariances and path analysis were worked as suggested by Dewey and Lu, 1959. Yellow Mosaic Virus disease was screened on the basis of 0-9 arbitrary scale according to Mohan et al. [11].
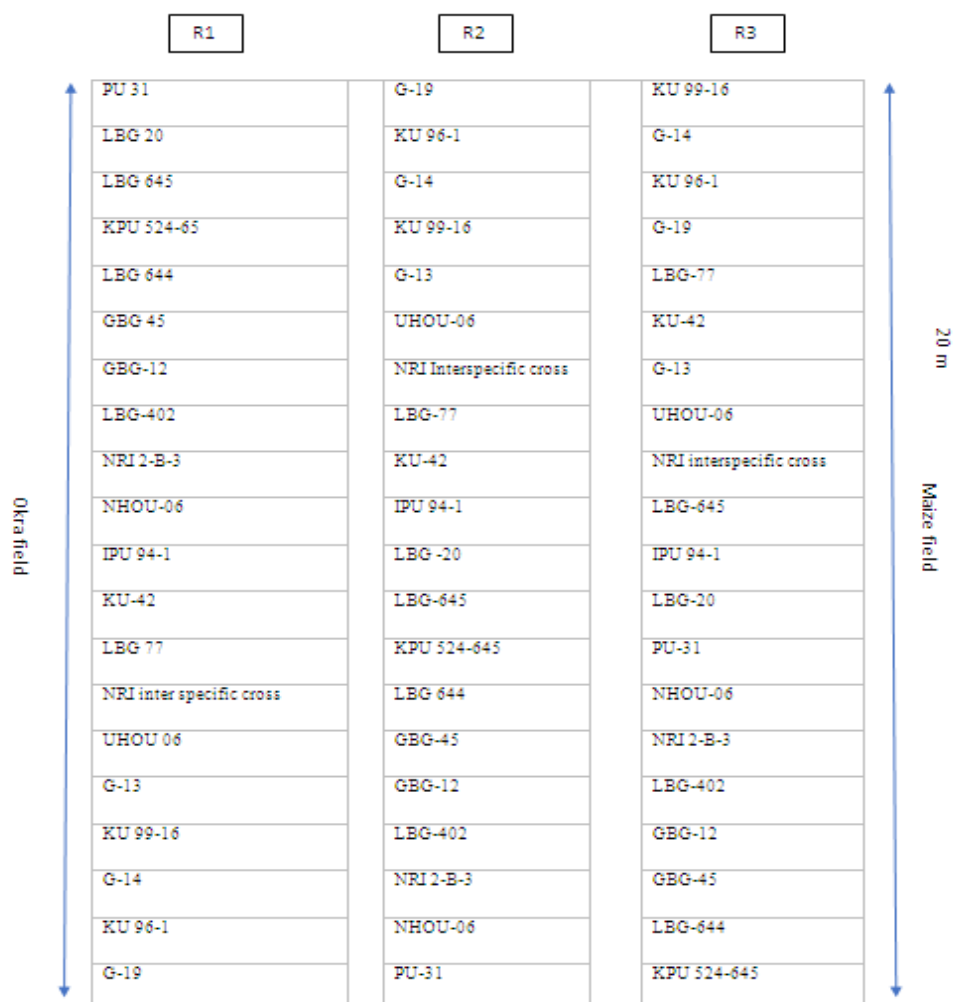

Fig. 1. Layout of experimental plot

3. RESULTS AND DISCUSSION

The analysis of variance was carried out for eleven quantitative characters. The variance due to treatment was highly significant for all eleven characters studied. This gives the evidence of magnitude of variability among genotypes was different significantly for all characters studied. The estimates of phenotypic coefficient of variation were higher than the corresponding genotypic coefficient of variation for all the characters which indicating the role of environment factors influencing the characters studied (Table 1). The present findings are in accordance with the findings of Gowsalya *et al.* [12] Panigrahi *et al.* [13] and Priyanka *et al* [14]. The phenotypic and genotypic coefficient of variation was found higher for number of pods per plant (28.24% and 27.023%) followed by number of clusters per plant (26.671% and 25.656%), number of primary branches (24.956% and 21.024%) and harvest index (21.149% and 20.265%). Similar results were reported by Kuralarasan *et al.* [15] and Priya *et al.* for plant height, number of clusters per plant, number of primary branches per plant and number of pods per plant. Suggesting that there is ample scope for selection for superior mutants due to preponderance of additive gene action.

Quantitative characters are influenced more by the environment. The phenotypic observed will not be transmitted to another generation entirely. Hence, study on heritable portion of variability is necessary. Heritability is a good index of transmission of characters from parents to their offspring and helps us a tool for selecting elite genotypes from diverse genetic population. It gives an exact idea of heritable portion of variability. In present investigation, high heritability was reported for the characters *viz.,* number of clusters per plant (92.536%), number of primary branches (92.032%), harvest index (91.814%), pods per plant (91.675%), seed index (91.303%), plant height (88.11%), seed yield per plant (85.834%) and biological yield (69.578%) indicating that these characters may serve as effective selection parameters during breeding programme for the improvement of blackgram productivity. These results are in agreement for number of clusters per plant, number of primary branches per plant, pods per plant, seed index and plant height by Gowsalya *et al.* [12], Hemalatha *et al.* [7], Konda *et al.* [16] Panigrahi *et al.* (2014), Priyanka *et al.* (2016), Reddy *et al.* [17] Singh *et al.* [18] and Sowmini and Jayamani

[19]. Moderate heritability was reported for days to maturity (38.823%), number of seeds per pod (34.019%), pod length (33.39%) and days to 50% maturity (32.179%) indicating that selection of these characters are likely to accumulate more additive genes leading to further improvement of their performance. The present findings are in accordance with the findings of Gowsalya *et al.* (2016) and Panigrahi *et al.* (2014) except for pod length.

Genetic advance predicts the genetic gain under selection. Genetic advance as percentage of mean is more reliable index for understanding the effectiveness of selection in improving the traits because estimated value is derived by involvement of heritability, phenotypic standard deviation and intensity of selection. High genetic advance as percent of mean was observed for number of pods per plant (53.301%), number of clusters (50.841%), number of branches (47.313%), seed index (41.384%), seed yield (40.452%), harvest index (40.001%), plant height (36.126%) and biological yield (21.084%). Similar findings were also observed by Aftab *et al.* [20] Low genetic advance as percent of mean was observed in pod length (5.363%), seed yield per pod (5.21%), days to 50% flowering (2.372%) and number of days to maturity (1.363%). Similar findings were also observed by Aftab *et al.* [20].

High heritability alone is not enough to make sufficient improvement through detection in advanced generations unless accompanied by substantial amount of genetic advance. The genetic advance as percent of mean is therefore a useful indicator to achieve the expected results on the traits of interest from a population after selection. In the present study, high estimates of heritability coupled with high genetic advance as percent of mean was observed for number of clusters (92.536% and 50.841%0, number of branches (92.032% and 47.313%), harvest index (91.814% and 40.001%), number of pods per plant (91.675% and 53.301%), seed index (91.303% and 41.384%), plant height (88.11% and 36.126%), seed yield per plant (85.834% and 40.001%) and biological yield (69.578% and 21.084%) respectively suggesting that there was preponderance of additive gene action governing the inheritance of this character and offers the best possibility of improvement through simple selection. These findings are in agreement with the results of Aftab *et al.* [20], Gowsalya *et al.* (2016), Kuralarasan *et al.* (2018) and Singh *et al.* [18].

The genotypic and phenotypic correlation coefficient among different characters of blackgram genotypes are presented in Table 2. In the present investigation, seed yield per plant showed positive significant association with harvest index, pod length, days to maturity, biological yield, number of primary branches per plant and days to 50% flowering at both phenotypic and genotypic level except for days to 50% flowering it showed non-significant positive association at phenotypic level. Similar findings were reported for number of primary branches, days to 50% flowering and days to maturity by Punia *et al.* [21]. Bharti *et al.* [22] reported similar findings for harvest index and biological yield. These results were in accordance with the findings of Shivade et al. [23] for pod length.

The estimates of correlation coefficient revealed only the relationship between yield components but did not show the direct and indirect effect of different traits on yield. This is because the attributes which are in association do not exist by themselves but are linked tother components. But the results of path coefficient analysis for grain yield and yield components can describe genotypic correlation to direct and indirect effects (Table 3). The highest positive direct effect on

seed yield per plant was exhibited by harvest index (0.989) followed by biological yield (0.967), seed index (0.245), number of pods per plant (0.177) and number of primary branches per plant (0.36) at genotypic levels and at phenotypic level high positive direct effect on seed yield per plant exhibited by harvest index (0.782), biological yield (0.481), number of pods per plant (0.041) and days to 50% flowering (0.041). hence selection based on these traits would be effective in increasing the seed yield.

On contrary, number of seeds per pod recorded negative direct effect on seed yield followed by number of clusters per plant, pod length, days to maturity, days to 50% flowering and plant height at genotypic level. At phenotypic level number of clusters per plant, days to maturity and seed index showed negative direct effect.

Considering the nature and magnitude of trait association and their direct and indirect effects, it can be inferred that simultaneous improvement of grain yield is possible through manifestation of harvest index, number of clusters per plant. Hence, it would be rewarding to lay stress on these characters in selection programme for increasing the grain yield.

Table 1. Genetic parameters for 12 quantitative characters of blackgram genotype

S. No.	Characters	Var Genotypical	Var Phenotypical	GCV	PCV	H^2 (Broad Sense)	Genetic Advancement	Gen. Adv as % of Mean
1	Days to 50 % flowering	0.943	2.931	2.03	3.579	32.179	1.135	2.372
2	Plant height	32.869	37.305	18.683	19.904	88.11	11.086	36.126
3	Number of pr branches plant	1.431	1.555	23.941	24.956	92.032	2.364	47.313
4	Number of clusters plant	2.241	2.421	25.656	26.671	92.536	2.966	50.841
5	Number of pods/ plant	8.577	9.356	27.023	28.224	91.675	5.776	53.301
6	Number of seeds per pod	0.085	0.248	4.337	7.436	34.019	0.349	5.211
7	Number of days to maturity	0.554	1.428	1.065	1.709	38.823	0.956	1.366
8	Pod length	0.04	0.12	4.505	7.796	33.39	0.238	5.363
9	Seed index	0.695	0.761	21.024	22.003	91.303	1.641	41.384
10	Biological yield	2.609	3.749	12.27	14.71	69.578	2.775	21.084
11	Harvest index	8.41	9.16	20.265	21.149	91.814	5.724	40.001
12	Seed yield per plant	0.16	0.187	21.195	22.878	85.834	0.765	40.452

Table 2. Genotypic Correlation and Phenotypic Correlation Coefficient between seed yield and its related traits of blackgram

Characters	Correlation coefficient	Plant height	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	Days to maturity	Pod length	Seed index	Biological yield	Harvest index	Seed yield per plant
Days to 50% flowering	r_g	-0.0610	0.480**	-0.1587	-0.1366	-0.369*	0.852**	0.1216	0.1659	-0.1416	0.508**	0.377*
	r_p	-0.0193	0.2516	-0.1212	-0.0683	-0.0939	0.340*	0.272*	0.1278	-0.0474	0.271*	0.2379
Plant height	r_g	**1.0000**	0.394*	-0.0047	-0.0345	-0.2196	-0.0770	0.329*	-0.0200	0.392*	-0.1060	0.1196
	r_p	**1.0000**	0.359*	-0.0046	-0.0164	-0.1376	-0.0524	0.1702	-0.0031	0.294*	-0.1249	0.0745
Number of primary branches per plant	r_g		**1.0000**	0.1500	0.1632	0.2477	0.549**	0.721**	0.0617	0.0694	0.384*	0.428**
	r_p		**1.0000**	0.1281	0.1632	0.1339	0.324*	0.430**	0.0494	0.0366	0.354*	0.336*
Number of clusters per plant	r_g			**1.0000**	0.768**	0.637**	0.0006	0.343*	0.318*	-0.0064	0.1940	0.1380
	r_p			**1.0000**	0.715**	0.444**	0.0856	0.1616	0.291*	0.0006	0.1838	0.1182
Number of pods per plant	r_g				**1.0000**	0.912**	0.1800	0.537**	0.309*	0.0091	0.2433	0.1881
	r_p				**1.0000**	0.538**	0.1419	0.311*	0.279*	-0.0083	0.1822	0.1550
Number of seeds per pod	r_g					**1.0000**	0.1348	0.822**	0.2535	0.0425	0.2303	0.2098
	r_p					**1.0000**	0.1269	0.2532	0.1618	0.1260	0.0862	0.1427
Days to maturity	r_g						**1.0000**	0.675**	0.1800	0.2167	0.479**	0.585**
	r_p						**1.0000**	0.2199	0.0576	0.1446	0.280*	0.271*
Pod length	r_g							**1.0000**	0.1227	0.657**	0.333*	0.738**
	r_p							**1.0000**	0.0381	0.263*	0.2112	0.383*
Seed index	r_g								**1.0000**	-0.266*	0.0163	-0.0737
	r_p								**1.0000**	-0.1594	-0.0013	-0.0847
Biological yield	r_g									**1.0000**	-0.1602	0.533**
	r_p									**1.0000**	-0.1313	0.397*
Harvest index	r_g										**1.0000**	0.803**
	r_p										**1.0000**	0.730**

* and ** indicates 5% and 1% level of significance respectively

Table 3. Direct and indirect effects at Genotypic level and Phenotypic level of different quantitative traits on seed yield

Characters		Days to 50% flowering	Plant height	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	Days to maturity	Pod length	Seed index	Biological yield	Harvest index	Seed yield per plant
Days to 50% flowering	**G**	**-0.1111**	0.0068	-0.0533	0.0176	0.0152	0.0410	-0.1285	-0.0135	-0.0184	0.0157	-0.0564	0.377*
	P	**0.0406**	-0.0008	0.0102	-0.0049	-0.0028	-0.0038	0.0138	0.0110	0.0052	-0.0019	0.0110	0.2379
Plant height	G	0.0177	**-0.2901**	-0.1142	0.0014	0.0100	0.0637	0.0223	-0.0955	0.0058	-0.1137	0.0307	0.1196
	P	-0.0003	**0.0144**	0.0052	-0.0001	-0.0002	-0.0020	-0.0008	0.0025	0.0000	0.0042	-0.0018	0.0745
Number of primary branches per plant	G	0.1731	0.1419	**0.3605**	0.0541	0.0588	0.0893	0.1979	0.2600	0.0223	0.0250	0.1386	0.428**
	P	0.0021	0.0031	**0.0085**	0.0011	0.0014	0.0011	0.0028	0.0037	0.0004	0.0003	0.0030	0.336*
Number of clusters per plant	G	0.0269	0.0008	-0.0254	**-0.1692**	-0.1299	-0.1077	-0.0001	-0.0580	-0.0538	0.0011	-0.0328	0.1380
	P	0.0077	0.0003	-0.0081	**-0.0634**	-0.0453	-0.0282	-0.0054	-0.0102	-0.0184	0.0000	-0.0116	0.1182
Number of pods per plant	G	-0.0242	-0.0061	0.0289	0.1359	**0.1771**	0.1614	0.0319	0.0950	0.0548	0.0016	0.0431	0.1881
	P	-0.0028	-0.0007	0.0067	0.0295	**0.0413**	0.0222	0.0059	0.0128	0.0115	-0.0003	0.0075	0.1550
Number of seeds per pod	G	0.0646	0.0384	-0.0433	-0.1114	-0.1595	**-0.1749**	-0.0236	-0.1955	-0.0444	-0.0074	-0.0403	0.2098
	P	-0.0012	-0.0018	0.0017	0.0058	0.0070	**0.0130**	0.0017	0.0033	0.0021	0.0016	0.0011	0.1427
Days to maturity	G	-0.1572	0.0105	-0.0746	-0.0001	-0.0245	-0.0183	**-0.1359**	-0.0917	-0.0245	-0.0295	-0.0651	0.585**
	P	-0.0180	0.0028	-0.0171	-0.0045	-0.0075	-0.0067	**-0.0529**	-0.0116	-0.0030	-0.0076	-0.0148	0.271*
Pod length	G	-0.0191	-0.0517	-0.1133	-0.0538	-0.0843	-0.1755	-0.1060	**-0.1570**	-0.0193	-0.1032	-0.0522	0.738**
	P	0.0217	0.0136	0.0343	0.0129	0.0248	0.0202	0.0176	**0.0798**	0.0030	0.0210	0.0169	0.383*
Seed index	G	0.0406	-0.0049	0.0151	0.0779	0.0757	0.0621	0.0440	0.0300	**0.2447**	-0.0651	0.0040	-0.0737
	P	-0.0010	0.0000	-0.0004	-0.0022	-0.0022	-0.0012	-0.0004	-0.0003	**-0.0077**	0.0012	0.0000	-0.0847
Biological yield	G	-0.1369	0.3788	0.0671	-0.0062	0.0088	0.0411	0.2095	0.6353	-0.2570	**0.9668**	-0.1549	0.533**
	P	-0.0228	0.1413	0.0176	0.0003	-0.0040	0.0606	0.0696	0.1266	-0.0767	**0.4811**	-0.0632	0.397*
Harvest index	G	0.5021	-0.1048	0.3801	0.1918	0.2406	0.2277	0.4736	0.3289	0.0161	-0.1584	**0.9886**	0.803**
	P	0.2118	-0.0977	0.2768	0.1437	0.1425	0.0674	0.2190	0.1652	-0.0010	-0.1027	**0.7821**	0.730**
Seed yield per plant	G	0.377*	0.1196	0.428**	0.1380	0.1881	0.2098	0.585**	0.738**	-0.0737	0.533**	0.803**	**1.0000**
	P	0.2379	0.0745	0.336*	0.1182	0.1550	0.1427	0.271*	0.383*	-0.0847	0.397*	0.730**	**1.0000**

Table 4. Grouping of genotypes based on scoring for yellow mosaic virus in blackgram

Rating	Reaction	Genotypes
1 to 2.0	Resistant (R)	PU-31
2.1 to 4.0	Moderately Resistant (MR)	LBG-645, LBG-644, GBG-45, LBG-402, NRI 2-B-3, NHOU-06, IPU-94-1, KU-42, NRI (interspecific cross), UHOU-06, G-13, KU-99-16, G-14, KU-96-1, G-19
4.1 to 5.0	Moderately Susceptible (MS)	KPU 524-645, GBG-12
5.1 to 7.0	Susceptible (S)	LBG-20, LBG-77
7.1 to 9.0	Highly Susceptible (HS)	-

A total of 20 genotypes of blackgram were screened against YMV disease during *kharif-2021* to identify tolerant/resistant genotypes for YMV. The data on disease resistance/susceptibility reaction of blackgram genotypes for YMV disease were presented in Table 4. In the present study 1 genotype showed resistant (R) with rating of 0.0. Fifteen genotypes showed moderately resistant reaction with a rating of 2.1 to 4.0 viz., LBG-645, LBG-644, GBG-45, LBG-402, NRI 2-B-3, NHOU-06, IPU-94-1, KU-42, NRI (interspecific cross), UHOU-06, G-13, KU-99-16, G-14, KU-96-1, G-19. Two genotypes showed moderately susceptible reaction (MS) with a rating of 4.1 to 5.0 viz., KPU 524-645, GBG-12. Remaining 2 genotypes showed susceptible reaction with a rating of 5.1 to 7.0 viz., LBG-20, LBG-77. Identification of resistant lines is essential in the ambit of integrated disease management which is an upcoming concept in the field of agriculture. PU-31 is the resistant genotype observed in the present study and can be utilized in resistance breeding programme.

4. CONCLUSION

From the present study, it can be concluded that genotypes which showed most difference among themselves *viz.,* KU-99-16, LBG-77, GBG-12 and KPU 524-645 for different yield contributing traits can be utilized as percent in crossing programme. Seed yield per plant showed positive and significant association with harvest index, pod length, days to maturity and biological yield. High direct effect on seed yield per plant at both genotypic and phenotypic levels with harvest index, biological yield, days to 50% flowering and number of pods per plant. Selection of plants on these traits would certainly lead to improvement in grain yield. Further harvest index followed by pod length, days to maturity and biological yield showed high correlation with seed yield per plant should be given importance while selecting for high yield. Lowest diseased genotypes PU-31 can be used to breed for resistance to YMV.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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