Original Research Article

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

Comment [AC1]: Title is too long, It is suggested: Genetic variability and character association studies on Blackgram (*Vigna mungo* (L.) Hepper) include the site where the work was performed

ABSTRACT

Analysis of variance showed highly significant differences among 20 genotypes of black gram 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 branches, harvest index, number of pods per plant, seed index, plant height, seed yield per plant, 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 biological yield, seed index, number of pods per plant and number of primary branches per plant at genotypic levels and at phenotypic level high positive direct effect on seed yield per plant 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.

Comment [AC2]: The abstract only presents the results in a descriptive way and does not include the problem, the justification, the objectives, the methodology of the work, nor are the main findings of the research presented.

Keywords: Blackgram, variability, correlation, Association.

Comment [AC3]: Consult international thesauri to make a better selection of keywords.

INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) known as urd-bean, 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 **(Gupta and Gopalakrishna, 2009)** and assumes considerable importance from the point of food and nutritional security in the world.

According to **Vavilov (1926),** blackgram has originated from Indian subcontinent. 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 **(Anon., 1999)** and hence lustre 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. It is mainly due to the repeated usage of few parents with high degree of relatedness in crossing programmes **(Jayamani and Sathya, 2013)**.

Comment [AC4]: Try to include more current references.

Success of yield improvement largely depends upon the magnitude and nature of genetic variability present in yield contributing traits **(Johnson *et al.*, 1955).**

The development of a suitable plant breeding program is dependent on the presence of genetic variability. Study of inheritance of various quantitative and qualitative traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance 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. Association studies give an idea about the contribution of different characters towards grain yield and it reveals the type, nature and magnitude of correlation between yield components with yield and among themselves. Estimation of correlation coefficient enables to eliminate the characters with little or no importance during selection. Path coefficient analysis suggested by (**Dewey and Lu, 1959)** 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.

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Comment [AC6]: More and updated references should be included in this part.

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). Mungbean yellow mosaic virus is one of the most prevalent and destructive viral pathogens in mungbean. It causes severe yield loss and a reduction in seed quality. Identifying resistant donors is a very complicated task due to the lack of reliable screening protocol for assessing the resistance/susceptibility of existing varieties. Realizing the importance and need for a comprehensive study in blackgram, the present investigation was undertaken to identify high yielding Blackgram genotypes for good quality traits, to establish a relationship between quantitative traits with seed yield and to identify the yellow mosaic virus resistant genotypes in Blackgram.

Comment [AC7]: In the introduction it is necessary to delve a little more into the research problem and the background studies must be focused within the international, national and regional context, no conclusive studies are presented to support the research.

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 Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P during *kharif*- 2021 season. In each replication, genotype was sown in a single row of four meter length with spacing of 30 x 10 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 accessions 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 (1967**). Phenotypic and genotypic coefficients

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of variation were calculated based on the method advocated by **Burton (1952**). Heritability and genetic advance as per-cent of mean were estimated as per formula given by **Johnson *et al.* (1955).**The phenotypic and genotypic correlation coefficients were calculated from phenotypic and genotypic variances and covariances and path coefficients analyses were worked out as suggested by **Dewey and Lu (1959).**

Comment [AC9]: It is suggested to better organize the methodology so that it is more understandable as follows: Location, Plant material where a table can be included presenting the general characteristics of the accessions used and also the place of origin. Then continue with the Experimental design, clearly specifying the experimental unit, the repetitions and the treatments. The variables should be better described in terms of how they were measured and the frequency of measurement and end with the Analysis of the information.

RESULTS AND DISCUSSION

The analysis of variance was carried out for twelve quantitative characters. The variance due to treatment was significant for all eleven characters studied. This gives the evidence of magnitude of variability among genotypes were differed 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 that the environment factors influencing the characters studied (Table 1). The present findings are in accordance with the findings of **Panigrahi *et al.* (2014), Priyanka *et al.* (2016) and Gowsalya *et al.* (2016**). The phenotypic and genotypic coefficient of variation was found higher for number of pods per plant (28.224%, 27.023) followed by number of clusters per plant (26.671% and 25.656%), number of primary branches (24.956% and 23.941%), seed yield per plant (22.878% and 21.195), seed index (22.003% and 21.024%) and harvest index (21.149% and 20.265%). Similar results are reported by **Panigrahi *et al.* (2014)** except for plant height. Suggesting that sufficient phenotypic variability was present for these traits.

Comment [AC10]: Hence the importance of determining where they come from or what is the origin of the genetic materials evaluated.

Comment [AC11]: The discussion is not only about mentioning the studies, but it is necessary to argue why they are related, where they were carried out and in what species.

Quantitative characters are influenced more by the environment. The phenotype observed will not be transmitted to another generation entirely. So, 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 as 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 character viz., number of cluster 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%) and seed yield per plant (85.834%) and biological yield (69.578%) (Table 2) 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 cluster per plant, number of primary branches per plant, pods per plant, seed index and plant height with the results of **Gowsalya *et al.* (2016), Hemalatha *et al.* (2017) Konda *et al.* (2009), Panigrahi *et al.* (2014), Priyanka *et al.* (2016), Reddy *et al.* (2012), Singh *et al.* (2014) and Sowmini and Jayamani (2013).**

Comment [AC12]: These arguments must be supported by bibliographical references.

Comment [AC13]: Take into account the previous observation.

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 accumulates more additive genes leading to further improvement of their performance. The present findings are in accordance with the findings of **Panigrahi *et al.* (2014) and Gowsalya *et al.* (2016)** 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 its 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.* (2018).** Low genetic advance as percent of mean was observed in pod length (5.363), seed yield per pod (5.21%), day to 50% flowering (2.372%) and number of days to maturity (1.363%). Similar findings were also observed by **Aftab *et al.* (2018).**

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Comment [AC15]: There is no discussion at the biological, agronomic and genetic level of the results found, the comparative studies are not discussed, and many of them are outdated.

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 a percent of mean is therefore a useful indicator to achieve the expected result 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 cluster (92.536%, 50.841%), number of branches (92.032%, 47.313%), harvest index (91.814%, 40.001%), number of pods per plant (91.675%, 53.301%), seed index (91.303% and 41.384%), plant height (88.11%, 36.126%), seed yield per plant (85.834%, 40.001%), biological yield (69.578%, 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. The findings are in agreement with the results of **Aftab *et al.* (2018), Gowsalya *et al*. (2016), Kuralarasan *et al.* (2018) and Singh *et al*. (2014).**

Comment [AC16]: Take into account the previous observations.

The genotypic and phenotypic correlation coefficients among different characters of blackgram genotypes are presented in Table 3 and Table 4. 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 levels 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 **Punia *et al.* (2014)**. **Bharti *et al.* (2013)** reported similar findings for harvest index and biological yield. These results were in accordance with the findings of **Shivade *et al.* (2011)** for pod length.

The estimates of correlation coefficients revealed only the relationship between yield components, but did not show the direct and indirect effects of different traits on yield. This is because the attributes which are in association do not exist by themselves, but are linked to other components. But the result of path coefficient analysis for grain yield and yield components can describe genotypic correlations 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 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.

Yellow Mosaic Virus disease was screened on the basis of 0-9 arbitrary scale according to **Mohan *et al.* (2014)**. Out of twenty genotypes screened for resistance to yellow mosaic virus (YMV), not a single genotypes showed Free (F) or Highly Resistant (HR) reaction. One genotypes namely Pant U-31 showed resistant reaction; whereas fifteen genotypes namely 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 showed moderate resistance reaction against the yellow mosaic virus. Genotypes namely KPU 524-645, GBG-12 showed moderately susceptible reaction whereas two genotypes namely LBG-20, LBG-77 showed susceptible reaction against YMV. The details are presented in Table 5.

Comment [AC17]: This must be included in the methodology.

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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 parent 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.

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

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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 per 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

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**

Comment [AC20]: The meaning of the abbreviations used should be explained.

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

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

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**

Comment [AC21]: Take into account the previous observations.

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

Table 4: Grouping of genotypes based on scoring for yellow mosaic virus in blackgram evaluated during *kharif* 2021 at Prayagraj

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)	-