Original Research Article

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Estimation of Genetic Variability and Character Association for Yield Characters in Blackgram (*Vigna mungo* (L.) Hepper)

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ABSTRACT

Keywords

Black gram, GCV, PCV, Variability, Heritability, Correlation, Path analysis

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The present investigation was carried out with a view to study the magnitude of variability, correlation and path analysis excluding reciprocals involving 25 genotypes in Black gram during *Kharif* - 2019. The experimental material was planted in randomized block design with three replications at the Field Experimentation Centre, Department of Genetics and Plant Breeding, SHUATS, Prayagraj, U.P. The analysis of variance indicated that parents were significant for all the characters, indicating presence of considerable amount of genetic variability in the germplasm tested. Number of clusters per plant, seed yield per plant exhibited high GCV, PCV and genetic parameters revealed that heritability (broad sense) and genetic advance as % of mean values were high for days to maturity, harvest index, but in case of genetic advance and genetic advance as % of mean values were high for seed yield per plant indicating that selection would be fruitful for improvement of these traits. Correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant association with Number of branches per plant, harvest index, Number of pods per plant, Number of seeds per pod. The Path coefficient analysis indicated that selection for days to maturity, Plant height, Number of clusters per plant, seed index, harvest index, would directly increase seed yield. The genotypes SHEKAR -3, IPU862 X IPU96-1, SHEKAR, and G.C 9120 X IC106194 were observed as promising genotypes for importance quantitative traits.

Introduction

Black gram (*Vigna mungo* L. Hepper, 2n=22) is an important self-pollinated and short duration legume crop belonging to the family Leguminosae and sub-family Papilionaceae. India is the center of origin of black gram (Mehra *et al.*, 2016). It is popularly known as “urd bean and mash” is an important short duration and self pollinated *Kharif* legume

crop and is an important part of Indian diet. It is rich source of protein (25-28%), carbohydrates (62-65%), fiber(3.5- 4.5%), ash (4.5-5.5%), oil (0.5- 1.5%), amino acids like lysine, vitamins like thiamine, niacin, riboflavin and much needed iron and phosphorus (Sohel *et al.*, 2016). Black gram was sown over an area of 50.31 lakh/ha and recorded a production of 32.84 lakh tonnes and yield level of 653 kg/ha in India. Where

as the total coverage under Black gram in Uttar Pradesh is 5.88 Lha with a production 3.05 Lt. and the productivity 520 kg/ha (*Directorate Pulse Development, Ministry of Agriculture & Farmers Welfare-2018-19*). The per capita availability of pulses has declined from 60.7 g/day in 1951 to 35.5 g day⁻¹ in 2007 as against the FAO/WHO's recommendation of 80 g/day (Economic Survey, 2008-09). Blackgram has a wide range of economic value. It is well known that 50 g pulses/person/day should be consumed in addition to other sources of protein such as cereals, milk, meat and egg which is very difficult task to achieve as the production and productivity of pulse crops including the blackgram is very low. Hence, there is a strong need to improve the productivity of crop. This could be achieved by studying the genetic architecture of this crop for yield improvement.

Materials and Methods

Description of the Study Area

The present investigation was carried out at the Field Experimentation Centre, Department of Genetics and Plant Breeding, SHUATS, Prayagraj (U.P.) during *Kharif*, 2019. The University is situated on the left side of Prayagraj - Rewa National Highway, about 5 km away from Prayagraj city. All types of facilities necessary for cultivation of successful crop including field preparation, inputs and irrigation facilities were provided from the Department of Genetics and Plant Breeding, SHUATS, Prayagraj (U.P.).

2.2 Experimental Design and Procedure.

The experiment was conducted in randomized block design with 25 genotypes which were replicated 3 times. Genotypes were randomly arranged in each replication divided into 75 plots. The gross area of experiment was 180m² and each plot size was 1 x 1 m. The

row to row spacing was 30 cm and plant to plant distance was 10 cm.

2.3 Data source and analysis.

Data were recorded from 13 characters viz, days to 50 % flowering, days to 50% pod setting, days to maturity, plant height (cm), number of branches per plant, number of cluster per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed index (g), biological yield (g), harvest index and seed yield per plant (g).

The 5 competitive plants from each of the replication were tagged and observations were taken from these tagged plants at various stages of the crop plant growth.

Mean values were computed and data were analysed for analysis of variance as suggested by (Fisher, 1936) and coefficient of variances as well as heritability (in broad sense), as suggested by Burton and Devane (1953). The estimates of genetic advance were obtained by the formula suggested by Lush (1949) and Johnson *et al.*, (1955). Phenotypic and genotypic correlation and path coefficients of variation were computed as per the method given by Dewey and Lu(1959).

Results and Discussion

Analysis of variance

Mean sum of squares data for 13 characters were subjected to analysis of variance for experimental design.

The analysis of variance for different characters is presented in Table 1. The mean squares due to genotypes showed highly significant differences ($\alpha = 0.01$) for all characters which showed significant differences ($\alpha = 0.05$) indicating the presence of substantial amount of genetic variability among the Black gram genotypes.

Table.1 Analysis of variance for 13 Quantitative characters in Black gram

S. No	Character	Mean sum of squares		
		Replication (d.f.=2)	Treatment (d.f.=19)	Error (d.f.=38)
1	Days to 50% flowering	24.3735	5.041**	2.193
2	Days to 50% Pod setting	27.3735	4.83**	2.123
3	Days to maturity	0.2165	9.18**	0.108
4	Plant height (cm)	1754.24	73.58**	24.23
5	Number of branches/plant	0.9835	1.89**	0.631
6	Number of clusters /plant	20.845	14.92**	1.85
7	Number of pods /plant	43.8655	28.68**	7.122
8	Number of seeds / pod	0.0195	0.071**	0.015
9	Pod length (cm)	0.459	0.69**	0.235
10	Seed index (g)	0.0225	0.13**	0.04
11	Biological yield	2.4155	14.38**	2.489
12	Harvest Index	8.8205	118.73**	25.293
13	Seed yield / plant	0.805	0.86**	0.05

* Significance at 5% level, ** Significance at 1% level

Table.2 Genetic parameters for 13 Quantitative traits of Blackgram genotypes

S.No	Character	GCV	PCV	h^2bs	GA	GA as % mean
1	Days to 50% flowering	2.166	3.94	30.216	1.103	2.453
2	Days to 50% pod setting	1.791	3.278	29.846	1.07	2.016
3	Days to maturity	2.459	2.506	96.342	3.52	4.973
4	Plant height	6.796	10.687	40.446	5.314	8.904
5	No. of branches/ plant	7.161	11.328	39.962	0.844	9.326
6	No. of clusters/ plant	17.475	20.857	70.195	3.602	30.16
7	No. of pods /plant	13.567	19.144	50.221	3.913	19.805
8	No. of seeds / plant	6.703	10.679	39.393	0.505	8.666
9	Pod length	3.341	4.509	54.904	0.208	5.1
10	Seed index	4.71	7.165	43.222	0.237	6.379
11	Biological yield	13.564	17.307	61.422	3.214	21.899
12	Harvest index	9.061	9.869	84.287	0.98	17.136
13	Seed yield / plant	13.964	18.797	55.186	8.541	21.369

VG= Genotypic variance VP = Phenotypic variance

GCV=Genotypic coefficient of variation PCV= Phenotypic coefficient of variation

 h^2 (bs) = Heritability broad sense GA= Genetic advance

Table.3 Correlation coefficient between yield and its related traits in Blackgram genotypes at genotypic level

Characters	Days to 50% flowering	Days to 50% pod setting	Days to Maturity	Plant height	No. of branches / plant	No. of clusters / plant	No of pods / plant	No. of seed /pod	Pod length	Seed index	Biological yield	Harvest Index	Seed yield/plant
Days to 50% flowering	1	0.136	-0.163	0.513**	0.228*	0.229*	0.085	0.252*	-0.752**	-0.045	-0.213	-0.548**	-0.217
Days to 50% pod setting		1	0.845**	0.250*	-0.249*	0.270*	0.273*	0.021	0.286*	0.275*	0.185	0.205	0.066
Days to Maturity			1	-0.020	-0.055	0.207	0.027	-0.020	0.512**	-0.037	-0.087	0.115	0.201
Plant height				1	0.652**	-0.034	0.000	0.144	-0.416**	0.169	0.093	0.122	-0.248*
No. of branches /plant					1	-0.250*	-0.188	0.018	-0.226*	0.246*	-0.157	0.213	0.285*
No. of cluster s/plant						1	0.680**	0.713**	0.179	0.052	0.114	0.173	0.254*
No of pods /plant							1	0.716**	0.050	0.512**	0.272*	0.367**	0.037
No. of seed /pod								1	0.090	0.134	0.111	0.380**	0.340**
Pod length									1	0.039	0.041	0.196	0.214
Seed index										1	0.375**	0.203	-0.151
Biological yield											1	0.275*	0.735**
Harvest Index												1	0.440**
Seed yield /plant													1

* Significance at 5% level, ** Significance at 1% level

Table.4 Correlation coefficient between yield and its related traits in Blackgram genotypes at phenotypic level

Characters	Days to 50% flowering	Days to 50% pod setting	Days to Maturity	Plant height	No. of branches / plant	No. of clusters / plant	No of pods / plant	No. of seed /pod	Pod length	Seed index	Biological yield	Harvest Index	Seed yield/plant
Days to 50% flowering	1	-0.009	-0.109	0.159	0.267*	0.107	-0.047	0.030	-0.363**	0.011	0.217*	-0.267*	-0.037
Days to 50% pod setting		1	0.425**	-0.029	-0.113	0.251*	0.035	-0.026	0.226*	0.001	-0.021	0.181	0.161
Days to Maturity			1	-0.009	-0.034	0.158	0.267*	-0.047	0.367**	0.003	-0.072	0.271*	0.152
Plant height				1	0.332**	0.008	0.085	0.081	0.262*	0.131	0.177	0.312**	-0.096
No. of branches /plant					1	0.084	0.167	-0.244	-0.040	-0.277	0.251*	0.087	0.389**
No. of clusters/plant						1	0.624**	0.564**	0.247*	0.044	0.180	0.153	0.419**
No of pods/plant							1	0.455**	0.149	0.281*	0.259*	0.262*	-0.027
No. of seed /pod								1	0.184	0.363**	0.175	-0.343*	0.403**
Pod length									1	-0.029	0.421**	-0.413**	0.014
Seed index										1	0.251*	0.107	-0.128
Biological yield											1	0.143	-0.808**
Harvest Index												1	0.443**
Seed yield /plant													1

* Significance at 5% level, ** Significance at 1% level

Table.5 Direct and indirect effects between yield and its different traits in Blackgram genotypes at genotypic level

Characters	Days to 50% flowering	Days to 50% pod setting	Days to Maturity	Plant height	No. of branches / plant	No. of clusters / plant	No of pods / plant	No. of seed /pod	Pod length	Seed index	Biological yield	Harvest Index	Seed yield/plant
Days to 50% flowering	-0.4987	-0.17244	-0.24187	0.63912	-0.2967	0.11538	-0.06361	0.1528	1.0095	-0.0503	0.31385	0.12439	-0.217
Days to 50% pod setting	-0.20408	-0.2663	0.25448	0.31126	0.32402	0.1362	-0.2035	0.0129	-0.38352	0.30971	- 0.27163	0.04645	0.066
Days to Maturity	0.24429	-0.07056	0.48388	-0.0251	0.07102	0.10453	-0.02041	-0.01216	-0.68642	-0.04217	0.12825	0.0261	0.201
Plant height	-0.76879	-0.31636	-0.02989	0.2459	-0.8488	-0.0171	-0.00032	0.08732	0.55801	0.19033	-0.13624	0.02768	-0.248
No. of branches /plant	-0.34141	0.315	-0.0809	0.81183	-0.303	-0.1259	0.13981	0.01117	0.30279	0.27635	0.23057	0.04828	0.285
No. of cluster s/plant	-0.34259	-0.3417	0.30731	-0.0423	0.325	0.5048	-0.50631	0.43238	-0.24059	0.05895	- 0.16783	0.03925	0.254
No of pods/plant	-0.12808	-0.34625	0.0407	0.00054	0.24469	0.34339	-0.74426	0.43418	-0.06671	0.57589	- 0.40023	0.08334	0.037
No. of seed /pod	-0.37788	-0.02695	-0.02978	0.17953	-0.024	0.36014	-0.53322	0.60601	-0.12109	0.15083	- 0.16363	0.08626	0.34
Pod length	0.12776	-0.36202	0.75925	-0.5182	0.294	0.09052	-0.03701	0.0547	-0.3415	0.04392	0.05821	0.04455	0.214
Seed index	0.06697	-0.34845	-0.0556	0.21069	-0.3198	0.02644	-0.3808	0.08121	-0.05234	0.12555	- 0.55128	0.04597	-0.151
Biological yield	0.31974	-0.23382	-0.12936	0.11539	0.20416	0.05759	-0.20248	0.06741	0.05308	0.42178	-	0.06235	0.735
Harvest Index	0.8213	-0.25912	0.17063	0.15194	-0.277	0.08728	-0.27325	0.23029	-0.26331	0.22794	- 0.40407	0.22699	0.44

* Significance at 5% level, ** Significance at1%level Residual effect0.06678

Table.6 Direct and indirect effects between yield and its different traits in Blackgram genotypes at phenotypic level

Characters	Days to 50% flowering	Days to 50% pod setting	Days to Maturity	Plant height	No. of branches / plant	No. of clusters / plant	No of pods / plant	No. of seed /pod	Pod length	Seed index	Biological yield	Harvest Index	Seed yield/plant
Days to 50% flowering	-0.04378	-0.00034	-0.00037	0.00304	0.00091	0.00073	-0.00334	-0.00102	0.00115	0.00028	0.14968	-0.14411	- 0.037
Days to 50% pod setting	0.00039	0.0381	0.00145	-0.0006	0.00152	0.00086	0.00251	0.0009	-0.00072	0.00001	0.01949	0.09745	0.161
Days to Maturity	0.00479	0.01619	0.0034	-0.0002	0.00046	0.00108	0.00077	0.00161	-0.00116	0.00008	0.0659	0.05929	0.152
Plant height	-0.00697	-0.0011	-0.00003	0.0191	-0.0045	0.00006	0.00604	-0.00278	0.00038	0.00327	-0.16162	0.05192	-0.096
No. of branches /plant	0.00297	-0.00432	-0.00012	0.00635	-0.013	0.00058	0.0118	-0.00042	0.00013	0.00272	-0.00788	0.04709	0.389
No. of clusters/p lant	-0.00468	0.00477	0.00054	0.00015	-0.0011	0.0068	0.04415	-0.01923	-0.00078	0.0011	-0.16408	0.08249	0.419
No of pods/plant	0.00206	0.00135	0.00004	0.00163	-0.0022	0.00427	0.07077	-0.01553	-0.00047	0.00703	-0.23701	0.14119	- 0.027
No. of seed /pod	-0.00131	-0.00101	-0.00016	0.00156	-0.0002	0.00386	0.03222	-0.0341	-0.00058	0.00187	-0.15973	0.11619	0.403
Pod length	0.01591	0.00863	0.00125	-0.0023	0.00054	0.00169	0.01053	-0.00627	-0.0032	-0.00072	-0.06367	0.0518	0.014
Seed index	-0.00049	0.00002	0.00001	0.0025	-0.0015	0.0003	0.01986	-0.00254	0.00009	0.02506	-0.22947	0.05786	- 0.128
Biological yield	0.00717	-0.00081	-0.00025	0.00338	-0.0001	0.00123	0.01836	-0.00596	-0.00022	0.00629	-0.91376	0.07698	- 0.808
Harvest Index	0.0117	0.00688	0.00037	0.00184	-0.0012	0.00105	0.01852	-0.00734	-0.0003	0.00269	-0.13038	0.53948	0.443

* Significance at 5% level, ** Significance at 1% level Residualeffect0.02103

Parameters of genetic variability

The parameters of genetic variability such as mean, range, phenotypic coefficient of variation (pcv), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance as percent of mean were estimated for all quantitative characters are presented in table 2. The Phenotypic coefficient of variation (PCV) ranged from 2.50 (days to maturity) to (20.85) number of clusters per plant. High PCV were recorded for number of clusters per plant (20.85). Low PCV were recorded for seed index (7.16), pod length (4.50), days to 50% flowering (3.94), days to 50% podsetting (3.27), days to maturity (2.50). Similar results are reported by Gowsalya *et al.*, (2016), Hemalatha *et al.*, (2017). Genotypic coefficient of variation ranged from days to 50% of podsetting (1.79) to number of clusters per plant (17.47). High GCV were recorded for number of clusters per plant (17.47).

Low GCV were recorded for number of seeds per plant (6.70), followed by seed index (4.71), pod length (3.34), days to maturity (2.45), days to 50 % of flowering (2.166), and days to 50% of podsetting (1.79). Similar results are reported by Kumar *et al.*, (2015), Gowsalya *et al.*, (2016), and Hemalatha *et al.*, (2017).

Heritability

The estimate of heritability (%) in the broad sense for 13 characters studied which range from 29.84 (days to 50 % of pod setting) to 96.34 (days to maturity). The highest heritability (broad sense) were recorded for characters i.e. days to maturity (96.34), harvest index (84.28), number of clusters per plant (70.19), and biological yield (61.42). The lowest heritability (broad sense) were recorded for characters plant height (40.44), number of branches per plant (39.96), number

of seeds per plant (39.39), days to 50 % of flowering (30.21), and days to 50 % of pod setting (29.84). Similar results are reported by Gowsalya *et al.*, (2016), Patel *et al.*, (2014).

Genetic advance (%)

The genetic advance (%) which ranged from 8.54 (seed yield per plant) to 0.208 (pod length). The highest genetic advance were recorded for seed yield per plant (8.54) followed by plant height (5.31), number of pods per plant (3.91), number of clusters per plant (3.60), days to maturity (3.52). The lowest genetic advance were recorded for harvest index (0.98), number of branches per plant (0.84), number of seeds per plant (0.50), pod length (0.23), and pod length (0.208). Similar results are reported by Priya *et al.* (2018).

Genetic advance as % of mean

The genetic advance as percent of mean varied from 30.16 (number of clusters per plant) to 2.0 (days to 50% of pod setting). The highest genetic advance as % of mean were recorded for no of clusters per plant (30.16) followed by biological yield (21.8), seed yield per plant (21.36), number of pods per plant (19.8) and harvest index (17.13). The lowest genetic advance as % of mean were recorded for days to maturity (4.9), days to 50% of flowering (2.4) and days to 50% of pod setting (2.0). Similar results are reported by Gowsalya *et al.*, (2016), Patel *et al.*, (2014), Punia *et al.*, (2014).

Correlation coefficient analysis

The correlation coefficient is a statistical measure which is used to find out the degree (strength) and direction of the relationship between two or more variable components (Panigrahi *et al.*, 2014).

Correlation with seed yield

Correlation coefficient analysis among grain yield and its contributing characters are shown in table 3 and table 4. Genotypic correlation coefficient analysis revealed that seed yield per plant showed highly significant and positive association with biological yield (0.735**), harvest index (0.440**), number of seeds per plant (0.340**), number of branches per plant (0.285*), number of clusters per plant (0.254*), and negative significant association with plant height (-0.248*). It also showed positive but non-significant association with Days to 50% of pod setting (0.066), number of pods per plant (0.037), pod length (0.214), days to maturity (0.201). While negative but non-significant association was recorded for Days to 50% flowering (-0.217), seed index (-0.151). Similar results are reported by Rajasekhar *et al.*, (2017), Mehra *et al.*, (2016), Kumar *et al.*, (2015). Phenotypic correlation coefficient analysis revealed that Seed yield per plant showed highly significant and positive association with harvest index (0.443**), number of seeds per plant (0.403**), number of clusters per plant (0.419**), number of branches per plant (0.389**). Positive non-significant association with pod length (0.014), days to maturity (0.152), days to 50% of pod setting (0.161). Negative significant association with biological yield (-0.808**). Negative non-significant association with seed index (-0.128), number of pods per plant (-0.027), plant height (-0.096), days to 50% of flowering (-0.037), these findings were in accordance with Rajasekar *et al.*, (2017), Mehra *et al.* (2016), Kumar *et al.* (2015), Punia *et al.*, (2014), Bharti *et al.*, (2014).

Path coefficient analysis

Path coefficient analysis is an efficient statistical technique specially designed to qualify the interrelationship of different

components and their direct and indirect effects on yield (Pushpa *et al.*, 2013).

Seed yield with other yield traits

Genotypic path coefficient analysis revealed that character seed yield per plant showed positive direct effect with Number of seeds per pod (0.60) followed by number of clusters per plant (0.540), days to maturity (0.48), plant height (0.24), harvest index (0.22) and seed index (0.12) where as it showed negative direct effect with days to 50 % of pod setting (-0.26) followed by pod length (-0.34) number of branches per plant (-0.30), biological yield (-0.47) days to 50 % of flowering (-0.49), and number of pods per plant (-0.74). Aijaz *et al.*, (2002), Singh *et al.*, (2009), Muzibul *et al.* (2010), and Reni *et al.*, (2013). Phenotypic path coefficient analysis revealed that character seed yield per plant showed positive direct effect with harvest index (0.539) followed by number of pods per plant (0.070), days to 50% of pod setting (0.038), days to maturity (0.0034), seed index (0.025), plant height (0.019) and number of clusters per plant (0.006). Whereas it showed negative direct effect with Biological yield (-0.91) followed by days to 50% of flowering (-0.04), number of branches per plant (-0.013), number of seeds per pod (-0.034), and pod length (-0.003) Rajasekhar *et al.*, (2017) Baudhbharti *et al.*, (2014), Mishra *et al.*, (2014) (Table 5 and 6).

From the present investigation it is concluded that analysis of variation showed significant variation to all the characters. Among 25 genotypes of black gram on the basis of mean performance SHEKAR -3 followed by IPU862 X IPU96-1, SHEKAR and G.C 9120 X IC 106194 was found to be superior and showed possessed maximum seed yield.

Number of clusters per plant, seed yield per plant exhibited high GCV, PCV and Genetic

parameters revealed that heritability (broad sense) were high for days to maturity, harvest index, but in case of genetic advance and genetic advance as % of mean values were high for seed yield per plant. High estimates of heritability coupled with high genetic advance as percent of mean recorded for number of clusters per plant and followed by biological yield.

Correlation coefficient analysis revealed that with number of branches per plant, harvest index, number of pods per plant, number of seeds per pod, exhibited positive significant association with seed yield per plant at both genotypic and phenotypic levels.

Path analysis revealed that the characters days to maturity, Plant height, number of clusters per plant, seed index, harvest index, exhibited positive direct effect on seed yield at both phenotypic and genotypic levels.

All four genotypes mentioned above with these characters can be used for further improvement and development of blackgram.

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References

Ali, M.N., Gupta Suparna, Bhattacharyya Somnath and Sarkar, H.K. (2008). Evaluation of black gram (*Vigna mungo* (L.) Hepper) germplasm using multi-varietal analysis *journal of Environment and Ecology*, 26(2): 943-945.

Bakshi, A., Bala, S. and Dostisder, K.G. (2006). Character association for seed yield components in blackgram (*Vigna mungo* (L.) Hepper) *journal of Environment and Ecology*, 24(3): 943-945.

Bharti, Singh, S. and Kumar, P. (2014). Study on correlation and path analysis in blackgram (*Vigna mungo* (L.) Hepper). *Journal of Legume Research*, 18 (2): 25-28.

Chauhan, M.P., Mishra A.C. and Singh A.K. (2007). Correlation and path analysis in urd bean. *Journal of Legume Research* 30(3): 205-208.

Dadepeer, P., Ravikumar, R.L. and Salimath, P.M. (2009). Genetic variability and character association in local greengram (*Vigna radiata* (L.) Wilczek.) genotypes of Karnataka. *Journal of Environment and Ecology*, 27(1): 165-169.

Deepshikha, Lavanya, G.R. and Kumar, S. (2014). Assessment of Genetic variability for Yield and Its Contributing Traits in Blackgram (*Vigna mungo* (L.) Hepper). *journal of Trends in Biosciences*, 7(18) : 2835-2838

Dewey, D. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, 51: 515-518.

Falconer, D.S. (1981). Introduction to Quantitative genetics, 3rd ed. Longman, New York. Pp. 340.

Fisher, R.A. (1918). The correlation between relatives of the supposition of Mendelian inheritance. *Journal of France Royal Society of Edinburgh*, 52: 399-433.

Gowsalya, P., Kumaresan, D. Packiaraj, D. and Bapu, K.J.R. (2016). Genetic variability and character association for biometrical traits in blackgram (*Vigna mungo* L. Hepper). *Electronic Journal of Plant Breeding*. 7(2): 317-324.

- Hemalatha, K., Sapna, S.L. and Gabriel, M.L. (2017). Study on Genetic Variability and Correlation in Blackgram (*Vigna mungo* L. Hepper). *Journal of Pharmacognosy and Phytochemistry*, 6(4): 674-676
- Isha Parveen, S., Reddy Sekhar, M., Mohan Reddy, D. and Sudhakar, P. (2011). Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper). *International Journal of Applied Biology and Pharmaceutical Technology*, 2(3): 619-625.
- Jayamani, P. and Sathya. (2013). Genetic diversity in pod characters in blackgram. *Journal of Legume Research*, 36(3): 220-223.
- Jyothsna, S., Patro, T.S.S.K., Ashok, S. Sandhya Y., Rani and Neeraja, B (2016). Character association and Path analysis of Seed Yield and its Yield Components in Black gram (*Vigna mungo* (L.) Hepper). *International Journal of Theoretical & Applied Sciences*, 8(1): 12-16.
- Konda, C.R., Salimath, P.H. and Mishra, M.N. (2008). Correlation and path coefficient analysis in blackgram (*Vigna mungo* (L.) Hepper). *Journal of Legume Research* 31(3): 202-205.
- Konda, C., Salimath, P. and Mishra, M. (2008). Correlation and path coefficient analysis in black -gram (*Vigna mungo* (L.) Hepper). *Legume Research-An International Journal*, 31(3) : 202-205.
- Kumar, G. V., Vanaja, M., Lakshmi, N. J and Maheswari, M. (2015). Studies on variability, heritability and genetic advance for quantitative traits in blackgram (*Vigna mungo* (L.) Hepper). *Agricultural Research Journal*, 52(4) : 28-31.
- Loganathan, P., Sarvanan, K. and Ganesan, J. (2001). Genetic variability in greengram *Journal of .Research Crops*, 2(3) : 396-397.
- Mehra, Reena, Tikle, A.N., Saxena, Ashok., Munjal, Ashok., Rekhakhandia and Singh, Mahipal (2016). Correlation, path-coefficient and genetic diversity in Blackgram (*Vigna mungo* L. Hepper). *International Research Journal of Plant Science*, 7(1): 001-011.
- Panigrahi, K.K. and Baisakh, B. (2015). Correlation analysis for quantitative traits in blackgram (*Vigna mungo* (L.) Hepper) in different seasons. *International Journal of Scientific and Research publications*, 5, Issue 4.
- Punia, S., Gautam, N., Ram, B., Verma, P., Dheer, M., Jain, N.K and Jat, V.S. (2014). Genetic variability and correlation studies in urd-bean (*Vigna mungo* L. Hepper). *Journal of Legume Research*, 37(6):580- 584.
- Parameswarappa, S.G. and Lamani, K.D. (2005). Genetic estimates, association and path coefficient analysis in blackgram (*Vigna mungo* (L.) Hepper). *Karnataka Journal of Agricultural Sciences*, 18(1): 21-23.
- Parveen, S.I., Sekhar, M.R., Reddy, D.M. and Sudhakar, P. (2011). Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo*(L.)Hepper). *International Journal of Applied Biology and Pharmaceutical Technology*, 2(3):619-625.
- Pradhan, K.C. and Misra, P.K. (2005). Character association in blackgram (*Vigna mungo* (L.) Hepper). *Journal of Environment and Ecology* ,23(4) : 737-742.
- Rahim, M.A., Mia, A.A. Mahmud, F. Zeba N. and Afrin. K.S. (2010). Genetic variability, character association and genetic divergence in mung bean (*Vigna radiata* L. Wilczek). *Pakistan orthodontic Journal*, 3(1): 16.
- Rajan, R.E., Wilson, D. and Kumar, V.

- (2001). Correlation and path analysis of blackgram (*Vigna mungo*(L.) Hepper). *Madras Agriculture Journals*, 87(10/12) : 590-593.
- Rajasekhar,D., Sapna, S.L. and Gabriel, M.L. (2017).Character association and path analysis for seed yield and its components in blackgram [*Vigna mungo* (L.) Hepper]. *Journal of Plant Archives*, 17(1): 467- 471.
- Rao, M., Rao Y.K. and Reddy M.V. (2006). Evaluation of mung bean germplasm for yield and yield components. *Journal of Legume Research*, 29(1): 73-75.
- Singh, I.P., Kumar, A., Singh, J.D. and Singh, K.P. (2007). Genetic variation, character association and path analysis between grain yield and its component in blackgram (*Vigna mungo* (L.) Hepper) *International Research Journal of Plant Science*, 7(1): 001-011.
- Sreelakshmi, C and Reddy Sekhar, M. (2011). Comparison between correlation and path analysis studies in the full sib progenies and F3 bulk population among yield and its attributes in two crosses of greengram (*Vigna radiata* (L.) Wilczek). *Electronic Journal of Plant Breeding*, 2(2): 258-262.
- Umadevi, M. and Ganesan, N.M. (2007). Variability, correlation and path analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper). *Journal of Crop Research*, 31(2) : 253-257.
- Veeramani, N., Venkatesan, M. Thangavel P. and Ganesan J. (2005). Genetic variability, heritability and genetic advance analysis in segregating generation of black gram (*Vigna mungo* (L.) Hepper). *Journal of Legume Research*, 28(1): 49 - 51.
- Vijiyalaxmi and Bhattacharya A. (2006). Mung bean seed yield: III. Effect of yield attributing traits and phenology. *Journal of Legume Research*, 29(1): 11-17.
- Wani, S.K., Sridevi, O. and Salimath, P.M. (2007). Studies on genetic variability correlation and path analysis in chilli (*capsicum annum*). *Journal of Annals of Biological Sciences*, 23(2): 117-121.
- Zukovskiji, P.M. (1962). Cultivated plants and their wild relatives, Commonwealth Agriculture Bureau, London.

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