

**GENETIC VARIABILITY, PHENOTYPIC, GENOTYPIC
CORRELATION AND PATH COEFFICIENT ANALYSIS OF BLACK
GRAM (*VIGNA MUNGO* (L) HAPPER)**

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ABSTRACT

To utilize blackgram (*Vigna mungo* (L) Happer) gene pool effectively study on genetic variability, heritability, genetic advance and their correlations were conducted during *yala* 2013 & *maha* 2014/15. Data of ten quantitative characters were recorded. Heritability estimates were high (60%) for days to 50% flowering, plant height, 1000 seed weight, number of pods per plant, days to maturity and number of main branches. Number of main branches, plant height, pods per plant and seed yield showed higher (25%) phenotypic coefficient of variance (PCV) and number of main branches, plant height, pods per plant and grain yield showed higher (>20%) genotypic coefficient of variance (GCV). The correlation studies exhibited significant positive association of yield with number of main branches, plant height, pods per plant, seeds per pod and pod length in both phenotypic and genotypic manner. Correlation coefficients were further partitioned in to components of direct and indirect effect by path coefficient analysis. The number of main branches had the maximum direct effect on yield followed by plant height, number of pods per plant and pod length. Hence selection based on these characters would be effective in increasing the seed yield.

Keywords: black gram, heritability, genetic advance, correlation, path coefficient analysis

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INTRODUCTION

Blackgram is an important pulse crop cultivated in tropical and sub tropical countries and mainly grown in India, Pakistan, Burma, Sri Lanka and some south east Asian countries. In Sri Lanka blackgram is a popular legume crop as it suitable for dry and unfertile marginal lands in dry and intermediate zones. It is a short duration crop grown as sole crop as well as a component of inter and multiple cropping systems. On the other hand blackgram helps to improve the nutrient status of soil through atmospheric nitrogen fixation. Annual production and extent of blackgram is around 11,000mt and 9,000mt respectively. However, average productivity is around 0.83t/ha which is very low. (Agstat,2014). Therefore, it is crucial to improve its yield. For yield improvement, it is essential to start an efficient breeding programme. Breeders need sound knowledge on genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability and genetic advance (Misra and Sahu. 1985). The coefficient of correlation between yield and its contributing traits show a complex relationship. Path coefficient analysis partitions the components of correlation coefficient into direct and indirect effects and visualizes the relationship in a more meaningful way (Wright 1921). Genetic diversity is one of the criteria of parent selection in a hybridization programme. Therefore, the present study was conducted to study the effects of different yield components on seed yield using parameters which indicate the relative importance of different traits, like variability, heritability, genetic advance, correlation and path coefficient.

MATERIALS AND METHODS

The research for the present investigation was conducted at Field Crops Research and Development Institute, Mahailupplama during *yala* 2013 & *maha* 2014/15. Forty blackgram germplasm (Table 01) was sown in randomized complete block design (RCBD) with two replicates. Each plot was accommodating three rows of 4m length with 30cm & 10cm distance between rows and plants receptively. Recommended agronomic and plant protection activities were practiced during the cultivation period. Data of ten morphological characters, Days to 50% flowering (FF), Days to maturity (DM), Number main branches (MB), Plant height (PH), Number of clusters per plant (CP), Number of

pod per plant (PP), Number of seed per pod (SP), Pod length (PL), Thousand seed weight (SW) and Plot yield (Y) were recorded.

Table 1. Forty blackgrsm genotypes

No	Line	No	Line	No	Line	No	Line
1	AC0224	11	AC8632	21	AC31186	31	AC2951
2	AC0337	12	AC8724	22	AC31303	32	AC1998
3	AC0355	13	AC8816	23	AC31263	33	MIBG117-21
4	AC0460	14	AC8986	24	AC31322	34	MIBG117-A
5	AC0500	15	T9	25	AC31173	35	MIBG 85
6	AC0784	16	AC6565	26	AC31200	36	MIBG 23
7	AC1816	17	AC31196	27	Nirmal 7	37	MIBG 62
8	AC6563	18	AC31215	28	BLG0067-1	38	AC 8734
9	AC7624	19	AC 31175	29	BLG0072-3	39	AC 7623
10	AC8301	20	AC31265	30	AC778	40	AC1454

Statistical analysis

Analysis of variance (ANOVA) was used to statistically analyse the data of each trait. F-test followed by least significant difference (LSD) test was applied for mean analysis. The genetic, phenotypic and environmental variance for each traits were estimated using following formula suggested by Johnson *et al.*, (1955).

Environmental variance $\sigma_e^2 \sigma_e^2 = \text{Error means square}$

Genetic variance $\sigma_g^2 \sigma_g^2 = \frac{(\text{Genotypic means square} - \text{Error mean square})}{\text{Number of replicates}}$

Phenotypic variance $\sigma_p^2 \sigma_p^2 = \text{Genetic variance} + \text{Environmental Variance}$

Broad sense heritability ($h_{bs}^2 h_{bs}^2$) was estimated by the formula suggested by Johnson *et al.* (1955), Hanson *et al.*, (1956)

$$h_{bs}^2 h_{bs}^2 = \frac{\sigma_g^2 \sigma_g^2}{\sigma_p^2 \sigma_p^2} \times 100$$

Phenotypic and genotypic coefficient of variation (PCV & GCV) were calculated by the formula suggested by Burton (1952).

Phenotypic coefficient of variation (PCV)

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$$PCV = \frac{\sigma_p \sigma_p}{\bar{n} \bar{n}} \times 100$$

where as, $\sigma_p \sigma_p$ = Phenotypic standard deviation , $\bar{n} \bar{n}$ = Population mean
Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sigma_g \sigma_g}{\bar{n} \bar{n}} \times 100$$

where as, $\sigma_g \sigma_g$ = Genotypic standard deviation , $\bar{n} \bar{n}$ = Population mean
The expected genetic advance (GA) for different characters under selection was estimated using the formula suggested by Johnson *et al.*, (1955).

$$GA = \frac{\sigma_g^2 \sigma_g^2}{\sigma_p^2 \sigma_p^2} \times k \times \sigma_p \sigma_p$$

where as, k = selection differential, the value of which is 2.06 at 5%
selection intensity

Genetic advance in percentage of mean was calculated from the formula given by Johnson *et al.*, (1955).

$$GA\% = \frac{\text{Genetic advance}}{\text{Population mean}} \times 100$$

The coefficient of variability (CV) of each character was calculated by using following formula

$$CV = \frac{\text{Error means Square}}{\text{Population mean}} \times 100$$

The formula suggested by Miller *et al.*, (1958), Hanson *et al.*, (1956) and Johnson *et al.*, (1955) was used to calculate the genotypic and phenotypic correlation coefficient for all possible combinations. The genotypic correlation coefficient (r_g) components between two traits and phenotypic correlation coefficient (r_p) components between two traits were derived in the same way as for the corresponding variance components. These covariance components were used to compute genotypic and phenotypic correlation between the pair of characters.

Correlation coefficients were further partitioned in to components of direct and indirect effect by path coefficient analysis originally developed by Wright (1921). Seed yield as taken as the dependent character, its coefficient of correlation with other independent characters was partitioned in to direct and indirect effects. Phenotypic & genotypic correlation coefficients and path coefficients were computed using SATA computer software.

RESULTS AND DISCUSSION

Analysis of variance

Sound knowledge of the existing genetic variation for yield and its component characters is required develop improved varieties. The combined pooled ANOVA for morphological characters is given in table 02. The mean sums of squares due to genotype were highly significant at 1% level for all tested characters. This pointed out the existence of high variability for all tested traits in the blackgram germplasm. Same results were observed by Chauhan *et al.*,(2007), Veeranjanyulu *et al.*,(2007), Praveen *et al.*,(2011) and Mehra *et al.*,(2011).

Table 2. Analysis of variance of blackgram genotypes for tested traits

Characters	Replication	Genotype	Error	r ²
FF	1.25	27.6**	0.14	0.994
DM	43	204.6**	3.211	0.87
MS	0.112	0.53**	0.086	0.859
PH	7.62	497.8**	2.862	0.951
CL	0.8	1.84**	0.517	0.782
PP	48.03	214.1**	3.461	0.861
SP	0.312	1.06**	0.36	0.746
PL	0.125	0.249**	0.101	0.711
SW	21.45	54.94**	3.07	0.94
Y	0.6	0.491**	0.173	0.71

** Significant in 1% level of significant

FF - days to 50 % flowering, DM - Days to maturity, MS - Number of main stems, PH- Plant height in cm, CL - Number of clusters per plant, PP- number of pods per plant, SP- number of seed per pod, PL - Pod length in cm, SW- thousand seed weight in g, Y- Grain yield in t/ha.

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Parameters of genetic variability

The estimate of heritability (h_{bs}^2), genotypic (GCV) and phenotypic (PCV) coefficient of variance genetic advance (GA), coefficient of variation (CV%) and grand mean (GM) (two consecutive seasons *yala* 2013 & *maha* 2014/15) for ten morphological characters of the forty blackgram germplasm are given in table 03.

Table 3. Genetic & phenotypic variance, heritability, genetic advance, genotypic & phenotypic coefficient

Characters	GM	h_{bs}^2	GCV	PCV	GA	GA %	CV (%)
FF	40.43	98.99	9.17	9.21	7.50	18.56	0.35
DM	81.98	72.87	11.33	13.27	16.50	20.13	3.92
MB	2.19	72.08	21.54	25.37	0.82	37.32	3.93
PH	46.19(cm)	89.13	33.16	35.12	29.33	63.51	6.2
CP	13.30	56.13	6.12	8.16	1.25	9.36	3.89
PP	34.70	72.16	27.29	32.13	16.41	47.28	9.97
SP	6.51	49.40	9.10	12.95	0.85	13.07	5.53
PL	4.72	42.29	5.76	8.86	0.36	7.63	2.14
SW	49.66(g)	89.42	10.26	10.85	9.84	19.82	6.18
Y	1.69(t/ha)	47.89	23.58	34.07	0.54	31.74	10.23

GM-Grand mean, σ_g^2 - Genotypic variance, σ_p^2 - Phenotypic variance, h_{bs}^2 - Heritability(broad seance), GCV- Genotypic coefficient of variance, PCV- Phenotypic coefficient of variance, GA- Genetic advance (5%), GA% - Genetic advance in percentage of mean

Heritability, Genotypic coefficient of variance, Phenotypic coefficient of variance, Genetic advance

The estimates of phenotypic coefficient of variation (PCV) were slightly higher than the genotypic coefficient of variation (GCV) for all characters. It revealed that there is environmental influence to some extent in the expression of these characters. The highest value (>20%) of GCV were estimated for plant height (33.16), number of pods per plant (27.29), number of main branches (25.37), & grain yield (23.58). whereas higher PCV values (>25%) were recorded for plant height (35.12), grain yield (34.07), number of pods per plants (32.13) and number of main branches (25.37). Higher estimate of PCV measured for all the morphological characters validates the positive influence of environmental factors in expression of different morphological traits under different environment than that of corresponding GCV. Higher value of GCV for plant height, number of pods per plants, grain yield, and number of main branches indicate better chance for selection for these traits to be successful. GCV shows the range of genetic variability expressed by the plant traits and helps to compare genetic variability present in germplasm for various traits. Higher PCV suggested that the environmental factors were influencing in expression of these traits. However, along with the GCV not possible to determined the amount of variation that is heritable. Mehar *et al.*, (2016) were found that number of pods per plants, number of main branches have higher and Jyothsna *et al.*, (2016) were observed plant height, pods per plants and number of main branches showed higher GCV.

Higher values of broad sense heritability (h_{bs}^2) (>70%) were recorded for days to 50% flowering (98.99), 1000 seed weight (89.4), Plant height (89.13), Days to maturity (72.8) and number of pods per plant (72.1).

Expected genetic advance at 5% selection intensity expressed as percentage of population mean, ranged from 7.63% of pod length to 63.51% for plant height. Higher genetic advance associated with high heritability value indicated genetic effect in controlling the characters and had considerable value to the breeder for plant selection (Panse, 1957).

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Correlation coefficient

Table 04 shows the phenotypic and genotypic correlations between all pairs of characters. For most of the yield related traits, the genotypic correlation coefficient with yield was higher than the corresponding phenotypic correlation coefficient. This indicating that the environmental influences were marked enough to change the degree of association all characters. (Rohman *et al.*(2003), Rani *et al.*(2013,)

Days to 50% flowering

Days to 50% flowering shows negative phenotypic and genotypic correlations with number of days to maturity and grain yield indicating yield could be reduced with increasing days to 50% flowering. This character had significant positive correlations with number of main branches, plant height and number of seeds per plant (Table 04) which indicated that increase of days to 50% flowering increase the value of above traits. Rohuman *et al.*(2003) found negative correlation between grain yield and days to 50% flowering.

Days to maturity

Days to maturity represented significant positive correlation with grain yield and plant height and positive phenotypic correlation with other traits. which indicated that late maturing tall plants gave higher yield. Genotypic correlation of days to maturity shows negative correlation with days to 50% flowering and number of main braches and significant positive correlation with plant height. Rest of the traits showed positive correlation with number of days to maturity. Kousar *et al* (2007), observed number of days to maturity positively correlated with plant height.

Number of main branches

Number of main branches per plant showed significant phenotypic correlation with days to flowering, number of clusters per plant, plant height and grain yield. Genotypic correlation of days to 50% flowering, plant height and number of clusters per plant showed significant positive correlation with number of main branches. this feature indicated that increased of number of main branches would lead to increased grain yield, plant height and number of clusters per plant. Similar results have been reported by Chanuhan *et al.*, (2007), Reddy *et al.*,(2011), Mehra *et al.*,(2016).

Plant height

Plant height showed significant positive correlation with days to 50% flowering, Days to maturity. Number of main branches, number of pods per plant, number of seed per pods and grain yield at phenotypic and genotypic level indicated that these characters would increase with increasing height. Similar association of plant height have been reported earlier with pod length (Goud *et al.*, 1977), seeds per pod (Santha and Paramasivam 1999), 1000 seed weight and number days to maturity (Nagarjuna *et al.*, 2001).

Number of clusters per plant

Number of cluster of plant exhibit highly significant positive phenotypic and genotypic association with number of main branches, number of seeds per pod and pod length which indicated that selection of the plants with more number of clusters may increase the number of main branches, number of seeds per pod and pod length. Genotypic correlation of grain yield showed negative association with number of clusters per plant which revealed that selection of more number of clusters lead to decreased grain yield. Similar significant positive association of clusters per plant were reported earlier with seeds per pod (Gopi Krishhnan *et al.*, (2002) and with pod length (Preveen *et al.*, 2011).

Number of pods per plant

Number of pods per plant was found to show significant positive correlations both genotypic and phenotypic with plant height, seeds per pod, pod length and grain yield. Results reveal that the number of pods per plant increase with ncrease of plant height and ultimately number of seeds per pod, pod length and grain yield. Number of pods per plant showed positive correlation with all traits. Significant positive association of number of pods per plant with number of seeds per pod and pod length were also reported by Rohman *et al.*, 2003.

Table 4. Phenotypic correlation coefficient (r_p) and genotypic correlation coefficient (r_g) of black gram traits

Traits	F	M	MB	PH	CL	PP	SP	PL	SW	Y
F	P 1	-0.02	0.269*	0.585**	0.116	0.197	0.331**	0.090	0.189	-0.032
	G 1	-0.12	0.293*	-0.600	0.122	0.215	0.389*	0.102	0.200	-0.040
M	P 1	1	0.162	0.347**	0.001	0.012	0.114	0.089	0.190	0.280*
	G 1	1	-0.015	0.343	0.028	0.133	0.039	0.136	0.064	0.165
MB	P 1	1	1	0.265*	0.222**	0.126	0.090	0.066	0.053	0.120*
	G 1	1	1	0.29*	0.24**	0.158	0.169	0.081	0.058	0.088**
PH	P 1	1	1	1	0.144	0.396**	0.277*	0.084	0.020	0.033*
	G 1	1	1	1	0.180	0.385**	0.329**	0.104	0.041	0.007**
CL	P 1	1	1	1	1	0.215	0.134**	0.281**	0.193	0.030*
	G 1	1	1	1	1	0.251*	0.230*	0.345*	0.228*	-0.081
PP	P 1	1	1	1	1	1	0.329**	0.254*	0.058	0.07**
	G 1	1	1	1	1	1	0.371*	0.304**	0.084	0.212*
SP	P 1	1	1	1	1	1	1	0.664	0.288	0.223*
	G 1	1	1	1	1	1	1	0.564**	0.220*	0.149
PL	P 1	1	1	1	1	1	1	1	.3180**	0.164
	G 1	1	1	1	1	1	1	1	0.387*	0.266**
SW	P 1	1	1	1	1	1	1	1	1	0.184
	G 1	1	1	1	1	1	1	1	1	0.186
Y	P 1	1	1	1	1	1	1	1	1	1
	G 1	1	1	1	1	1	1	1	1	1

FF - days to 50 % flowering, DM - Days to maturity, MS - Number of main stems, PH-Plant height in cm, CL - Number of clusters per plant, PP- number of pods per plant, SP- number of seed per pod, PL - Pod length in cm, SW- thousand seed weight in g, Y- Grain yield in t/ha.

Number of seeds per pod

In case of number of seeds per pod significant positive relationships were observed with days to 50% flowering, plant height number of clusters per plant, number of pods plant and pod length as both genotypic and phenotypic correlations while days to maturity and number of main braches show non- significant positive correlations. Number of seeds per pod showed significant positive genotypic correlation with grain yield. Grain yield showed highly significant genetic correlations with number of seeds per pod and significant positive phenotypic correlation with 1000 seed weight. All traits were positively correlated with number of seeds per pod which suggested that all traits increased with increased number of seeds per pod. These finding are in agreement with the results obtain by Gowda *et al.*, (1997) and Previn *et al.*, (2007)

Pod length

Pod length showed positive genotypic and phenotypic correlations with all traits while it is significant with number of clusters per plant, 1000 seed weight and number of pods per plant. Grain yield showed significant positive genotypic correlation with pod length indicating that grain yields have increased with the increase of pod lengths. Pod length showed positive significant association with 1000 seed weight both genotypic and phenotypic. This indicated that seed weight also increased with the increase of pod length. On the other hand, Parveen *et al.*, (2011) while working on 75 germplasm accessions of blackgram found significant positive correlation of pod length with number of pods per plant and 100 seed weight.

1000 seed weight

The significant positive association both genotypic and phenotypic of 1000 seed weight was found only with pod length. This indicated that the increase of seed weight is directly related to the increase of pod length. Number of seeds per pod showed significant positive correlation with 1000 seed weight while number of clusters per plant showed significant positive genotypic associations with 1000 seed weight. Number of main branches, plant height and pod length were significantly and positively associated with plant height and grain yield at genotypic levels. (Nagarjuna *et al.*, 2001 and Chauhan *et al.*, 2007).

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Grain yield

Grain yield of blackgram showed significant phenotypic correlations with days to maturity (0.280) and number of cluster per plant (0.03). Days to 50% flowering (-0.03, -0.04) showed significant negative phenotypic and genotypic correlations with grain yield. Number of clusters per plant (-0.081) was negatively associated with grain yield in genotypic manner. Number of main branches (0.088), plant height (0.007) and pod length (0.266) were significantly and positively associated with grain yield at both genotypic and phenotypic level. At genotypic level number of clusters per plant was negatively correlated with grain yield while significantly positive association was observed at phenotypic level. These results agree with the findings of Mehara (2016), Sohel *et al.*, (2016) and Arulblachandra *et al.*, (2010).

Path coefficient

The estimations of correlation coefficients showed only the relationship between yield and yield associated characters, but did not show the direct and indirect effect of different traits on yield. This is because the traits which are in association do not exhibit by themselves, but are linked into other components. The path coefficient analysis originally developed by Wright (1921 & 1923) and suggested by pacified the effective measure of direct and indirect Dewey and (1959) sources of association and also depicts the relative importance of each factor involved in contributing to the yield (Selvaraj *et al.*, 2011). In order to find out source effect relationship between yield and its related characters, path analysis was taken up in the present investigation.

The results of genotypic path analysis are given in table 05. Number of main branches had the highest positive direct effect followed by Plant height (0.190), number of pods per plant (0.162) and 1000 seed weight (0.109). Mehra *et al.*, (2016) noted greatest contribution of plant height on yield in blackgram whereas Parveen *et al.* (2011) acknowledged the highest contribution of number of main branches.

Number of main branches had highest effect with all other tested traits. This resulted high significant association between number of main branches and grain yield.

Plant height (0.190) showed positive direct effect and positive indirect effect with all other traits, finally showing a highly significant relationship with grain yield.

Number of pods per plant (0.129) had a moderate positive direct effect on yield and negative indirect effects through days to fifty percent flowering and days to maturity. All other traits indicated positive indirect effects and it lead to a significant correlation with grain yield

Pod length (0.096) showed a moderate positive direct effect and negative indirect effects through number of main branches. But a higher positive indirect effects through seeds per pod enable a high significant correlation with grain yield.

1000 seed weight (0.109) also had a moderate direct effect and strong negative effects through number of main branches. This resulted in a non significant relationship with grain yield.

These results are in conformity with the findings of Mehra *et al.*, (2005), Chauhan *et al.*, (2007) and Konda (2008) for pods per plant and pod length. the present finding is supported by finding of Mishra *et al.*, (2005) Chauhan *et al.*, (2007) for plant height and number of main branches.

Table 5. Direct (Diagonal) and indirect effect of yield contributing characters on grain yield in 40 blackgram genotypes

Traits	F	M	MB	PH	CI	PP	SP	PL	SW	R2
F	-0.005	0.002	-0.001	0.027	0.038	0.953	0.000	0.017	-0.254	-0.040
M	-0.066	0.016	0.003	0.013	0.008	0.184	-0.002	0.001	-0.052	0.165
MB	0.041	0.008	0.217	0.001	0.013	1.172	0.046	0.025	0.207	0.088**
PH	2.513	0.511	1.515	0.190	0.010	0.013	0.008	0.003	0.011	0.007**
CI	-0.004	-0.007	0.401	0.008	-0.049	-0.001	0.034	0.027	0.367	-0.081
PP	-0.361	-0.166	0.404	0.343	1.577	0.162	0.004	0.006	0.028	0.212*
SP	0.075	0.012	-0.080	-0.004	0.044	0.022	-0.049	0.000	0.874	0.223*
PL	-0.007	0.002	-0.002	-0.003	0.082	0.003	0.274	0.096	0.007	0.266**
SW	0.529	0.147	-0.535	-0.112	0.674	0.015	-0.034	3.185	0.109	0.186

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FF - days to 50 % flowering, DM - Days to maturity, MS - Number of main stems, PH-Plant height in cm, CL - Number of clusters per plant, PP- number of pods per plant, SP- number of seed per pod, PL - Pod length in cm, SW- thousand seed weight in g, Y- Grain yield in t/ha.

CONCLUSIONS

According to this study there was significant genetic variability among genotypes for all traits. Plant height, number of pods per plant and number of main branches showed high heritability along with high genetic advance. Hence these characters were possess high genetic variability and are less influenced by environments. Number of main branches, plant height, and number of pods per plant and pod length had highly significant and positive correlations with seed yield and also among themselves. Hence selection of these characters simultaneously would bring improvement in yield. Number of branches followed by plant height, pods per plant and pod length showed highest direct effect on the grain yield. Hence, direct selection of these traits would be worthwhile.

REFERENCES

- AgStat, 2014. Socio -Economic and Planning Centre, Department of Agriculture, Peradeniya, Sri Lanka. XI. 22-24
- Arulbalachandran, D., L. Mullainathan, S. Velu, and C. Thilagavathi 2010. Genetic variability, heritability and genetic advance of quantitative traits in blackgram by effects of mutation in field trial. *African Journal of Biochemistry*, 9(19): 2731-2735.
- Chauhan, M.P., A.C. Mishra and A.K. Singh 2007. Correlation and Path Analysis on urdbean. *Legume Research - An International Journal*, 30(3):205-208.
- Dewey, D.R., K.H. Lu 1959. A correlation and path –coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, Madison, V51, n.8, p 515-518.

- Gopi Krishnan, A., M. Reddissekhar, K.R. Reddy and K.S. Reddy 2002. Character association and path analysis in urdbean (*Vigna mungo* (L.) Hepper). Madras Agriculture Journal. 89(4-6) 31-318.
- Goud J.V., B. C. Viraktamath, and P.V. Luxmi 1977. Variability and correlation studies in Blakgram (*Vigna mungo* (L.) Hepper). Msore Journal of Agriculture Sciences 23 (2):56-64.
- Gowda M.B., J.C. Prakash, J. Shantala 1997. Estimation of genetic variability and heritability in blackgram. Crop Research 13(2): 369-372.
- Hanson, C.H., H.F. Robinson, R.E. Comstok 1956. the biometrical studies on yield in segregating population of Korean lespedeza. Agronomy Journal 48:268-272.
- Johnson, H.F., H. F. Robinson and R.E. Comstock (1955). Estimation of genetic and environmental variability in soybean. *Agron* Journal 47:314-318.
- Jyothsna, S. T.S.S.K. Patro, A. Ashok, Y. S. Rani and B. Nirraja 2016. Character association and path analysis of seed yield and its yield componants in blackgram (*Vigna mungo* (L.) Hepper). International Journal of Theoretical and Applied Scncs 8(1)12-16.
- Konda C.R., P.M. Salimath and M.N. Mishra 2008. Correlation and path coefficient analysis in blackgram. Legume Rsearch 31(3):2012-205
- Kousar, M., A. Garard J. Arif and A.K.Sing 2007. Genetic variability and correlations studies yield and its component of (mungbean) (*Vigna radiata* (L.)Wilezck. J. Agron , 6(1) ; 216 - 218
- Mehra, R., A.T. Tikle, A.Suxena, A. Munjal, Rekhakhandia and M. Singh 2016. Correlation, path-coefficient and genetic diversity in black gram (*Vigna mungo* (L.) Hepper). International Research Journal of Plant Science 7(1): 01-011.

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- Misra, R.C. and B.C. Sahu 1985. Genetic parameters, correlation and coefficient analysis in greengram (*Vigna radiata* Wilczek). The Andhra Agriculture Journal 32(2):7-97.
- Miller, P.A., . Willianis, H.F. Roginson and R.E. Comstock 1958 . Estimates of genotypic and phenotypic and environmental variance and covariance and their implication in section. Agron Journal 50:126-131.
- Nagarjuna, M., K. Sagar, and M. R. Sekhar 2001. Character association studies in black gram (*Vigna mungo* (L.) Hepper). Madras Agriculture Journal 88: 222-224.
- Rani, Y.P., Y.K. Rao, Y. Satish and S. Babu 2013. Estimation of genetic parameters and path analysis in blackgram (*Vigna mungo* (L) Happer). International Journal of Plant, Anomal and Environment Sciences. 3(4) 231-234.
- Reddy, D.K., R. O. Venkateswarlu, M. N. Narkhede 2011. Heritability studies in black gram. journal of Legume research. 34(2) 149-152
- Rohuman, M.M., A.S.M.I. Hussain, M.S. Arifin, Z. Akhter and M. Hasanuzzaman 2003. Genetic variability, correlation and path analysis in mungbean. Asian Journal of Plant sciences.2(14-24) 1209-1211.
- Panse, V.G., 1957. Genetic and quantitative characters in relation to plant breeding. Indian Journal of Genetic and Plant Breeding. 17: 318-328.
- Preveen, S.I., M.R. Sekhar, D.M.Reddy and P. Sudhkar 2011. Correlation & 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.
- Pervin, M. A., M. B. Polash, S.M. Rahman, A. C. Deb 2007. Variability study in blackgram. Journal of Biological Sciences 7(1): 169-175.
- Santha, S., K. Paramasivam 1999. correlation and path analysis for rice fallow blackgram (*Vigna mungo* (L.) Hepper). Madras Agriculture Journal 86: 397-400.

- Selvaraj, I.C., P. Nagarajan, K. Thiyagarajan, M. Bharthi and R Rabindran 2011. Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes among rice blast disease resistance genotypes of rice (*Oryza sativa* L.). African Journal of Biotechnology 1(17):2322-2334.
- Sohel, M. H., R. Miah, S. J. Mohiuddin, A. K. M. S. Islam, M. Rahman and A. Haque 2016 Correlation and path coefficient analysis of blackgram (*Vigna mungo* L.). Journal of Bioscience and Agriculture Research 7(2): 621-629.
- Veeranjaneyulu, A., K.B. Wswari, V.S. Roi, and J.V.Ramana 2007. Association analysis of yield and its components in blackgram (*Vigna mungo* (L.) Hepper). The Andhra Pradesh Agricultural Journal. 54:134-138.
- Wright, S., 1921. correlation and causation. Journal of Agriculture Research 20:557-587.