

Original Research Article

<https://doi.org/10.20546/ijcmas.2020.912.046>

Association Analysis in Black gram (*Vigna mungo* L. Hepper)

Vikky Kumar*, Prafull Kumar and Subhash Soni

S. G. College of Agriculture & Research Station, IGKV, Jagdalpur (C.G.), India

*Corresponding author

ABSTRACT

Keywords

Black gram
Vigna mungo

Article Info

Accepted:
04 November 2020
Available Online:
10 December 2020

The present experiment was conducted at Research cum Instructional Farm of SGCARS Kumhrawand, Jagdalpur, Bastar (C.G.). The experiment was conducted in Randomized Complete Block Design (RCBD) with two replications. Crop was grown proper spacing 30×10cm during *Kharif* 2019. The study was undertaken on the 80 black gram genotypes along with two checks (Indira Urd Pratham and T.U. 94-2) to study the correlation and path analysis. Analysis of variance showed highly genetically significant differences among (80+2 check) black gram genotypes for 13 quantitative characters studies. Correlation coefficient studies revealed that Seed yield per plant has showed positive and highly significant association with number of pods per cluster, test weight of 1000 seed (g), petiole length (cm), number of pods per plant, days to maturity, days to 50% flowering, days to first mature pod and number of seeds per pod at genotypic level. Path analysis revealed that number of pods per cluster was main component for improving the single pant yield. Hence selection of these traits would improve yield in black gram breeding programs.

Introduction

Pulses are the major source of dietary protein. Black gram (*Vigna mungo* (L.) Hepper), popularly known as urdbean in India, is an important short duration pulse crop and self pollinating diploid (2n=22) with a small genome size estimated to be 0.56pg/1C (574 Mbp) (Gupta *et al.*, 2008). Black gram is a protein rich food, containing about 26 percent protein, which is almost three times that of cereals. It ranks fourth among the major pulses cultivated in India. Black gram supplies a major share of protein requirement of vegetarian population of the country. It is consumed in the form of split pulse as well as

whole pulse, which is an essential supplement of cereal based diet. According to Vavilov (1926) black gram has originated from Indian subcontinent. Center of genetic diversity for black gram is found in India (Zeven *et al.*, 1982).

India is the largest producer and consumer of black gram cultivated in an area about million hectares with a production of 1.92 million tonnes (AICRP report, 2016). Besides Gujarat, Andhra Pradesh is one of the major black gram producing state grown in an area about 4.49 million hectares with a Productivity of 651kg ha⁻¹ (Website <http://www.dacnet.nic.in/ean> 2017). Among

the various pulses, black gram or urdbean (*Vigna mungo* L. Hepper) is an important grain legume with easily digestible protein and low flatulence contents. It is highly prized pulse, rich in phosphoric acid. Black gram grain contains about 25% protein, 56% carbohydrates, 2% fat, 4% minerals and 0.4% vitamins. Black gram used as dry season intercrop in rice or wheat as it has a beneficial effect on soil nutrient status (Parashar, 2006). Black gram is extensively used as a nutritious pulse. Its seeds may be eaten raw, roasted, parched or boiled in split form. Low and uneven rainfall pattern of the state since last few years have urged the need to develop early maturing varieties of black gram to avoid yield losses due to long dry span during maturity. Though, India is the world's largest producer of black gram, it imports a large amount to meet the growing domestic needs. Black gram is grown in varying agro-ecological conditions and cropping systems with diverse cultural practices, so it needs appropriate plant type for each growing situation.

The breeding progress has been slow and uneven because several desirable traits need to be combined for developing appropriate plant type for a particular growing region and cropping system. Correlation is the relationship which can reveal whether the change in one variable would cause change in the other or not. Such relationship between the two sets of characters or variables can be expressed quantitatively by the degree of relationship, called Correlation Coefficient. It is important to know the association of yield and its components in order to identify a suitable plant type. At the same time, knowledge about causes of genetic correlation will also give an idea about the extent of possible improvement of the character. The important cause's underlined genetic correlations are linkage, pleiotropy, physiological association and heterozygosity.

The genetic causes of correlation are chiefly due to pleiotropy. Through linkage is a cause of transient correlation, particularly in population derived from crosses between two species. Pleiotropy is simply a property of a gene, which affects two or more character. Path coefficient is standardized partial regression coefficient. In biological system, the relationships may exist in a very complex form and the correlation coefficients are only the indications of simple associations between variable.

The magnitude of association between two variables is always proved to effect and simultaneous variability in other related characters. The correlation and path-coefficient analysis provide information about the relative importance of various yield components in the expression of yield and thus, help in formation of appropriate selection strategy. In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959).

Materials and Methods

The present experiment entitled "Diversity analysis in black gram [*Vigna mungo* (L.) Hepper] was conducted at "Research cum Instructional Farm, Shaheed Gundadhoor College of Agriculture and Research Station, Kumhrawand, (Jagdapur), Indira Gandhi Krishi Vishwa vidyalaya, Raipur (Chhattisgarh)" located at N 19°5'39" longitude E 81°59'33" latitude and at an altitude 553.400 meters above mean sea level (MSL) with an annual rainfall 14.39 mm.

The experimental material comprised of eighty two black gram genotypes along with two check varieties Indira Urd Pratham and T.U. 94-2. The experimental material was planted in a Randomized Complete Block

Design with two replications during *kharif* 2019. Each genotype was planted in two rows of 3 m length \times 1 m width having 30 \times 10 cm spacing between rows and plants. The observations were recorded on five randomly selected plants per replication for each accession. The analysis of variance for different characters was carried out using the mean data through method given by Ponce and Sukhatme (1964).

Genotypic and phenotypic correlation coefficient was worked out using the formula given by Al-Jibouri *et al.*, (1958) with the help of correlation coefficients scales given by Searle, (1965) and path coefficient analysis was calculated using the formulae given by Dewey and Lu (1959). TNAUSATAT software was used for analysis of correlation and path coefficient analysis (Manivannan, 2014). The R software was used preparing correlation chart. The direct and indirect effects were classified based on scale (Lenka and Mishra, 1973).

Results and Discussion

Analysis of variance was performed for thirteen quantitative traits including yield and yield attributes of 82 genotypes. From the analysis of variance it was observed that mean sum of squares due to genotypes was significant for all characters at 5% level of significance under study.

Study on correlation coefficient analysis

The statistics that measures the degree and direction of association between two or more variables is known as correlation coefficient. It is denoted by r and its value lies between -1 to 1. The term coefficient of correlation was first used by Karl Pearson in 1902. It computes the mutual association between various plant character pairs and defines the component characters on which selection can

be depend on for improvement in seed yield. Through correlation coefficient analysis emphasis can be given for selecting character which is genetically correlated with the dependent character. To know the nature and magnitude of relationship existing between the traits under study correlation coefficient was estimates both at phenotypic as well as genotypic levels. Data presented in table 1 and 2 respectively.

At phenotypic level (Table 1) seed yield per plant exhibited significant positive correlation with test weight of 1000 seed (0.370**), trailed by number of pods per cluster (0.347**), petiole length (0.250**) and number of pods per plant (0.210**). At genotypic level (Table 2) number of pods per cluster (0.446**) trailed by 1000 seed weight (0.395**), petiole length (0.295**), number of pods per plant (0.255**), days to maturity (0.251**), days to 50% flowering (0.223**), days to first mature pod (0.220**) and number of seeds per pod (0.184*) were correlated with seed yield per plant. Similar result reported by Sathees *et al.*, (2019) for number of pods per plant and number of seeds per pod, Pushpa *et al.*, (2013) and Panigarahi *et al.*, (2014) seed yield per plant (g) positive significant correlation with number of pods per plant (0.958**, 0.911**), number of seeds per pod (0.393**, 0.317**) and test weight (0.934**, 0.741**) at genotypic and phenotypic level respectively. If the value of correlation (r) is significant the association between two characters is high and genotypic correlation coefficient (r_g) is higher than the phenotypic correlation coefficient (r_{ph}), it means that there is strong association between these two characters genetically. Similar result positive association of number of pods per plant with seed yield was reported earlier by Venkatesan *et al.*, (2004), Umadevi and Ganesan (2005), Chauhan *et al.*, (2007) and Reddy *et al.*, (2011).

Table.1 Phenotypic correlations coefficient analysis for seed yield and its component traits in black gram

Characters	DFF	NPBPP	NPPP	PL	PH	NSPP	DFMP	DM	PeL	NPPC	HI	TW	SYPP
DFF	1.000	0.162*	0.236**	0.143	0.174*	0.113	0.169*	0.092	0.262**	0.067	0.049	0.321**	0.112
NPBPP			0.163*	0.271**	0.271**	0.170*	0.151	0.191*	0.238**	0.027	-0.110	0.310**	0.022
NPPP				0.208**	0.216**	0.450**	0.166*	0.183*	0.196*	0.334**	0.178*	0.517**	0.210**
PL (cm)					0.195*	0.211**	-0.003	0.066	0.210**	0.174*	-0.138	0.291**	0.107
PH (cm)						0.318**	0.339**	0.244**	0.308**	-0.069	-0.019	0.146	0.013
NSPP							0.160*	0.127	0.142	0.232**	0.222**	0.387**	0.146
DFMP								0.532**	0.204**	-0.050	0.067	0.223**	0.122
DM									0.167*	-0.024	0.071	0.182*	0.136
PeL (cm)										0.360**	0.030	0.342**	0.250**
NPPC											0.157*	0.302**	0.347**
HI												0.133	-0.019
1000 Seed weight (g)													0.370**
SYPP (g)													1.000

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

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, NPBPP= Number of primary branches per plant, NPPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, NSPP= Number of seeds per pod, NPPC=Number of pods per cluster, DFMP=Days to first mature pod, HI= Harvest index, SYPP= Seed yield per plant, TW= Test weight of 1000 seed

Table.2 Genotypic correlations coefficient analysis for seed yield and its component traits in black gram

Characters	DFF	NPBPP	NPPP	PL	PH	NSPP	DFMP	DM	PeL	NPPC	HI	TW	SYPP
DFF	1.000	0.194*	0.400**	0.296**	0.240**	0.313**	0.428**	0.599**	0.411**	0.100	0.125	0.526**	0.223**
NPBPP			0.203**	0.367**	0.296**	0.237**	0.215**	0.573**	0.279**	0.019	-0.115	0.344**	0.050
NPPP				0.355**	0.285**	0.701**	0.318**	0.447**	0.205**	0.514**	0.223**	0.585**	0.255**
PL (cm)					0.272**	0.288**	-0.055	-0.040	0.236**	0.242**	-0.184*	0.386**	0.117
PH (cm)						0.419**	0.474**	0.597**	0.363**	-0.061	-0.014	0.157*	0.030
NSPP							0.415**	0.522**	0.276**	0.344**	0.363**	0.570**	0.184*
DFMP								1.792**	0.213**	-0.119	0.050	0.359**	0.220**
DM									0.439**	0.075	0.037	0.477**	0.251**
PeL (cm)										0.483**	0.034	0.389**	0.295**
NPPC											0.229**	0.370**	0.446**
HI												0.144	-0.019
1000 Seed weight (g)													0.395**
SYPP (g)													1.000

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

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, NPBPP= Number of primary branches per plant, NPPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, NSPP= Number of seeds per pod, NPPC=Number of pods per cluster, DFMP=Days to first mature pod, HI= Harvest index, SYPP= Seed yield per plant, TW= Test weight of 1000 seed

Table.3 Phenotypic path coefficient analysis (direct and indirect) for seed yield per plant and its component traits in black gram

Characters	DFF	NPBPP	NPPP	PL	PH	NSPP	DFMP	DM	PeL	NPPC	HI	TW	SYPP
DFF	-0.0008	-0.0195	-0.0069	-0.0038	-0.0067	0.0017	0.0065	0.0091	0.0205	0.0174	-0.0063	0.1015	0.112
NPBPP	-0.0001	-0.1202	-0.0048	-0.0073	-0.0104	0.0025	0.0058	0.0188	0.0186	0.0071	0.0142	0.0980	0.022
NPPP	-0.0002	-0.0196	-0.0293	-0.0056	-0.0083	0.0066	0.0064	0.0180	0.0153	0.0866	-0.0229	0.1633	0.210**
PL (cm)	-0.0001	-0.0325	-0.0061	-0.0269	-0.0075	0.0031	-0.0001	0.0065	0.0164	0.0452	0.0178	0.0918	0.107
PH (cm)	-0.0001	-0.0326	-0.0063	-0.0053	-0.0384	0.0046	0.0130	0.0239	0.0240	-0.0178	0.0025	0.0460	0.013
NSPP	-0.0001	-0.0204	-0.0132	-0.0057	-0.0122	0.0146	0.0061	0.0125	0.0110	0.0602	-0.0286	0.1223	0.146
DFMP	-0.0001	-0.0181	-0.0049	0.0001	-0.0130	0.0023	0.0382	0.0521	0.0159	-0.0129	-0.0086	0.0706	0.122
DM	-0.0001	-0.0230	-0.0054	-0.0018	-0.0093	0.0019	0.0203	0.0980	0.0130	-0.0062	-0.0092	0.0575	0.136
PeL (cm)	-0.0002	-0.0286	-0.0058	-0.0056	-0.0118	0.0021	0.0078	0.0164	0.0780	0.0933	-0.0039	0.1080	0.250**
NPPC	-0.0001	-0.0033	-0.0098	-0.0047	0.0026	0.0034	-0.0019	-0.0024	0.0280	0.2595	-0.0203	0.0955	0.347**
HI	0.0000	0.0133	-0.0052	0.0037	0.0007	0.0032	0.0026	0.0070	0.0023	0.0408	-0.1290	0.0419	-0.019
1000 Seed weight (g)	-0.0003	-0.0373	-0.0152	-0.0078	-0.0056	0.0057	0.0085	0.0178	0.0267	0.0785	-0.0171	0.3158	0.370**

Residual effect = 0.763

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, NPBPP= Number of primary branches per plant, NPPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, NSPP= Number of seeds per pod, NPPC=Number of pods per cluster, DFMP=Days to first mature pod, HI= Harvest index, SYPP= Seed yield per plant, TW= Test weight of 1000 seed

Table.4 Genotypic path coefficient analysis (direct and indirect) for seed yield per plant and its component traits in black gram

Characters	DFF	NPBPP	NPPP	PL	PH	NSPP	DFMP	DM	PeL	NPPC	HI	TW	SYPP
DFF	0.1009	-0.0179	-0.0823	-0.0226	0.0186	-0.0160	0.0152	0.0608	-0.0501	0.0548	-0.0209	0.1826	0.223**
NPBPP	0.0196	-0.0921	-0.0418	-0.0280	0.0229	-0.0122	0.0076	0.0582	-0.0340	0.0107	0.0192	0.1196	0.050
NPPP	0.0404	-0.0187	-0.2057	-0.0270	0.0221	-0.0359	0.0113	0.0453	-0.0249	0.2828	-0.0375	0.2031	0.255**
PL (cm)	0.0298	-0.0338	-0.0730	-0.0762	0.0210	-0.0147	-0.0019	-0.0040	-0.0288	0.1332	0.0309	0.1342	0.117
PH (cm)	0.0242	-0.0273	-0.0587	-0.0207	0.0773	-0.0214	0.0168	0.0606	-0.0442	-0.0336	0.0024	0.0546	0.030
NSPP	0.0315	-0.0219	-0.1443	-0.0220	0.0324	-0.0512	0.0147	0.0530	-0.0337	0.1890	-0.0611	0.1979	0.184*
DFMP	0.0431	-0.0198	-0.0653	0.0042	0.0366	-0.0213	0.0354	0.1819	-0.0259	-0.0652	-0.0084	0.1246	0.220**
DM	0.0604	-0.0528	-0.0919	0.0030	0.0461	-0.0267	0.0635	0.1015	-0.0534	0.0415	-0.0062	0.1655	0.251**
PeL (cm)	0.0415	-0.0257	-0.0421	-0.0180	0.0281	-0.0142	0.0075	0.0445	-0.1218	0.2659	-0.0058	0.1351	0.295**
NPPC	0.0100	-0.0018	-0.1058	-0.0185	-0.0047	-0.0176	-0.0042	0.0077	-0.0589	0.5501	-0.0384	0.1285	0.446**
HI	0.0126	0.0106	-0.0459	0.0140	-0.0011	-0.0186	0.0018	0.0037	-0.0042	0.1258	-0.1680	0.0501	-0.019
1000 Seed weight (g)	0.0530	-0.0317	-0.1203	-0.0295	0.0121	-0.0292	0.0127	0.0484	-0.0474	0.2035	-0.0242	0.3474	0.395**

Residual effect = 0.667

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, NPBPP= Number of primary branches per plant, NPPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, NSPP= Number of seeds per pod, NPPC=Number of pods per cluster, DFMP=Days to first mature pod, HI= Harvest index, SYPP= Seed yield per plant, TW= Test weight of 1000 seeds

Study on path coefficient analysis

Path analysis was proposed by Wright in 1921 and was used first for plant selection by Dewey and Lu in 1959. Path analysis is simply standardized partial regression coefficient partitioning the correlation coefficients into the measures of direct and indirect effects of set of independent variables on the dependent variable. It is also known as cause and effect relationship. If the correlation between yield and a character is due to direct effect of a character, it reveals true relationship between them and direct selection for this trait will be rewarding for yield improvement. Phenotypic path in Table 3 revealed that revealed that traits test weight of 1000 seeds (g) (0.3158), number of pods per cluster (0.2595), days to maturity (0.0980), petiole length (cm) (0.0780), days to first mature pod (0.0382) and number of seeds per pod (0.0146) have positive direct effect on seed yield per plant. Harvest index (%) (-0.1290), number of primary branches per plant (-0.1202), plant height (cm) (-0.0384), number of pods per plant (-0.0293), pod length (-0.0269) and days to 50% flowering have negative direct effect on seed yield per plant. These results are in agreement with the findings of Blessy and Naik (2018) reported number of primary branches (-0.233), followed by days to 50% flowering (-0.121) number of pods per plant (-0.120), pod length (cm) (-0.120) harvest index

In order to get yield, yield components and quality traits were investigated through path coefficient analysis (Table 4) revealed that characters number of pods per cluster (0.5501), test weight of 1000 seeds (g), days to maturity (0.1015), days to 50% flowering (0.1009), plant height (0.0773) and days to first mature pod (0.0354) have positive direct effect on seed yield per plant (g) similar result reported by Chauhan *et al.*, (2007) for the trait plant height (cm). While the traits number of

Pods per plant (-0.2057), harvest index (%) (-0.1680), petiole length (-0.1218), number of primary branches per plant (-0.0921), pod length (-0.0762) and number of seeds per pod (-0.0512) have negative direct effect on seed yield per plant at genotypic level.

The residual effect observed in present study (0.763 and 0.667) for both phenotypic and genotypic path coefficient analysis respectively other remaining character can be further studied.

References

- Al-Jibouri, H.A., Mullar P.A. and Rabinsion, H.F. (1958) Genetic and environmental variances and co-variances in an upland cotton cross of inter specific origin. *Journal of Agronomy*, 50:633-636.
- Blessy, V. and Pavan Naik, B. 2018. Studies on Correlation and Path Analysis in Black gram (*Vigna mungo* (L.) Hepper). *Int.J.Curr.Microbiol.App.Sci*. 7(08): 1991-1997.
- Chauhan, M.P., Mishra, A.C. and Singh, A.K. 2007. Correlation and path analysis in urd bean. *Legumes Res.*, 30(3): 205-208.
- Dewey, D.I., Lu, K.H. A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production. *Agronomy Journal*. 1959; 51:515-518.
- Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal.*, 51:515-518.
- Gupta, S.K., Souframanien, J, Gopalakrishna, T. Construction of a genetic linkage map of black gram based on molecular markers and comparative studies. *Genome*. 2008; 51:628.
- Lenka, D. and Mishra, B. 1973. Path

- coefficient analysis of yield in rice varieties. *Indian. J. Agric. Sci.*, (43): 376-379.
- Manivannan, N. (2014). TNAU STAT-Statistical package. Retrieved from <https://sites.google.com/site/tnaustat>.
- Panigrahi, K., Baisakh, B., Kar, M. and Mohanty, A. 2014. Research Note Genetic divergence in mutants and land races of black-gram [*Vigna mungo* (L.) Hepper] from Odisha. *Electronic Journal of Plant Breeding*, 5(3):567-572.
- Parashar SMP. Post harvest profile of black gram. MRPC-71, Ministry of Agriculture, Directorate of marketing and inspection, India, 2006.
- Pearson, Karl (1905). On the General Theory of Skew Correlation and Non-linear Regression. London: Dulau & Co.
- Ponse, V.G. and Sukhatme, P.V. (1967). Statistical methods for Agricultural Research Workers.III edition, ICAR, New Delhi.
- Pushpa, R.Y., Koteswara, R. Y., Satish, Y, Sateesh, B. J. 2013 Estimates of genetic parameters and path analysis in black gram (*Vigna mungo* (L.) Hepper). *Int. J. of Plant, Animal and Environ. Sci.*, 3:4.
- Reddy, D.K.R., Venkateswarlu, O., Jyothi, G.L.S. and Obaiah, M.C. 2011. Genetic parameters and inter-relationship analysis in black gram. *Legume Res.*, 34: 149-154.
- Sathees, N., Shoba, D., Saravanan, S., S. Merina Perm Kumari and Arumugam Pillai, M. (2019). Studies on Genetic Variability, Association and Path Coefficient Analysis in Black Gram (*Vigna mungo* L. Hepper). *Int.J.Curr.Microbiol.App.Sci.* 8(06): 1892-1899.
- Umadevi, M and Ganesan, N.M. 2005. Correlation and path analysis for yield and yield components in black gram (*Vigna mungo* L. Hepper). *Madras Agricultural Journal*, 92 (10-12): 731-734.
- Vavilov N. Studies on the origin of cultivated plants. *Inst. Appl. Bot. Plant Breed, Leningard*, 1926, 248.
- Venkatesan, M., Prakash, M. and Ganesan, J. 2003. Genetic divergence in black gram [*Vigna mungo* (L.) Hepper]. *Legume Res.*, 26 (4): 268-271.
- Venkatesan, M., Veeramani, N., Anbuselvam, Y and Ganesan, J. 2004. Correlation and path analysis in black gram (*Vigna mungo* L. Hepper). *Legume Res.*, 27 (3): 197-200.
- Wright, s. 1921a. Correlation and causation. *J. Agric. Res.* 20:557-585.
- Zeven, A. C. and De, Wet J M J (1982) Dictionary of cultivated plants and their regions of diversity. Center for Agricultural Publishing and Documentation. Wageningen.

How to cite this article:

Vikky Kumar, Prafull Kumar and Subhash Soni. 2020. Association Analysis in Black gram (*Vigna mungo* L. Hepper). *Int.J.Curr.Microbiol.App.Sci.* 9(12): 365-371.
doi: <https://doi.org/10.20546/ijcmas.2020.912.046>