



ISSN (E): 2277- 7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2021; 10(10): 983-986  
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www.thepharmajournal.com  
Received: 11-08-2021  
Accepted: 17-09-2021

**P Sravani**  
Department of Genetics and  
Plant Breeding, M. S.  
Swaminathan School of  
Agriculture, Centurion  
University of Technology &  
Management, Paralakhemundi,  
Odisha, India

**Praveen Kumar**  
Department of Genetics and  
Plant Breeding, M. S.  
Swaminathan School of  
Agriculture, Centurion  
University of Technology &  
Management, Paralakhemundi,  
Odisha, India

**K Krishnam Raju**  
Department of Genetics and  
Plant Breeding, M. S.  
Swaminathan School of  
Agriculture, Centurion  
University of Technology &  
Management, Paralakhemundi,  
Odisha, India

**Raghu Gogada**  
Department of Biochemistry and  
Plant Physiology, M M. S.  
Swaminathan School of  
Agriculture, Centurion  
University of Technology &  
Management, Paralakhemundi,  
Odisha, India

**Corresponding Author:**  
**Praveen Kumar**  
Department of Genetics and  
Plant Breeding, M. S.  
Swaminathan School of  
Agriculture, Centurion  
University of Technology &  
Management, Paralakhemundi,  
Odisha, India

## Studies on inter-relationship and cause effect for yield and its attributes of Black gram (*Vigna mungo* L. Hepper) genotypes

**P Sravani, Praveen Kumar, K Krishnam Raju and Raghu Gogada**

DOI: <https://doi.org/10.22271/tpi.2021.v10.i10o.8259>

### Abstract

The experiment was carried out during late *Rabi* season, 2019-20 with twenty seven blackgram genotypes at Bagusala Farm, M. S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha to study the inter-relationship and cause effect for yield and its attributes of Blackgram in randomized complete block design with three replications. The results highlighted that the yield per plant had significant to highly significant positive correlation at phenotypic level with plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, pod weight, and seeds per pod. The magnitude of genotypic correlations was found to be higher than phenotypic correlations for all the quantitative characters under studied indicating the prominence of additive x additive gene action and less effect of environment. Path coefficient analysis showed highest positive direct effect on the dependent character like yield per plot by 100-seed weight followed by number of clusters per plant, days to 50% flowering, protein content, number of secondary branches, pod weight per plant at phenotypic level. Henceforth, these traits would be given an importance during selection procedures to improve yield and scope for simultaneous improvement of these traits.

**Keywords:** Additive gene action, genotypic correlation, phenotypic, path coefficient

### Introduction

Pulses are the major source of dietary protein in India. Among them, Blackgram (*Vigna mungo* (L.) Hepper) is one of the important crops which are reported to be originated and majorly cultivated in India from ancient times. India is the primary center of origin for Blackgram (Vavilov, 1926). Blackgram is also known as urad bean, mungo bean or black matpe bean belongs to the family leguminosae with diploid chromosome number,  $2n=22$  and domesticated from *Vigna mungo varsilvestris* (Lukoki *et al.* 1980). It gives vegetable protein as well as cereal based diet that contain 26% protein, which is three times more than that of cereals and other vitamins. Apart from protein, it is also a source of carbohydrates (62-65%), fiber (3.5-4.5%), oil (0.5-1.5%), amino acids (lysine), vitamins, iron (9mg/100g) and phosphoric acid (385mg/100g) (sohel *et al.* 2016) [7]. Despite of its importance, there are constraints for the low production due to some environmental changes. Correlation studies provide an opportunity to study the magnitude and direction of association between yield and its component characters. The inter-relationship of various characters contributing to the yield in a single genotype can be accumulated through path coefficient analysis (Panigrahi *et al.* 2014). Keeping in view of above discussed points, present instigation was carried out to study the inter-relationship and cause effect for yield and its attributes of 27 Black gram genotypes.

### Materials and Methods

The experimental material consists of twenty seven blackgram genotypes collected from Regional Agriculture Research Station, LAM Farm, Guntur. The experiment was conducted during late *Rabi* 2019-2020 at Bagusala Farm of M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha. The genotypes were sown in Randomized Complete Block Design (RCBD) with three replications. Each genotype was planted in 4 rows with spacing of 30 cm x 10 cm. All the recommended package of practices was followed to raise the healthy crops. Observations were recorded on fifteen quantitative traits like plant height (cm), number of primary branches, number of secondary branches, number of cluster per plant, number of pods per cluster, number of pods

per plant, number of seeds per pod, pod weight (g), pod length (cm), 100 seed weight (g), yield per plant (g), total soluble sugars (%) and protein content (mg/g) from five randomly selected plants in each genotype in each replication, while days to maturity, days to 50% flowering, and yield per plot were recorded on the plot basis. The genotypic and phenotypic correlations were computed by utilizing the various components of variance and co-variance by using the formula suggested by Al-Jibouri *et al.*, (1958). Path coefficients analysis was performed by solving simultaneous equations which gives basic relationship between correlations given by Wright (1921), Dewey and Lu (1959).

## Results and Discussion

The genotypic and phenotypic correlations of sixteen quantitative characters of twenty seven blackgram genotypes were furnished in table 1 and table 2, respectively.

### Genotypic correlation

The results on genotypic correlation highlighted that the traits yield per plot had significant to highly significant positive correlation with plant height (0.259\*), number of primary branches (0.349\*\*), days to 50% flowering (0.456\*\*), number of cluster of per plant (0.279\*), and 100-seed weight (0.459\*\*). Yield per plant also showed significant to highly significant positive correlation with plant height (0.453\*\*), number of clusters per plant (0.331\*\*), number of pods per cluster (0.478\*\*), number of pods per plant (0.468\*\*), pod length (0.297\*), pod weight (0.463\*\*), and seeds per pod (0.517\*\*). These results are in close conformity with the finding of Rasel Miah *et al.*, (2016) [7, 9], C R. Konda *et al.*, (2018) [12], Sridhar *et al.*, (2019) [17], Shalini *et al.*, (2019) [19] and Bhanu Pratap *et al.*, (2019) [18]. Negative significant association exhibited by pod length (-0.225\*) with the yield per plot. This result was in agreement with Panigrahi *et al.*, (2013) and Manipatsingh Yadav *et al.*, (2020) [21]. Plant height showed significant positive correlation with pod length (0.845\*\*\*). Similar results were reported by Isha Parveen *et al.* (2011) [1] and Shalini *et al.*, (2019) [19]. Number of clusters per plant showed a highly significant positive correlation with number of pods per plant (0.752\*\*), number of pods per cluster (0.285\*), and pod weight (0.465\*\*). These results were in consonance with Isha Parveen *et al.*, (2011) [1], Gowsalya *et al.*, (2016) [10], Mohan Lal *et al.*, (2018) [13] and Sridhar *et al.*, (2019) [17] which indicating that the selection of plants with more number of clusters may increase the number of pods per plant, pods per cluster and pod weight. The

magnitude of genotypic correlations of all characters were higher than phenotypic correlations indicating the prominence of additive x additive gene action (Falconer 1981) and strong inherent genetic association between traits and less effect of environment on genotypes.

### Phenotypic correlation

The result on phenotypic correlation showed yield per plot had a strong significant to highly significant positive association days to 50% flowering (0.268\*), number of cluster per plant (0.216\*), and 100-seed weight (0.370\*\*). Yield per plant also showed significant to highly significant positive correlation with number o cluster per plant (0.256\*), number of pods per cluster (0.391\*\*), number of pod per plant (0.412\*\*), pod length (0.264\*), pos weight (0.471\*\*), and seeds per pod (0.540\*\*). These results are in close conformity with the finding of Rasel Miah *et al.*, (2016) [7, 9], C R. Konda *et al.*, (2018) [12], Sridhar *et al.*, (2019) [17], Shalini *et al.*, (2019) [19] and Bhanu Pratap *et al.*, (2019) [18]. Days to 50% flowering had highly significant positive association with days to maturity (0.515\*\*). Similar result was reported by Gowsalya *et al.*, (2016) [10].

### Path coefficient analysis

Path coefficient analysis was evaluated with yield per plot as dependent factor and its attributing traits as independent variables. As in plant breeding studies phenotypic path analysis plays a crucial role which would provide better index for selection. Henceforth, the results of phenotypic path were furnished in table 3. Path coefficient analysis was partitioned into direct and indirect effects on the yield according to Lenka and Mishra (1973). The study on path coefficient analysis showed that the trait 100-seed weight (0.456) had highest positive direct effect on the dependent character like yield per plot. The second highest positive direct effect on yield per plot was recorded for the trait number of cluster per plant (0.299). These results were similar with earlier studies of MS Devi *et al.*, (2011) [3], Kanimoli Mathivathana *et al.*, (2015) [4], Arya Gopinath *et al.*, (2018), and CR Konda *et al.*, (2018) [12]. The traits like days to 50% flowering, protein content, number of secondary branches, and pod weight showed positive direct effects on yield per plot. Negligible positive direct effect was showed by seeds per pod and plant height on the yield. These results were supported by earlier findings of Isha Parveen *et al.*, (2011) [1], Vijay Kumar *et al.*, (2014), Shalini *et al.*, (2019) [19], Sathees *et al.*, (2019) and Mahipat Singh *et al.*, (2020) [21].

**Table 1:** Genotypic correlation coefficient of the morphological and biochemical parameters to the yield per plot

	PH	NPB	NSB	DF	DM	NCP	NPC	NPP	PL	PWP	SP	100 SW	YP	TSS	PC
PH	1.000	0.554**	-0.023	0.065	0.079	0.174	0.725**	0.552**	0.845**	0.102	-0.107	0.374**	0.453**	0.449**	-0.010
NPB		1.000	0.278*	0.677**	0.221*	-0.434**	-0.201	-0.138	0.675**	-0.252*	0.333**	0.293*	-0.118	-0.174	0.675**
NSB			1.000	-0.060	-0.374**	-0.046	0.090	0.060	0.153	-0.094	0.043	-0.226*	-0.192	-0.052	-0.041
DF				1.000	0.409**	-0.043	0.256*	0.135	0.796**	0.274*	0.238*	0.154	0.106	0.192	0.580**
DM					1.000	-0.049	-0.044	-0.068	0.187	0.184	0.215	0.134	-0.187	0.086	0.522**
NCP						1.000	0.285*	0.752**	0.478**	0.465**	0.274*	-0.011	0.331**	0.126	-0.181
NPC							1.000	0.836**	0.834**	0.306**	0.457**	0.161	0.478**	0.168	-0.209
NPP								1.000	0.767**	0.471**	0.382**	0.157	0.468**	0.153	-0.198
PL									1.000	-0.679**	-0.026	0.397**	0.297*	0.101	0.050
PWP										1.000	0.360**	-0.169	0.463**	0.398**	-0.127
SP											1.000	0.137	0.517**	0.347**	-0.025
100 SW												1.000	0.137	0.083	-0.179
YP													1.000	0.324**	-0.272*
TSS														1.000	0.098
PC															1.000
YPP	0.259	0.349**	0.020	0.456**	0.156	0.279*	-0.010	0.158	-0.225*	0.076	0.098	0.459**	0.084	0.063	0.199

\*\*Significant at 5%, \* Significant at 1%; PH: Plan height; NPB: Number of primary branches; NSB: Number of secondary branches; DF: Days to 50% flowering; DM: Days to maturity; NCP: Number of clusters/ plant; NPC: Number of pods/ cluster; NPP: Number of pods/ plant; PL: Pod length; SP: Number of seeds / pod; PWP: 5 pod weight; 100SW:Hundred seed weight; YP: Yield/ plant; YPP: Yield/ plot; TSS: Total soluble sugars content; PC: Total Protein content.

**Table 2:** Phenotypic correlation coefficient of the morphological and biochemical parameters to the yield per plot

	PH	NPB	NSB	DF	DM	NCP	NPC	NPP	PL	PWP	SP	100 SW	YP	TSS	PC
PH	1.000	0.068	-0.115	0.200	0.035	-0.079	0.192	0.165	0.395**	0.193	0.171	0.185	0.275*	0.195	-0.0007
NPB		1.000	0.413**	0.260 *	0.120	0.142	0.147	0.158	0.150	-0.029	0.055	0.113	-0.016	-0.062	0.277*
NSB			1.000	0.008	-0.285**	0.143	0.204	0.171	-0.021	-0.061	0.031	-0.138	-0.154	-0.046	-0.030
DF				1.000	0.515**	-0.0002	0.163	0.062	0.020	0.014	0.010	0.083	0.003	0.118	0.329
DM					1.000	-0.022	-0.039	-0.055	0.063	0.142	0.117	0.046	-0.148	0.056	0.422**
NCP						1.000	0.331*	0.748**	0.151	0.234*	0.187	0.010	0.256*	0.109	-0.144
NPC							1.000	0.804**	0.195	0.129	0.291**	0.135	0.391**	0.151	-0.148
NPP								1.000	0.235	0.271*	0.284**	0.131	0.412**	0.143	-0.161
PL									1.000	0.281*	0.325**	0.164	0.264*	0.055	-0.015
PWP										1.000	0.465**	-0.031	0.471**	0.255*	-0.113
SP											1.000	0.159	0.540**	0.292**	-0.018
100 SW												1.0000	0.129	0.057	-0.143
YP													1.000	0.297	-0.253*
TSS														1.000	0.093
PC															1.000
YPP	0.120	0.110	0.016	0.268**	0.138	0.216**	0.005	0.145	0.025	0.140	0.145	0.370**	0.130	0.068	0.172

\*\*Significant at 5%, \* Significant at 1%; PH: Plan height; NPB: Number of primary branches; NSB: Number of secondary branches; DF: Days to 50% flowering; DM: Days to maturity; NCP: Number of clusters/ plant; NPC: Number of pods/ cluster; NPP: Number of pods/ plant; PL: Pod length; SP: Number of seeds / pod; PWP: 5 pod weight; 100SW:Hundred seed weight; YP: Yield/ plant; YPP: Yield/ plot; TSS: Total soluble sugars content; PC: Total Protein content.

**Table 3:** Phenotypic path association of the morphological and biochemical parameters to the yield per plot

	PH	NPB	NSB	DF	DM	NCP	NPC	NPP	PL	PWP	SP	100 SW	YP	TSS	PC
PH	0.093	0.006	-0.01	0.018	0.003	-0.007	0.017	0.015	0.036	0.018	0.016	0.017	0.025	0.018	0.018
NPB	-0.009	-0.131	-0.054	-0.034	-0.015	-0.018	-0.019	-0.02	-0.019	0.003	-0.007	-0.014	0.002	0.008	0.008
NSB	-0.018	0.067	0.162	0.001	-0.046	0.0103	0.033	0.027	-0.003	-0.01	0.005	-0.022	-0.025	-0.007	-0.007
DF	0.043	0.056	0.001	0.215	0.11	0	0.035	0.013	0.004	0.003	0.002	0.0051	0	0.025	0.025
DM	-0.001	-0.005	0.0079	-0.025	-0.048	0.001	0.001	0.002	-0.003	-0.007	-0.005	-0.002	0.007	-0.002	-0.002
NCP	-0.023	0.042	0.042	0.0001	-0.006	0.299	0.099	0.224	0.045	0.07	0.056	0.003	0.0712	0.032	0.032
NPC	-0.038	-0.029	-0.04	-0.032	0.007	-0.062	-0.199	-0.16	-0.038	-0.025	-0.058	-0.027	-0.078	-0.03	-0.03
NPP	-0.002	-0.002	-0.002	-0.001	0.042	-0.012	-0.013	-0.016	-0.003	-0.004	-0.004	-0.002	-0.006	-0.002	-0.002
PL	-0.054	-0.02	0.002	-0.002	-0.008	-0.02	-0.027	-0.032	-0.138	-0.038	-0.045	-0.022	-0.036	-0.007	-0.007
PWP	0.025	-0.003	-0.008	0.001	0.018	0.03	0.016	0.035	0.036	0.13	0.0734	-0.004	0.061	0.033	0.033
SP	0.001	0.0125	0.0003	0.0368	0.001	0.001	0.002	-0.0071	0.0064	0.0086	0.008	0.001	0.004	0.0627	0.002
100 SW	0.084	0.051	-0.063	0.038	0.021	0.004	0.062	0.06	0.075	-0.014	0.073	0.457	0.059	0.026	0.026
YP	0.039	-0.002	-0.022	0.0006	-0.021	0.036	0.0515	0.059	0.038	0.067	0.077	0.018	0.143	0.042	-0.120
TSS	-0.029	0.009	0.006	-0.017	-0.008	-0.016	-0.022	-0.021	-0.008	-0.038	-0.043	-0.008	-0.044	-0.149	-0.013
PC	-0.0001	0.058	-0.006	0.069	0.088	-0.03	-0.031	-0.033	-0.003	-0.023	-0.003	-0.03	-0.053	0.019	0.21
YPP	0.120	0.11	0.016	0.268	0.138	0.216	0.005	0.145	0.025	0.140	0.145	0.370	0.130	0.068	0.172

Residual effect = 0.398; PH: Plan height; NPB: Number of primary branches; NSB: Number of secondary branches; DF: Days to 50% flowering; DM: Days to maturity; NCP: Number of clusters/ plant; NPC: Number of pods/ cluster; NPP: Number of pods/ plant; PL: Pod length; SP: Number of seeds / pod; PWP: 5 pod weight; 100SW:Hundred seed weight; YP: Yield/ plant; YPP: Yield/ plot; TSS: Total soluble sugars content; PC: Total Protein content

## Conclusion

From the present investigation the results showed that characters days to 50% flowering, number of cluster per plant, and 100-seed weight had significant to highly significant positive association with yield per plot at phenotypic level. Yield per plant also showed significant to highly significant positive association with number of cluster per plant, number of pods per cluster, number of pod per plant, pod length, pod weight, and seeds per pod. The characters 100-seed weight, and number clusters per plant exhibited maximum positive direct effect on dependent variable like yield per plot. Henceforth, these traits would be given importance during selection procedures to improve yield and scope for simultaneous improvement of these traits.

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