



Assessment on Genetic Variability Correlation and Path Analysis for Quantitative Traits in Blackgram (*Vigna mungo* L. Hepper)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Based on mean performance of 22 genotypes of Blackgram. Seed yield per plant was highest in case of KU-48 (6.08) followed by LBG-752 (6.00) genotypes. On the basis of Analysis of variance, significant difference was recorded for all the seed yield and its components indicating presence of large amount of variability in the genotypes. The magnitude of GCV and PCV recorded highest for seed yield per plant, number of pods per plant, biological yield per plant, number of clusters per plant, harvest index. High heritability coupled with high genetic advance as percent of mean was recorded for seed yield per plant, number of pods per plant, biological yield per plant, number of clusters per plant. Correlation at both genotypic and phenotypic level, seed yield per plant exhibited non-significant positive association with number of pods per plant, number of clusters per plant, number of primary branches per plant, days to maturity, biological yield per plant, plant height, harvest index, number of seeds per pod, pod length, days to 50% pod setting. Path analysis revealed that number of pods per plant harvest index registered high and positive direct effect on seed yield per plant. It indicates true relationship between these traits and direct selection for these traits will be rewarding for yield improvement.

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1. INTRODUCTION

Blackgram (*Vigna mungo* L. Hepper, 2n=22), popularly known as urdbean, is an important self-pollinating diploid grain legume (Naga et al., 2006) and belongs to the family Leguminosae and subfamily Papilionaceae. Center of genetic diversity for Blackgram is found in India (Zeven et al., 1982). It has been in cultivation from ancient times and is one of the most highly prized pulse of India. It is an economically important grain legume crop in Asia, widely cultivated on marginal lands with low inputs during Kharif, Rabi and summer seasons. Blackgram seeds are mainly a staple food, dehulled and split seeds are a common dish in South Asia [1,2]. It is extensively used in culinary preparation like dosa, idli, vada and papad. The by-product of dal processing (chunior bran) constitutes about 15-20% of the seed weight and comprises hulls, germs and broken seeds. Chuni is a potential feed resource and large quantities are available in India and other Southern Asian countries where Blackgram is a popular food (Reddy et al., 2000). It is very nutritious and is recommended for diabetics, as are other pulses.

Blackgram is an erect, sub-erect or trailing, densely hairy annual herb. The tap root produces a branched root system with smooth, rounded nodules [3-5]. The pods are narrow, cylindrical and up to 6 cm. long. The pod is hairy and has a short-hooked beak. It contains 4-10 ellipsoid black or mottled seeds (Ecocrop, 2011). Many *Vigna mungo* cultivars exist, each one adapted to specific environmental conditions. Early maturing, disease resistant and easily cultivated cultivars have been obtained (Jansen, 2006). This is one of the most important short duration legume crops utilized in the food, fodder, soil conservation, integrated farming systems, reclaiming of degraded pastures and symbiotic nitrogen fixation [6-10].

Blackgram is the fourth important pulse crop in India which holds about 13 per cent of the total pulse area and contributing about 10 per cent to the total pulse production. It is mostly grown in Andhra Pradesh, Uttar Pradesh, Maharashtra, Madhya Pradesh, Tamil Nadu, Rajasthan, Orissa and Bihar. In India 2019-20, area covered under blackgram is 37.52 lakh/ha as against 38.18 lakh/ha in last year with a production of 2.04

million tonnes and 651 kg/ha productivity. The states of Madhya Pradesh (16.50 lakh/ha), Uttar Pradesh (7.01 lakh/ha), Rajasthan (4.56 lakh/ha), are the major producers of blackgram in India.

It is often used as dry season intercrop in rice or wheat as it has a beneficial effect on soil nutrient status (Parashar, 2006). Blackgram is still cultivated on marginal lands under rainfed conditions and faces terminal drought which affects its productivity to a great extent. Low and uneven rainfall pattern of the state since last few years have urged the need to develop early maturing varieties of Blackgram to avoid yield losses due to long dry span during maturity [11-15].

Correlation coefficient analysis is a statistical technique which measures the degree and association between two or more variables. Estimates of correlation coefficient are useful in identifying the component traits which can be used for yield improvement of maize [16-18]. Path coefficient analysis provides a thorough understanding of contribution of various characters by partitioning the correlation coefficient into components of direct and indirect effects [19], which helps the breeder in determining the yield components. To accumulate optimum contribution of yield contributing characters, it is essential to know the association of various characters along with path coefficients (Bhutia et al. 2016). Therefore, present study was conducted to assess correlation and path analysis to identify component traits for developing high yielding varieties of maize.

1.1 Objectives

1. To examine the extent of genetic variability present in the germplasm
2. To estimate the association between different quantitative traits and grain yield
3. To study direct and indirect effects yield contributing characters

2. MATERIALS AND METHODS

The present investigation was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of

Agriculture, Technology and Sciences, Allahabad, U.P during Zaid-2021. A randomized block design was adopted with three replications and row to row spacing is 30cm and plant to plant spacing is 10 cm with plot size of 1mx1m. Replication wise data on the basis of five randomly taken competitive plants from each replication were recorded on following fourteen quantitative traits : 1) Days to 50% flowering, 2) Days to 50% pod setting, 3) Plant height, 4) Number of primary branches, 5) Number of clusters per plant, 6) Days to maturity, 7) Number of pods per plant, 8) Number of seeds per plant, 9) Pod length, 10) Biological yield, 11) Seed index, 12) Harvest index, 13) Seed yield per plant. The recorded for all the considered characters were subjected to analysis of variance with the formula suggested by Panse and Sukhatme. Further, different components of variance i.e., As per established methods, data were statistically analysed to determine genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as a percent mean. For the analysis of variance, genotypic coefficient of variation and phenotypic coefficient of variation, standard statistical methods were utilised Burton, heritability Burton and Devane [20] and genetic advance Johnson et al., [21], Ai Jibouri et al., used genotypic and phenotypic variances and co-variances to calculate genotypic and phenotypic correlation coefficients. The path coefficient study was carried out using the technique proposed by Dewey and Lu [22].

2.1 Layout Description

- Crop: Black gram (*Vigna mungo* L.)
- Season: ZAID, 2021
- Experimental design: Randomized Block Design
- Number of genotypes: 22
- Number of replications: 03
- Gross area: 144 sq.m
- Net area: 66.sq.m
- Individual plot size: 1x1 Sq m
- Spacing: 30 X 10 cm
- Date of sowing: 22-02-2021
- Recommended Fertilizer dose: N : P : K @ 20:40:20 kg/ha

2.2 Experimental Material

The Source of Experimental materials for the present study were obtained from the Department of Genetics and Plant Breeding, SHUATS, Prayagraj.

3. RESULTS AND DISCUSSION

For all of the traits studied, the analysis of variance indicated substantial differences between the genotypes (Table 1). As a result, it revealed a significant level of genetic heterogeneity among twenty-two Blackgram genotypes. Evaluation of genetic characteristics, correlation and path coefficient analysis aid in the examination of significant traits during the selection process for optimizing maize productivity. (Table 2) displays the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance (GA) and genetic advance as a percent of mean GA (percent) for all yield contributing characteristics.

For all of the characters, PCV was higher than the matching GCV, indicating that the environment had an impact. The highest PCV and GCV were found for number of pods per plant (43.292 and 44.443), seed yield per plant (40.258 and 41.387), biological yield per plant (33.795 and 33.956), number of clusters per plant (31.742 and 35.020), days to maturity (31.260 and 33.140), harvest index (23.410 and 26.380) and days to 50% flowering (22.340 and 24.860). The results are in conformity with the findings of Kumar et al. (2015) and Babu et al. [23]. The genotypic coefficient of variation estimations reflects the overall amount of genotypic variability present in the material.

Heritability, on the other hand, reflects the fraction of this genotypic polymorphism that is passed down from parents to offspring [24,25]. Lush [26] proposed the broad sense heredity idea. It influences how effective genotypic variability may be used in a breeding programme. (Table 2) shows the heritability estimates obtained during the current investigation. The heritability of the qualities is moderate to high, ranging from harvest index (99.70), biological yield for plant (99.10), number of pods per plant (94.90), seed yield per plant (94.60), number of clusters per plant (82.20), number of seeds per plant (74.00), number of primary branches (56.80), plant height (56.70), seed index (51.28), pod length (35.60), days to 50% flowering (48.69), days to maturity (47.95), days to 50% pod setting (34.26). The high heritability values of the qualities examined in this study revealed that they were less influenced by the environment, allowing for successful selection of traits based on phenotypic appearance using a simple selection strategy

and indicating the possibility of genetic progress. Similar findings were reported by Panda et al. (2017) and Ozukum and Sharma [27].

High genetic advance was recorded for seed yield per plant (29.630), biological yield per plant (27.260), harvest index (21.140), Similar results were reported by Priya et al. [28] and Kuralarasan et al. [29].

High genetic advance as percent mean was observed for number of pods per plant (86.872), biological yield per plant (69.288), number of clusters per plant (59.268), seed yield per plant (32.260), harvest index (28.560), number of primary branches per plant (22.715). Similar results were reported by Priya et al. [28] and Kuralarasan et al. [29].

During the correlation study, associations between yield and yield contributing features were investigated under study. (Table 3) shows the phenotypic and genotypic correlation coefficients between the investigated features of 45 maize genotypes on different quantitative traits. In most cases, the genotypic correlation was higher than that of phenotypic correlation; reveal that association may be largely due to genetic reason (strong coupling linkage) (Sharma, 1988). At genotypic level, Seed yield per plant showed significant positive correlation with Number of pods per plant (0.966** and 0.911**), Number of clusters per plant (0.942** and 0.846**), Plant Height (0.926** and 0.709**), Biological yield per plant (0.884** and 0.855**),

Number of primary branches (0.844** and 0.642**), Seed index (0.787** and 0.501*), Pod length (0.760** and 0.429*), Harvest index (0.597** and 0.579**) are positively and significantly correlated with grain yield per plant in both genotypic and phenotypic correlation. Similar findings were reported by Reni et al. (2013), Miah et al. (2016), Mohanlal et al. [30] and Sushmitharaj et al. [31].

Path analysis is one of the most accurate statistical techniques for determining the interdependence of features and the degree of control of independent characters on seed production, either directly or indirectly Mushtaq et al. (2013). When it comes to choosing high yielding germplasm, the idea of direct and indirect influence of yield contributing traits on the final end product yield in any crop is crucial. (Table 4) depicted the direct and indirect effects of 13 different quantitative characters. In genotypic path analysis revealed that Seed yield per plant had positive direct effect on Number of clusters per plant (0.5393), Number of pods per plant (0.4111), Number of seeds per plant (0.2469), Biological yield per plant (0.1202), Pod length (0.0963), Seed index (0.0445), days to 50% flowering (0.0377), Plant Height (0.134), Harvest index (0.072). While the negative indirect effects were Number of primary branches per plant (-0.3038), days to maturity (-0.0781), days to 50% pod setting (-0.0139). Similar findings were reported by Juothsna et al. (2016), Arya et al. [32] and Sathya et al. [28].

Table 1. Analysis of variance (ANOVA) among 22 Blackgram genotypes for 13 quantitative traits

Traits	Mean sum of square		
	Replication	Genotype	Error
Degrees of freedom (df)	2	21	42
Days to 50% flowering	26.63	7.26**	12.36
DAYS to 50% pod setting	22.82	6.60**	6.25
Plant height (cm)	7.28	98.01**	10.59
Number of primary branches per plant	206.04	217.71**	4.63
Number of clusters per plant	7.29	8.38**	2.36
Days to maturity	10.06	22.26**	16.96
Number of pods per plant	54.48	10.97**	2.02
Number of seeds per plant	23.63	81.15**	3.14
pod length (cm)	10.07	9.15**	8.07
Biological yield (g)	42.68	37.01**	26.13
Seed index (g)	5.24	4.19**	2.63
Harvest index (%)	67.13	8.62**	11.06
Seed yield per plant (g)	47.01	34.01**	20.18

Level of significance at 5 %, ** Level of significance at 1%

Table 2. Genetic parameters for 13 quantitative characters in 22 Blackgram genotypes

Traits	GCV	PCV	Heritability (Broad sense) %	GA 5%	GAM 5%
Days to 50% flowering	22.340	24.860	48.69	1.460	2.840
DAYS to 50% pod setting	1.967	5.090	34.26	8.970	1.560
Plant height (cm)	12.018	15.961	56.70	3.541	18.642
Number of primary branches per plant	14.631	19.413	56.80	0.690	22.715
Number of clusters per plant	31.742	35.020	82.20	2.265	59.268
Days to maturity	31.260	33.140	47.95	0.480	0.611
Number of pods per plant	43.292	44.443	94.90	11.472	86.872
Number of seeds per plant	11.244	13.074	74.00	1.050	19.919
pod length (cm)	4.911	8.231	35.60	2.230	6.038
Biological yield (g)	33.795	33.956	99.10	27.260	69.288
Seed index (g)	11.260	15.590	51.28	1.480	0.446
Harvest index (%)	23.410	26.380	99.70	21.140	28.560
Seed yield per plant (g)	40.258	41.387	94.60	29.630	32.260

PCV: Phenotypic Coefficient of Variation, GCV: Genotypic Coefficient of Variation, h^2 bs: heritability (broad sense), GA: Genetic Advance, GAM: Genetic Advance as Percent of Mean

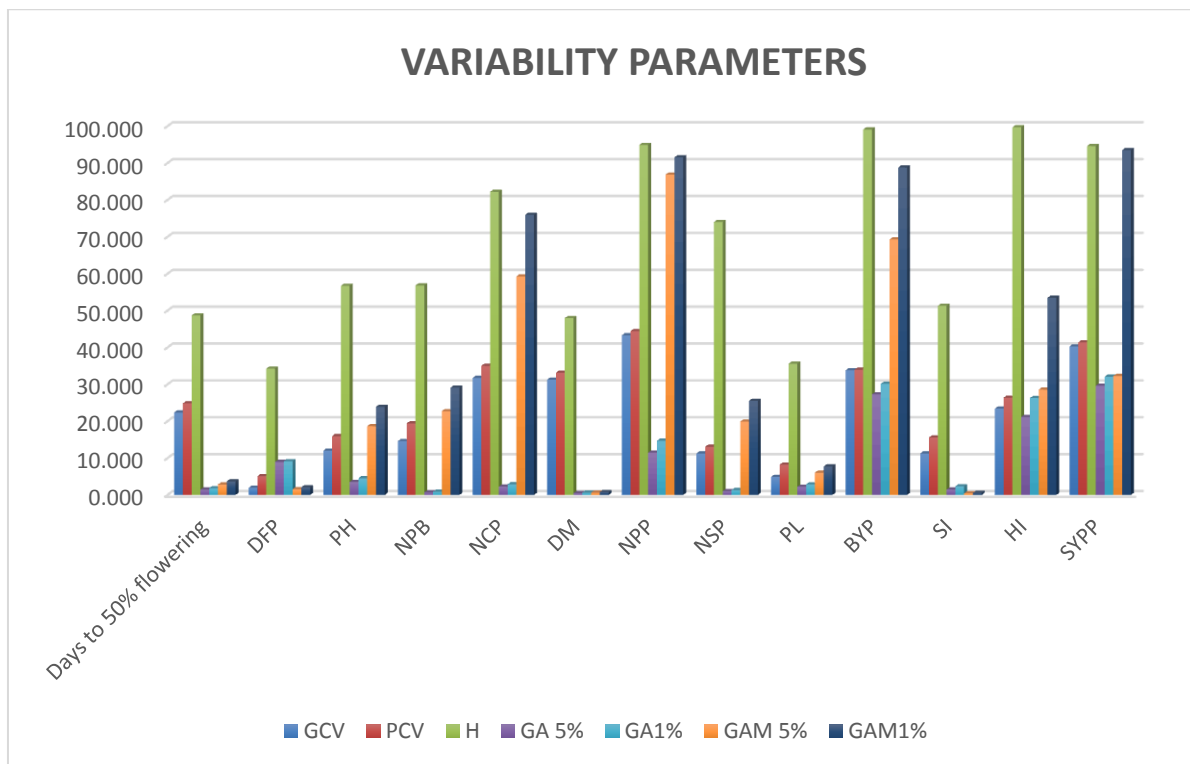


Fig. 1. Histogram depicting GCV, PCV, heritability and genetic advance for 13 quantitative characters of 22 Blackgram genotypes

In phenotypic path analysis revealed that Seed yield per plant had positive indirect effects were through biological yield per plant (0.4718), Number of pods per plant (0.2442), Number of seeds per plant (0.1287), Number of clusters per plant (0.0947), Harvest index (0.229), Seed index (0.0045), Plant Height (0.133), Number of

primary branches per plant (0.0041). While the negative indirect effects were days to maturity (-0.0561), days to 50% pod setting (-0.0266), days to 50% flowering (-0.0184), pod length (-0.098). Similar findings were reported by Juothesna et al. (2016), Arya et al. [32] and Sathya et al. [28].

Table 3. Genotypic and phenotypic correlation among the different traits evaluated in Blackgram during zaid-2021

Traits		Days to 50% flowering	DAYS to 50% pod setting	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Days to maturity	Number of pods per plant	Number of seeds per plant	Pod length (cm)	Biological yield (g)	Seed index (g)	Harvest index (%)	Seed yield per plant (g)
Days to 50% flowering	G	1	-0.112	0.147	0.191	-0.063	0.638**	-0.007	0.137	0.244	0.064	0.026	-0.11	-0.014
	P	1	0.131	0.021	0.229	-0.017	0.229	0.004	0.005	0.013	-0.022	-0.009	0.055	-0.03
DAYS to 50% pod setting	G		1	0.860**	0.578**	0.419*	0.575**	0.417*	0.36	0.25	0.431*	-0.882**	0.335	0.395
	P		1	-0.124	-0.063	-0.261	0.007	-0.415*	-0.276	-0.23	-0.146	-0.189	-0.125	0.256
Plant height (cm)	G			1	0.738**	0.920**	0.963**	0.803**	0.531**	0.698**	0.751**	0.832**	0.644**	0.926**
	P			1	0.479*	0.576**	0.189	0.576**	0.409	0.41	0.557**	0.253	0.480*	0.709**
Number of primary branches per plant	G				1	0.926**	0.964**	0.815**	0.585**	0.830**	0.675**	0.575**	0.764**	0.844**
	P				1	0.656**	0.247	0.643**	0.334	0.385	0.497*	-0.009	0.576**	0.642**
Number of clusters per plant	G					1	0.636**	0.946**	0.353	0.742**	0.891**	0.838**	0.527**	0.942**
	P					1	0.433*	0.842**	0.255	0.424*	0.809**	0.128	0.481*	0.846**
Days to maturity	G						1	1.001	0.354	-0.056	0.212	0.048	0.500*	0.026
	P						1	0.295	0.101	0.102	0.329	-0.092	0.139	0.014
Number of pods per plant	G							1	0.32	0.679**	0.914**	0.667**	0.510*	0.966**
	P							1	0.26	0.449*	0.885**	0.068	0.495*	0.911**
Number of seeds per plant	G								1	0.744**	0.242	0.09	0.667**	0.543**
	P								1	0.460*	0.205	0.103	0.570**	0.456*
Pod length (cm)	G									1	0.674**	-0.055	0.577**	0.760**
	P									1	0.392	-0.099	0.34	0.429*
Biological yield (g)	G										1	0.447*	0.176	0.884**
	P										1	0.1	0.175	0.855**
Seed index (g)	G											1	0.563**	0.787**
	P											1	0.122	0.501*
Harvest index (%)	G												1	0.597**
	P												1	0.579**
Seed yield per plant (g)	G													1.000
	P													1.000

G*: genotypic correlation, P*: phenotypic correlation

Table 4. Direct (Bold) and indirect effect at genotypic and phenotypic level for different quantitative traits on seed yield

Traits		Days to 50% flowering	DAYS to 50% pod setting	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Days to maturity	Number of pods per plant	Number of seeds per plant	Pod length (cm)	Biological yield (g)	Seed index (g)	Harvest index (%)	Seed yield per plant (g)
Days to 50% flowering	G	0.0377	-0.0042	0.0055	0.0072	-0.0024	0.024	-0.0003	0.0052	0.0092	0.0024	0.001	-0.0041	-0.014
	P	-0.0184	-0.0024	-0.0004	-0.0042	0.0003	-0.0042	-0.0001	-0.0001	-0.0002	0.0004	0.0002	-0.001	-0.03
DAYS to 50% pod setting	G	0.0156	-0.139	-0.1195	-0.0803	-0.0582	-0.0799	-0.0579	-0.05	-0.1737	-0.0599	0.1226	-0.0465	0.395
	P	-0.0035	-0.0266	0.0033	0.0017	0.0069	-0.0002	0.0037	0.0073	0.0061	0.0039	0.005	0.0033	0.256
Plant height (cm)	G	0.0197	0.1153	0.134	0.0989	0.1234	0.1559	0.1077	0.0712	0.0935	0.1007	0.1785	0.0863	0.926**
	P	0.0028	-0.0165	0.133	0.0637	0.0766	0.0251	0.0766	0.0543	0.0545	0.0741	0.0336	0.0638	0.709**
Number of primary branches per plant	G	-0.0581	-0.1755	-0.2241	-0.3038	-0.2814	-0.384	-0.2475	-0.1777	-0.2521	-0.2051	-0.1745	-0.2319	0.844**
	P	0.0009	-0.0003	0.0019	0.0041	0.0027	0.001	0.0026	0.0014	0.0016	0.002	0.0124	0.0023	0.642**
Number of clusters per plant	G	-0.0341	0.2259	0.4963	0.4996	0.5393	0.7474	0.5103	0.1903	0.4	0.4807	0.4519	0.2843	0.942**
	P	-0.0016	-0.0247	0.0546	0.0621	0.0947	0.041	0.0797	0.0241	0.0401	0.0766	0.0121	0.0455	0.846**
Days to maturity	G	-0.0498	-0.0449	-0.0908	-0.0987	-0.1083	-0.0781	-0.0782	-0.0276	0.0044	-0.0875	-0.222	-0.0391	0.026
	P	-0.0128	-0.0004	-0.0106	-0.0139	-0.0243	-0.0561	-0.0166	-0.0057	-0.0057	-0.0185	0.0051	-0.0078	0.014
Number of pods per plant	G	-0.0029	0.1714	0.3302	0.3349	0.389	0.4116	0.4111	0.1317	0.2789	0.3756	0.2743	0.2096	0.966**
	P	0.001	-0.0338	0.1407	0.1571	0.2056	0.0721	0.2442	0.0635	0.1097	0.2162	0.0165	0.121	0.911**
Number of seeds per plant	G	0.0339	0.0889	0.1312	0.1445	0.0871	0.0873	0.0791	0.2469	0.1836	0.0598	0.0221	0.1648	0.543**
	P	0.0006	-0.0355	0.0526	0.0429	0.0328	0.013	0.0335	0.1287	0.0592	0.0264	0.0133	0.0734	0.456*
Pod length (cm)	G	0.0235	0.1204	0.0672	0.0799	0.0715	-0.0054	0.0654	0.0716	0.0963	0.0649	-0.0053	0.0556	0.760**
	P	-0.0013	0.0225	-0.0402	-0.0377	-0.0415	-0.01	-0.044	-0.0451	-0.098	-0.0384	0.0097	-0.0333	0.429*
Biological yield (g)	G	0.0077	0.0518	0.0903	0.0812	0.1072	0.1347	0.1098	0.0291	0.081	0.1202	0.0537	0.0212	0.884**
	P	-0.0101	-0.0687	0.2628	0.2342	0.3815	0.1553	0.4177	0.0967	0.1848	0.4718	0.0471	0.0825	0.855**
Seed index (g)	G	0.0012	-0.0392	0.0592	0.0256	0.0373	0.1264	0.0297	0.004	-0.0025	0.0199	0.0445	0.0251	0.787**
	P	-0.0014	-0.0008	0.0011	0.0016	0.0006	-0.0004	0.0003	0.0005	-0.0004	0.0004	0.0045	0.0005	0.501*
Harvest index (%)	G	-0.0079	0.0241	0.0463	0.0549	0.0379	0.036	0.0367	0.048	0.0415	0.0127	0.0405	0.072	0.597**
	P	0.0127	-0.0286	0.1099	0.1318	0.1101	0.0318	0.1134	0.1306	0.0777	0.04	0.0279	0.229	0.579**

: genotypic path analysis, P: phenotypic path analysis

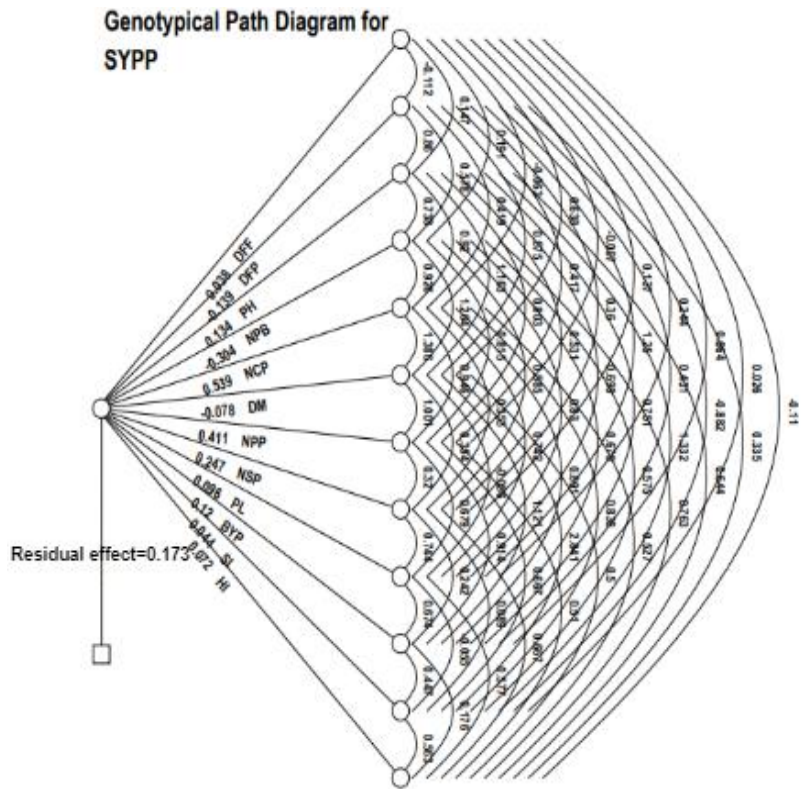


Fig. 2. Genotypic path diagram for grain yield per plant

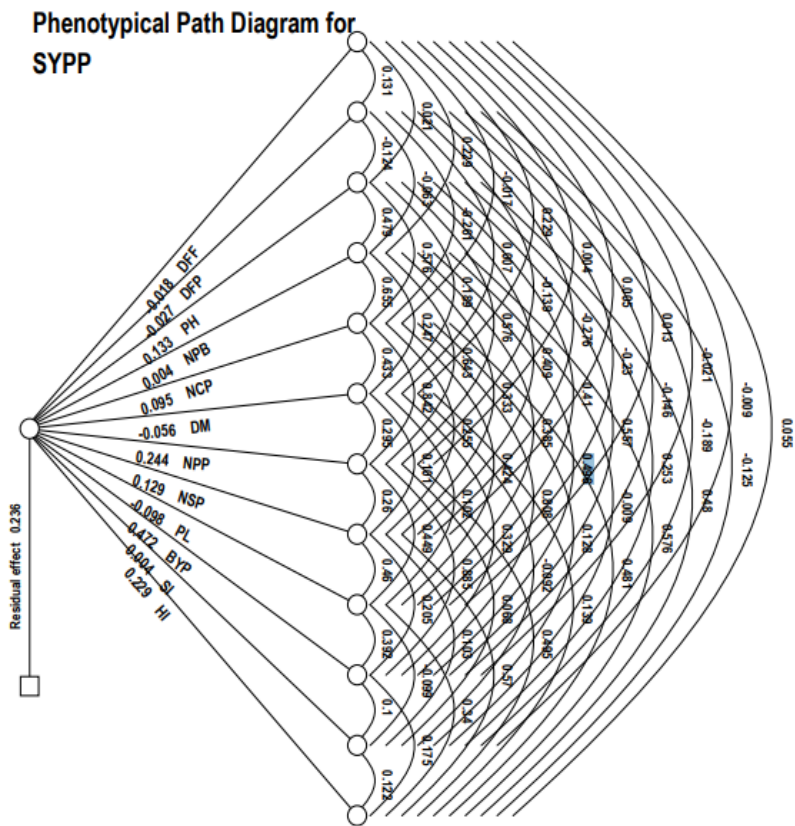


Fig. 3. Phenotypic path diagram for grain yield per plant

4. CONCLUSION

It is concluded that PCV is higher than GCV indicating that due to the influence of the environment on all the traits. Among twenty-two genotypes KU-48 (6.08 gm), LBG-752(6.00 gm), and KU-42 (3.85 gm) are the superior lines and, Number of pods per plant, Seed yield per plant had shown the highest GCV and PCV, high heritability recorded in Harvest index, biological yield per plant, Number of primary branches. A number of pods per plant, Number of clusters per plant, and biological yield per plant is positive and significantly correlated with seed yield per plant in genotypic and phenotypic correlation. path analysis revealed that the number of clusters per plant, Number of pods per plant had the highest direct effect in Seed yield per plant. Hence these characters should be given priority during selection for yield improvement in Blackgram.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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