

Original Research Article

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

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.

Key Words: **Blackgram** (*Vigna mungo* L. Hepper), Genetic variability, Heritability, Genetic advance, Genotypic correlation, Phenotypic correlation, Genotypic path analysis and Phenotypic path analysis.

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. 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. 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.

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.

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. Path coefficient analysis provides a thorough understanding of contribution of various characters by partitioning the correlation coefficient into components of direct and indirect effects (**Wright, 1921**), 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 study 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 Kharif-2021. A randomized block design was adopted with three replications and row to row spacing is 30cm and plant to plant spacing is 10cm 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., phenotypic, genotypic and environmental variance were estimated and genetic parameters like genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense, genetic advance as percent of mean and correlation analysis were conducted by following appropriate statistical procedure.

- 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

RESULT AND DISCUSSION

3.1 Analysis of Variance for Quantitative Characters in Blackgram (*Vigna mungo* L. Hepper)

The abundant scope for improving these characters including grain yield per plant provided the material is subjected to judicious selection programme. Due to diverse source of material taken as well as environmental influence affecting the phenotypes the presence of variability might be large. ANOVA for different characters is present in Table 1. The mean squares due to genotypes showed highly significant differences ($\alpha=0.01$) for all characters indicating the presence of substantial amount of genetic variability among the rice genotypes. In Table 2. which revealed a wide range of variation for all traits studies the mean values, the coefficient of variation (C.V.), standard error of the mean (SEm+), the critical difference (C.D.) at 5% and 1%, range of 20 genotypes for 13 quantitative characters are presented.

Genotypic coefficient of variation varied from 1.967 Days to 75% maturity to 43.292 for Grain yield per plant(gm). High magnitude of genotypic coefficient of variation was recorded for number of pods per plant (43.292), seed yield per plant (40.258), biological yield per plant (33.795), number of clusters per plant (31.742), days to maturity (31.260), harvest index (23.410) and days to 50% flowering (22.340), number of pods per plant (14.631), and moderate plant height (12.018), seed index (11.260), number of seeds per plant (11.244), pod length (4.911), days to 50% pod setting (1.967).

Phenotypic coefficient of variation

High magnitude of phenotypic coefficient of variation was recorded for number of pods per plant (44.443), seed yield per plant (41.387), number of clusters per plant (35.020), biological yield per plant (33.956), days to maturity (33.140), harvest index (26.380), days to 50% pod setting (24.860), number of primary branches plant (19.413), plant height (15.961), seed index (15.590), number of seeds per plant (13.074), pod length (8.231), days to 50% pod setting (5.090).

High broad sense heritability was observed for 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).

In the present study estimates of broad sense heritability are computed which includes both additive and non-additive gene effects. Higher values of broad sense

heritability for the traits harvest index, seed yield per plant, number of pods per plant, pod length, number of seeds per pod, number of clusters per plant, biological yield per plant, days to 50% flowering, plant height, seed index indicate that these characters are less influenced by environment effect and selection on the basis of phenotypic performance of genotypes would be more efficient in further improvement of these traits. High to moderate heritability for most of the traits in the present study indicated considerable potential for the development of high yielding varieties through desirable selection in succeeding generations.

Genetic advance

Moderate genetic advance was recorded for seed yield per plant (29.630), biological yield per plant (27.260), harvest index (21.140), number of pods per plant (11.472), days to 50% flowering (8.970), plant height (3.541), pod length (2.230), number of clusters per plant (2.265), seed index (1.480), days to 50% flowering (1.460), number of seeds per plant (1.050), number of primary branches per plant (0.690), days to maturity (0.480).

Genetic advance as percent of mean

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), number of seeds per plant (19.919), plant height (18.642), pod length (6.038), days to 50% flowering (2.840), days to 50% pod setting (1.560), days to maturity (0.611), seed index (0.446).

Genotypic Correlation Coefficient

At genotypic level, Seed yield per plant showed significant positive correlation with Number of pods per plant (0.966**), Number of clusters per plant (0.942**), Plant Height (0.926**), Biological yield per plant (0.884**), Number of primary branches (0.844**), Seed index (0.787**), Pod length (0.760**), Harvest index (0.597**), Number of seeds per plant (0.543**). It showed non-significant positive correlation with Days to 50% pod setting (0.395), Days to maturity (0.026). It showed non-significant negative correlation with days to 50% pod flowering (-0.014).

Phenotypic Correlation Coefficient

At genotypic level, Seed yield per plant showed significant positive correlation with Number of pods per plant (0.911**), Biological yield per plant (0.855**), Number of clusters per plant (0.846**), Plant Height (0.709**), Number of primary branches (0.642**), Harvest index (0.579**), Seed index (0.501*), Number of seeds per plant (0.456*), Pod length

(0.429*). It showed non-significant positive correlation with Days to 50% pod setting (0.256), Days to maturity (0.014). It showed non-significant negative correlation with days to 50% flowering (-0.03)

Genotypic Path Coefficient Analysis

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).

Phenotypic Path Coefficient Analysis

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)

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.

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

TRAITS	MEAN SUM OF SQUARE		ERROR
	REPLICATION	GENOTYPE	
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

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

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

• **Table: 3- Genotypic correlation coefficient between yield and its related traits in 22 Blackgram genotypes.**

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	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
Days to 50% pod setting		1	0.860**	0.578**	0.419*	0.575**	0.417*	0.36	0.25	0.431*	-0.882**	0.335	0.395
Plant height (cm)			1	0.738**	0.920**	0.963**	0.803**	0.531**	0.698**	0.751**	0.832**	0.644**	0.926**
Number of primary branches per plant				1	0.926**	0.964**	0.815**	0.585**	0.830**	0.675**	0.575**	0.764**	0.844**
Number of clusters per plant					1	0.636**	0.946**	0.353	0.742**	0.891**	0.838**	0.527**	0.942**
Days to maturity						1	1.001	0.354	-0.056	0.212	0.048	0.500*	0.026
Number of pods per plant							1	0.32	0.679**	0.914**	0.667**	0.510*	0.966**
Number of seeds per plant								1	0.744**	0.242	0.09	0.667**	0.543**
pod length (cm)									1	0.674**	-0.055	0.577**	0.760**
Biological yield (g)										1	0.447*	0.176	0.884**
Seed index (g)											1	0.563**	0.787**
Harvest index (%)												1	0.597**

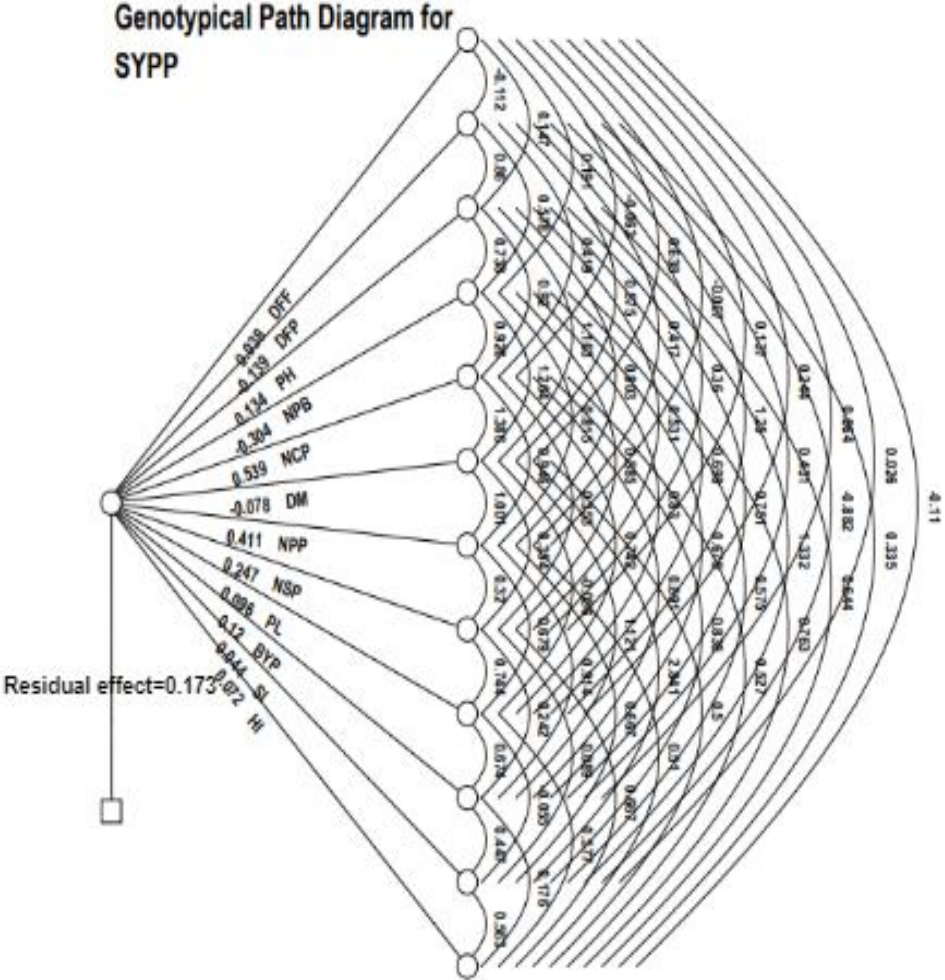
Table: 5- Direct and indirect effects for different quantitative characters on seed yield at the genotypic level.

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	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
Days to 50% pod setting	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
Plant height (cm)	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**
Number of primary branches per plant	-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**
Number of clusters per plant	-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**
Days to maturity	-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
Number of pods per plant	-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**
Number of seeds per plant	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**
pod length (cm)	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**
Biological yield (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**
Seed index (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**
Harvest index (%)	-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**

Table: 6- Direct and indirect effects for different quantitative characters on seed yield phenotypic level

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	-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	-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)	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	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	-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	-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	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	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)	-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)	-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)	-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 (%)	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**

Figure 2 : Genotypical path diagram for SYPP



Phenotypal Path Diagram for SYPP

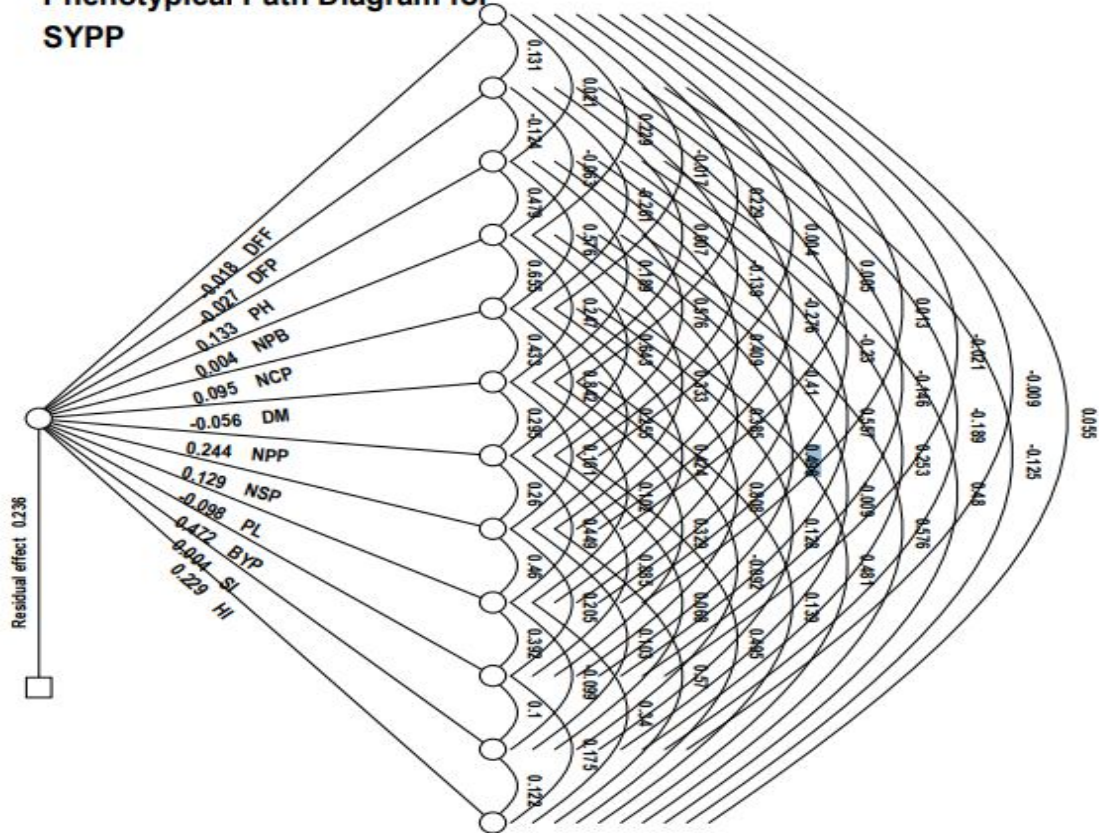


Figure 3 : phenotypal path diagram SYPP

REFERENCES

- Ali, M.N., Gupta, S., Bhattacharya, S., and Sarkar, H.K. (2008).** A character study in urdbean (*Vigna mungo* L. Hepper). *Environ. Eco.*, **26**: 952-954.
- Arya, P., Gaibriyal, M.L. and Lal, S.S. (2017).** Corelation and path analysis for yield and yield components in Blackgram (*Vigna mungo* L. Hepper). *International Journal of Advanced Biological Research*, **7**: 382-386.
- Atta, B.M., Haq, M.A. and Shah, T.M. (2008).** Variation and interrelationship of quantitative traits in Blackgram (*Cicer arietinum* L.). *Pakistan Journal of Botany*, **40**: 637-647.
- Babu, J.S., Reni, Y.P. and Ramana, M.V. (2016).** Character correlation and path coefficient in Blackgram (*Vigna mungo* L. Hepper). *International Research Journal of natural and Applied Sciences*, **3**: 178-185.
- Bandi, H.R.K., Rao, K.N., Krishna, K.V. and Srinivasulu, K. (2018).** Correlation and path-coefficient estimates of yield and yield component traits in rice fallow Blackgram (*Vigna mungo* L. Hepper). *International Journal of Current Microbiology and Applied Sciences*, **7**: 3304-3309.
- Bharti, B., Kumar, R., Bind, H.N., Kumar, A. and Sharma, V. (2014).** Correlation and path analysis for yield and yield components in Blackgram (*Vigna mungo* L. Hepper). *International journal of Plant Sciences*, **9**: 410-413.
- Chauhan, M.P., Mishra, A.C. and Singh, A.K. (2007).** Correlation and path analysis in urdbean. *Legume Research*, **30**: 205-208.
- Dewey, D.R. and Lu, K.H. (1959).** A correlation and path coefficient analysis of components of wheat grass seed production. *Agronomy Journal*, **51**: 515-518.
- Fisher, R.A. (1954).** Statistical methods for research workers. *Biological Monograph and Manuals*, **5**: 130-131.
- Gupta, S., Gupta, S.R., Dikshit, H.K. and Singh, R.A. (2001).** Variability and its characterization in Indian collections of Blackgram (*Vigna mungo* L. Hepper). *Plant Genetic Resources Newsletter*, **127**: 20-24.
- Hemalatha, K., Lal, S.S. and Lal, G.M. (2017).** Study on genetic variability and correlation in Blackgram (*Vigna mungo* L. Hepper). *Journal of pharmacognosy and phytochemistry*, **6**: 674-676

- Kuralarasan .V ,Vanniarajan .C, Kanchana.S ,Veni .K and S. Anandhi Lavanya (2018).**Genetic divergence, heritability and genetic advance in mutant lines of urd bean [Vigna mungo (L.) Hepper]. *Legume Research*, **41**(6) 2018: 833-836
- Mohanlal V. A. , Saravanan .K, Sabesan .T. (2018).** studies on genetic correlation and path coefficient analysis of Blackgram (*Vigna mungo* L. Hepper) genotypes under salinity. *journal of phytoogy*, 10: 09-11
- Sathya .P , Manivannan .N ,Mahalingam .A , Satya V.K. and Parameswari .C .(2018).** Association analysis for seed yield and component traits in segregating populations of Blackgram (*Vigna mungo* L. Hepper). *Electronic Journal of Plant Breeding*, **9** (2) : 741-746
- Suryawanshi N.A., Gabriyal M. Lal and Warkad S.D. (2018).** Correlation and Path Analysis for Yield and Yield Components in Blackgram [*Vigna mungo* L. Hepper] *Int.J. Curr.Microbiol.App.Sci. App.Sci* **7**(8): 612-621
- Sushmitharaj D.V., Shoba. D and Arumugam Pillai.M. (2018).** Genetic Variability and Correlation Studies in Black Gram (*Vigna mungo* L. Hepper) with Reference to YMV Resistance. *Int.J. Curr.Microbiol.App.Sci. App.Sci* Special Issue-6: 2849-2856
- Rolaniya D. Jinjwadiya M.K., Meghawal D.R. and Gabriyal M. Lal. (2017).** Studies on genetic variability in Black gram (*Vigna mungo* L. Hepper) germplasm. *Journal of Pharmacognosy and Phytochemistry*; **6**(4): 1506-1508
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955).** Estimation of genetic and environmental variability in soybean. *Agronomy Journal*, **47**: 314-318.
- Lush, J.L. (1949).** Heritability of quantitative characters in farm animals. Proceedings of 85th Congress on Genetics and Heriditas (Supplement), **35**: 356-375.
- Mehra, R., Tikle, A.N., saxena, A., Munjal, A., Rekhakhandia and Singh, M. (2016).** Correlation, path-coefficient and genetic diversity in Blackgram (*Vigna mungo* L. Hepper). *International Research Journal of Plant Science*, **7**: 001-011.
- Parveen, S.I., Sekhar, M.R., Reddy, D.M. and Sudhakar, P. (2011).** Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo* L. Hepper). *Int. J. Applied Biology and Pharmaceutical Technology*, **2**: 619-625.
- Patel, R.V., Patil, S.S., Patel, S.R. and Jadhav, B.D. (2014).** Genetic variability and character association in blackgram (*Vigna mungo* L. Hepper). *Trends in Biosciences*, **7**: 3795 3798.
- Patidar, M. and Sharma, H. (2017).** Correlation and path coefficient studies in Blackgram (*Vigna mungo* L. Hepper). *JPP*, **6**: 1626-1628.
- Burton, G.W. and Devane, E.M. (1953).** Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**: 478-481.

- Ozukum, C. and Sharma, M.B. (2017).** Variability among urdbean (*Vigna mungo* L. Hepper) for yield and yield components. *International Journal of Research and Innovation in Applied Science*, **2**: 26-28.
- Panse, V.G. and Sukhatme, P.V. (1985).** Statistical methods for agricultural workers, ICAR Publication, New Delhi. Parameswarappa, S.G. and Lamani, K.D. 2005. Genetic estimates, association and path coefficient analysis in Blackgram. *Karnataka Journal of Agricultural Sciences*, **18**: 21-23.
- Tank, H.K., Sharma, P.P., Nagar, K.K., Bairwa, L.L. and Meghawal, D.R. (2018).** Genetic variability and heritability studies in Blackgram (*Vigna mungo* L. Hepper). *International Journal of Chemical Studies*, **6**: 642-646.
- Thamodharan, G., Geetha, S. and Ramalingam, A. (2017).** Traits association and variability study in blackgram (*Vigna mungo* L. Hepper). *Agriculture Update*, **12**: 1019-1023.
- Umadevi, M. and Ganesan, N.M. (2005).** Correlation and path analysis for yield and yield components in Blackgram (*Vigna mungo* L. Hepper). *Madras Agric. J.*, **92**: 731-734.
- Vavilov, N.I. (1926).** Origin variation, immunity of cultivated plants. *Chronica Bot.*, **13**: 364.
- Wright, S. (1921).** Correlation and causation. *Journal of Agricultural Research*, **20**: 25-28.