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Correlation and path coefficient analysis for yield and quality traits in blackgram (*Vigna mungo* L.)

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ABSTRACT

The investigation was carriedout with 54 black gram genotypes using an Alpha Lattice design with three replications at the Regional Agricultural Research Station, Lam, Guntur, during rabi 2023-24. The observations were notedown days to 50% flowering, days to maturity, plant height, primary branches, clusters per plant, pods per plant, 100-seed weight, and seed yield. The ualified traits riceProtein, carbohydrate, methionine, tryptophan, and lysine contents were also estimated. The results revealed higher genotypic than phenotypic correlations, implying true associations among the charcters. Significant positive genotypic associations with seed yield were observed with days to 50% flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per plant, and test weight. Path analysis revealed strong direct effects on seed yield from pods per plant and days to maturity. The study concluded that traits like plant height, branches per plant, clusters per plant, pods per plant, and test weight, showing significant positive correlations with seed yield, are crucial for improving blackgram yield. Pods per plant, in particular, demonstrated a strong relationship with seed yield, making it a key trait for selection.

Key Words: *Blackgram,Correlation, Path analysis and Quality traits*

Blackgram, also known as "urd bean" or "mash," is an annual legume from the Fabaceae family, with a chromosome number of 2n=22. Orginated in the Indian subcontinent. It is a short-duration, self-pollinated crop. This crop grows best in well-drained loamy or sandy loam soils, especially black cotton soils. It thrives in regions with about 800 mm of annual rainfall but can tolerate as little as 650 mm. Blackgram is more tolerant of water logging than greengram (Singh *et al.* 2010).

The seeds of blackgram exhibit a substantial protein content, ranging from approximately 22% to 24%, alongside a predominant presence of carbohydrates constituting around 60%. Moreover, the seeds have 1.3% fat content and contain specific amino acids, notably lysine (0.43%), tryptophan (0.07%), and methionine (0.09%). Blackgram fixces nitrogen in soil which is a microbial conversion of atmospheric nitrogen gas into ammonia and plays a key role in improving the soil fertility and sustain the system productivity (Sekhon *et al.*2002).

High yield is the primary objective in breeding programs, but due to its low heritability, direct selection is often ineffective. Therefore, indirect selection through correlation analysis is preferred for yield improvement. The study estimated phenotypic and genotypic correlation coefficients between seed yield, yield components, and nutritional traits. By analyzing the correlation coefficient, one can assess the mutual relationships between different plant character pairs and identify the component characters that should be selected for yield improvement. Understanding character association is crucial for devising effective breeding strategies to develop high-yielding genotypes.

MATERIAL AND METHODS

The present investigation was conducted at Regional Agricultural Research Station (RARS) Lam, Guntur, during rabi 2023-24, with 54 genotypes of blackgram using Alpha Lattice design with three replications. Each plot consisted of two rows, of 4.0 meters length with roacing of 30 × 10 cm. Observations for days to 50% flowering and days to maturity were recorded on a plot basis. For single plant observations, five random plants from each replication were tagged to measure yield and other quantitative and qualitative traits. The mean values of these five plants were used for analysis. The traits plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, 100-seed weight, and seed yield per plant were noted. Protein content, carbohydrate content, methionine content, tryptophan content and lysine content were estimated. Phenotypic and genotypic correlations were worked out by using the formulae suggested by Falconer (1964). Path coefficient analysis was utilized to partition the phenotypic and genotypic correlation coefficients into direct and indirect effects of the yield and quality traits on seed yield. The analysis was carried out as per the procedures suggested by Wright (1921) and Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of genotypic and phenotypic correlation coefficients for 14 characters (Table 1) demonstrated that genotypic correlations were higher than their phenotypic counterparts. This suggests the true associations among the characters and no involuant of environment.

Days to 50% flowering showed a significant positive genotypic association and a non-significant positive phenotypic association with seed yield along with strong positive associations with days to maturity, plant height, and test weight at both levels. It also had non-significant positive associations with clusters per plant and carbohydrate content. Days to maturity had a significant positive genotypic association and a non-significant positive phenotypic association with seed yield, along with significant positive associations with plant height. It also showed non-significant positive associations with tryptophan and lysine contents. Plant height showed a significant positive association with seed yield per plant at both genotypic and phenotypic levels. Significant positive associations were observed with pods per plant, test weight, tryptophan content, and lysine content at both levels.

Branches per plant had a significant positive association with seed yield at both levels and showed a significant negative association with protein content and methionine content, along with significant positive associations with clusters and pods per plant. Clusters per plant had a significant positive association with seed yield, pods per plant, and methionine content. Pods per plant had a significant positive association with seed yield, and test weight. Non-significant positive associations with carbohydrate content and non-significant negative associations with protein content, methionine content, and lysine content. Test weight showed significant positive associations with seed yield and lysine content, while having non-significant negative associations with protein, carbohydrate, and methionine contents.

Protein content had non-significant negative associations with seed yield and significant positive associations with methionine, tryptophan, and lysine content. Carbohydrate content had non-significant positive association with seed yield and significant positive associations with tryptophan and lysine content, while showing non-significant negative associations with methionine content. Methionine content had non-significant negative associations with seed yield and significant positive associations with tryptophan and lysine contents. Tryptophan content had a significant negative association with seed yield at the genotypic level and a non-significant negative association at the phenotypic level, but showed significant positive association with lysine content. Lysine content had non-significant negative association with seed yield at both the levels.

From correlation studies of the present investigation, independent characters *viz.,* plant height (0.455** and 0.368**), branches per plant (0.251* and 0.222*), clusters per plant (0.263** and 0.221*), pods per plant (0.832** and 0.936**) and test weight (0.385* and 0.226*) showed highly significant association at both genotypic and phenotypic levels, respectively. So, it can be inferred that the above traits which are positive and significantly correlated with yield are important during selection for improvement of the dependent variable *i.e.,* seed yield per plant in the studied genotypes. Similar results were reported by Yadav *et al.* (2023) for all the characters and Kumar *et al.* (2014) and Partap *et al.* (2019) for plant height, branches per plant and test weight.

Path analysis

Correlation analysis simply shows the nature and degree of association between two characters while path analysis provides insight into the direct and indirect associations of characters and the relative contributions of various traits to seed yield. Consequently, the correlation coefficients were

Table 1. Phenotypic and genotypic correlations among seed yield and component characters in blackgram

		DFF	DM	PH	NPB	NCP	NPP	TW	PROTEIN	CHO	MET	TRP	LC	SYPP
DF	G	1	0.732**	0.586**	-0.212*	0.053	0.194*	0.309**	0.485**	0.127	-0.162*	0.289**	0.261**	0.225*
	P	1	0.468**	0.253*	-0.07	0.022	0.104	0.156*	0.114	0.061	-0.076	0.102	0.095	0.078
DM	G		1	0.488**	-0.276**	-0.174*	0.299**	0.207*	0.387**	0.200*	-0.254*	0.068	0.038	0.296**
	P		1	0.226*	-0.113	-0.112	0.093	0.05	0.051	0.084	-0.101	0.022	0.036	0.097
PH	G			1	-0.117	0.118	0.445**	0.414**	-0.06	0.166*	-0.214*	0.256*	0.221*	0.455**
	P			1	-0.118	0.089	0.384**	0.300**	-0.078	0.145	-0.204*	0.231*	0.205*	0.368**
NPB	G				1	0.295**	0.244*	-0.013	-0.157*	-0.002	-0.067	-0.189*	-0.203*	0.251*
	P				1	0.270**	0.235*	-0.005	-0.103	0.001	-0.064	-0.183*	-0.191*	0.222*
NCP	G					1	0.261**	0.145	0.117	-0.048	0.296**	0.08	0.055	0.263**
	P					1	0.223*	0.077	0.068	-0.033	0.275**	0.076	0.049	0.221*
NPP	G						1	0.380**	-0.072	0.066	-0.048	-0.162*	-0.11	0.832**
	P						1	0.231*	-0.075	0.063	-0.043	-0.151	-0.108	0.936**
TW	G							1	-0.066	-0.008	-0.058	0.133	0.160*	0.385**
	P							1	-0.034	-0.015	-0.04	0.083	0.121	0.226*
PROTEIN	G								1	0.017	0.423**	0.390**	0.311**	-0.082
	P								1	0.009	0.335**	0.320**	0.250*	-0.059
CHO	G									1	-0.049	0.207*	0.169*	0.068
	P									1	-0.051	0.203*	0.166*	0.061
MET	G										1	0.258**	0.160*	-0.049
	P										1	0.254*	0.155*	-0.043
TRP	G											1	0.918**	-0.161*
	P											1	0.907**	-0.154
LYSINE	G												1	-0.111
	P												1	-0.106
DF	G													1
	P													1

Days to maturity, PH-Plant height (cm), NPB- No. of Primary branches per plant, NCP- Clusters per plant, NPP- Pods per plant, TW-Test weight (g), PROTEIN -Protein content (mg/g), CHO-Carbohydrate content (mg/g), MET-Methionine content (µg/g), TRP- Tryptophan content (µg/g), LC-Lysine content (µg/g) and SYPP-Seed yield per plant (g).

Table 2. Phenotypic and genotypic direct and indirect effects of different traits on seed yield in blackgram

		DFF	DM	PH	NPB	NCP	NPP	TW	PROTEIN	CHO	MET	TRP	LC	SYPP
DF	**G**	**-0.014**	-0.025	-0.008	0.003	-0.001	-0.003	-0.004	-0.007	-0.002	0.003	-0.004	-0.004	**0.225***
	P	**-0.037**	-0.018	-0.01	0.003	-0.001	-0.004	-0.006	-0.005	-0.003	0.003	-0.004	-0.004	**0.078**
DM	**G**	0.058	**0.03**	0.015	-0.009	-0.006	0.009	0.007	0.012	0.006	-0.008	0.002	0.002	**0.296****
	P	0.011	**0.024**	0.006	-0.003	-0.003	0.003	0.002	0.002	0.002	-0.003	0.001	0.001	**0.097**
PH	**G**	-0.013	-0.011	**-0.022**	0.003	-0.003	-0.01	-0.009	0.002	-0.004	0.005	-0.006	-0.005	**0.455****
	P	0.006	0.006	**0.023**	-0.003	0.002	0.009	0.007	-0.002	0.004	-0.005	0.006	0.005	**0.368****
NPB	**G**	0.001	0.001	0.001	**-0.002**	-0.001	-0.001	0.001	0.001	0.001	0.001	0.001	0.001	**0.251***
	P	-0.001	-0.001	-0.001	**0.004**	0.001	0.001	0.001	-0.001	0.001	-0.001	-0.001	-0.001	**0.222***
NCP	**G**	-0.001	0.001	-0.001	-0.001	**-0.002**	-0.001	-0.001	-0.001	0.001	-0.001	-0.001	-0.001	**0.263****
	P	0.001	-0.002	0.002	0.005	**0.017**	0.004	0.002	0.002	-0.001	0.005	0.002	0.001	**0.221***
NPP	**G**	0.203	0.314	0.466	0.256	0.274	**0.849**	0.399	-0.075	0.069	-0.05	-0.17	-0.115	**0.832****
	P	0.096	0.085	0.352	0.216	0.205	**0.917**	0.212	-0.069	0.058	-0.039	-0.138	-0.099	**0.936****
TW	**G**	-0.004	-0.003	-0.005	0.001	-0.002	-0.005	**-0.012**	0.001	0.001	0.001	-0.002	-0.002	**0.385****
	P	0.002	0.001	0.004	-0.001	0.001	0.003	**0.012**	-0.001	-0.001	-0.001	0.001	0.002	**0.226***
PROTEIN	**G**	-0.014	-0.011	0.002	0.005	-0.004	0.002	0.002	**-0.029**	-0.001	-0.012	-0.011	-0.009	**-0.082**
	P	0.003	0.002	-0.002	-0.003	0.002	-0.002	-0.001	**0.026**	0.001	0.009	0.009	0.007	**-0.059**
CHO	**G**	-0.001	-0.002	-0.002	0.001	0.001	-0.001	0.001	-0.001	**-0.009**	0.001	-0.002	-0.002	**0.068**
	P	0.001	0.001	0.002	0.001	-0.001	0.001	-0.001	0.001	**0.008**	-0.001	0.002	0.002	**0.061**
MET	**G**	-0.001	-0.001	-0.001	-0.001	0.002	-0.001	-0.001	0.002	-0.001	**0.004**	0.001	0.001	**-0.049**
	P	0.001	0.001	0.001	0.001	-0.001	0.001	0.001	-0.001	0.001	**-0.001**	-0.001	-0.001	**-0.043**
TRP	**G**	0.017	0.004	0.015	-0.011	0.005	-0.01	0.008	0.023	0.012	0.015	**0.057**	0.053	**-0.161***
	P	-0.007	-0.002	-0.016	0.013	-0.006	0.011	-0.006	-0.022	-0.014	-0.018	**-0.069**	-0.063	**-0.154**
LYSINE	**G**	-0.008	-0.002	-0.007	0.006	-0.002	0.004	-0.005	-0.01	-0.005	-0.005	-0.028	**-0.03**	**-0.111**
	P	0.005	0.002	0.009	-0.009	0.003	-0.005	0.006	0.011	0.008	0.007	0.04	**0.044**	**-0.106**

* Significant at 5% level, ** Significant at 1% level, ** Significant at 0.1% level., Residual Effect at genotypic level = 0. 290 and at phenotypic level = 0.350

CHARACTERS: DF-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm), NPB- No. of Primary branches per plant, NCP- Clusters per plant, NPP- Pods per plant, TW-Test weight (g), PROTEIN -Protein content (mg/g), CHO- Carbohydrate content (mg/g), MET-Methionine content (µg/g), TRP- Tryptophan content (µg/g), LC-Lysine content (µg/g) and SYPP-Seed yield per plant (g).

divided into direct and indirect effects at both genotypic and phenotypic levels. In this study, seed yield per plant was treated as the dependent variable, the other traits were considered as independent variables. The path coefficient values of 13 traits among 54 blackgram genotypes are presented in Table 2.

Direct effects

Path analysis revealed stronger positive direct effects of pods per plant (0.849 and 0.917) and days to maturity (0.030 and 0.024) at both genotypic and phenotypic levels on seed yield per plant. Similar direct effects were reported by Karthik *et al.* (2022) and Dhillon *et al.* (2024).

Days to 50% flowering (-0.014 and -0.037) showed negative direct effects. These results were in conformity with Rajasekhar *et al.* (2017), Sagar *et al.* (2021), Mallikarjuna *et al.* (2021), Karthik *et al.* (2022) and Dhillon *et al.* (2024). Plant height, branches per plant, clusters per plant, test weight, protein content, carbohydrate content and lysine content showed negative direct effect at genotypic level and positive direct effect at phenotypic level. Methionine content and tryptophan content showed positive direct effect at genotypic level and negative direct effect at phenotypic level.

Indirect effects

Days to maturity, pods per plant recorded indirects effects via days to 50% flowering pods per plant *via* days to maturity, days to maturity and pods per plant *via* plant height, days to 50% flowering, pods per plant, carbohydrate content *via* no. of primary branches per plant, no. of pods per plant via clusters per plant, days to maturity *via* pods per plant, days to maturity, no. of branches per plant, pods per plant *via* test weight, days to maturity *via* protein content, days to maturity, no. of branches per plant, pods per plant via carbohydrate content, day to 50% flowering *via* methionine content, days to maturity via tryptophan content, days to maturity *via* lysine content on seed yield per plant.

Residual effect

The residual effect at genotypic level was 0.29 and at phenotypic level was 0.35 indicating that the characters included in the present investigation are contributing around 71% and 65% respectively at genotypic and phenotypic levels of variability pertaining to dependent variable *i.e.,* yield. Only 29% and 35% of contribution at genotypic and phenotypic levels is from the characters which are not included in the present study.

In the present investigation, path analysis revealed that pods per plant had true relationship with seed yield per plant by establishing significant positive association and positive direct effect. Hence, this trait can be considered during selection for obtaining high yielding genotypes.

LITERATURE CITED

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.

Dhillon K S, Mittal R K, Sood V K, Chaudhary H K, Kaur K, Verma S and Kumar N 2024. Correlation and path analysis for yield and yield contributing traits in advance generation of blackgram (*Vigna mungo* (L.) Hepper). *Plant Cell Biotechnology and Molecular Biology*. 25(1-2): 45-52.

Falconer D S 1964. *An Introduction to Quantitative Genetics*. Oliver and Boyd, Edinburgh. 312-324.

Karthik U, Lal G M, Bara B M, Yajavathi C and Gangadhar L 2022. Direct and indirect effects of yield contributing characters on seed yield in blackgram (*Vigna mungo* (L.) Hepper). *International Journal of Environment and Climate Change*. 12(11) :2016-2027.

Kumar G V, Vanaja M, Sathish P, Vagheera P, Shishodia S S and Razak A 2014. Correlation and path analysis of seed yield and yield contributing components of black gram (*Vigna mungo* L. Hepper) under rainfed condition from Andhra Pradesh, India. *International Journal of Applied Biology and Pharmaceutical Technology*. 5(3): 137-140.

Mallikarjuna G, Rao K N, Srinivas T and Ramesh D 2021. Correlation and path coefficient studies in blackgram. *The Andhra Agricultural Journal*. 68(3): 324-331.

Partap B, Kumar M, Kumar V and Kumar A 2019. Genetic variability and correlation studies of seed yield and its components in

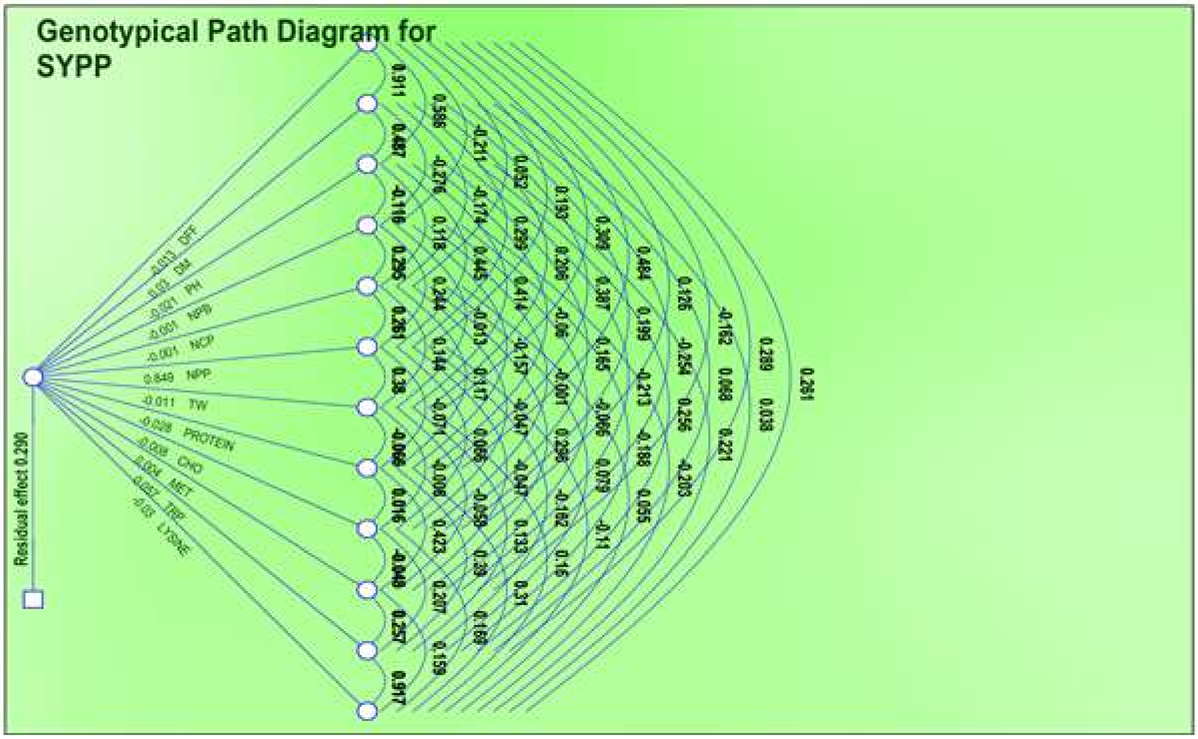

Fig 1. Genotypic Path diagram showing direct and indirect effects of yield components on seed yield per plant in blackgram

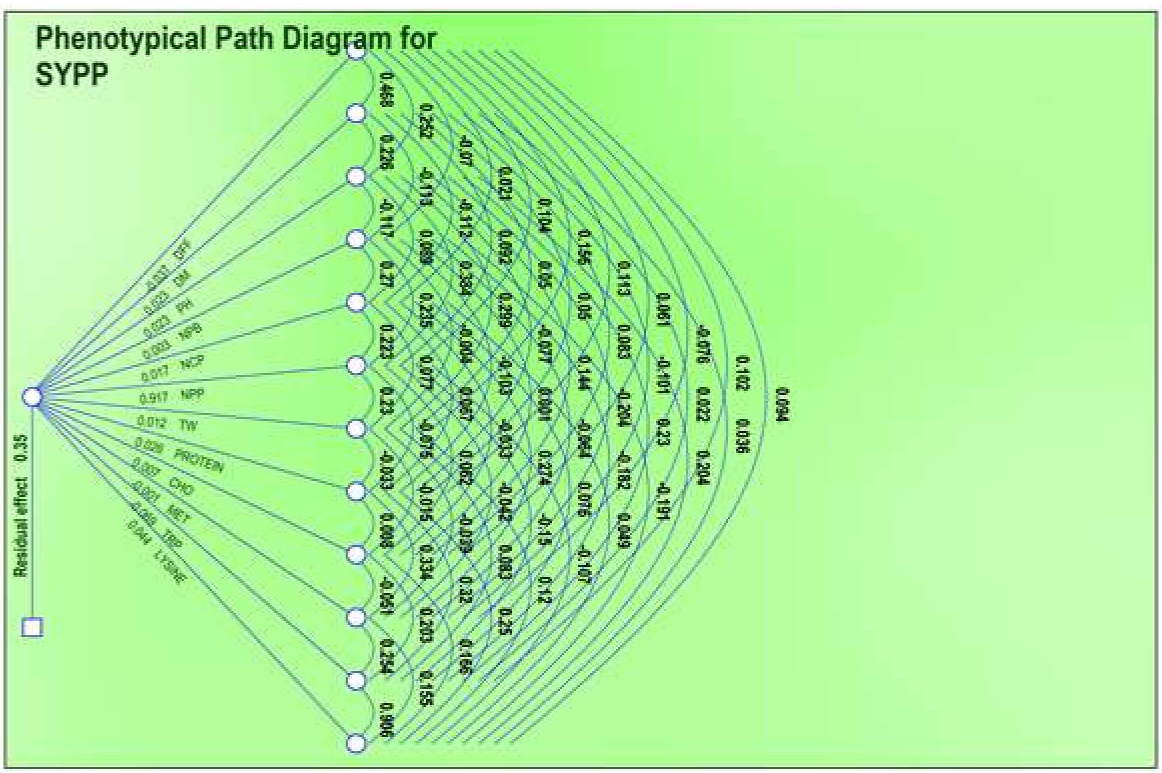

Fig 2. Phenotypic Path diagram showing direct and indirect effects of yield components on seed yield per plant in blackgram

blackgram (*Vigna mungo* (L.) Hepper). *Journal of Pharmacognosy and Phytochemistry*. 8(3): 2035-2040.

Rajasekhar D, Lal S S and Lal G M 2017. Character association and path analysis for seed yield & its components in blackgram [*Vigna mungo* (L.) Hepper]. *Plant Archives.* 17(1): 467-471.

Sagar K P, Suresh B G and Lal G M 2021. Correlation and path analysis for yield and yield contributing traits in black gram [*Vigna mungo* (L) Hepper.]. *Journal of Pharmacognosy and Phytochemistry*. 10(5): 299-302.

Sekhon H S, Singh G and Sharma P 2002. Biological nitrogen fixation. *Recent Advances in Agronomy.* 141-166.

Singh C, Singh P and Singh R 2010. *Modern techniques of raising field crops*. Oxford and IBH Publication Co., New Delhi. 2: 256-258.

Wright S 1921. Correlation and causation. *Journal of Agricultural Research.* 20: 557-585.

Yadav M, Meena A K, Rajput S S, Punia S S and Yadav A P 2023. Correlation and path analysis in M_4 generation of blackgram [*Vigna mungo* (L.) Hepper]. *The Pharma Innovation Journal*. 12(2): 1698-1701.

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