



# International Journal of Research in Agronomy

E-ISSN: 2618-0618

P-ISSN: 2618-060X

© Agronomy

[www.agronomyjournals.com](http://www.agronomyjournals.com)

2024; 7(3): 246-251

Received: 19-01-2024

Accepted: 26-02-2024

## Ritika

Section of Genetics and Plant  
Breeding, BTC College of  
Agriculture and Research Station,  
Bilaspur, Indira Gandhi Krishi  
Vishwavidyalaya, Raipur,  
Chhattisgarh, India

## Roshan Parihar

Section of Genetics and Plant  
Breeding, BTC College of  
Agriculture and Research Station,  
Bilaspur, Indira Gandhi Krishi  
Vishwavidyalaya, Raipur,  
Chhattisgarh, India

## DJ Sharma

Section of Genetics and Plant  
Breeding, BTC College of  
Agriculture and Research Station,  
Bilaspur, Indira Gandhi Krishi  
Vishwavidyalaya, Raipur,  
Chhattisgarh, India

## AP Agrawal

Section of Genetics and Plant  
Breeding, BTC College of  
Agriculture and Research Station,  
Bilaspur, Indira Gandhi Krishi  
Vishwavidyalaya, Raipur,  
Chhattisgarh, India

## Corresponding Author:

### Ritika

Section of Genetics and Plant  
Breeding, BTC College of  
Agriculture and Research Station,  
Bilaspur, Indira Gandhi Krishi  
Vishwavidyalaya, Raipur,  
Chhattisgarh, India

## Correlation and path analysis of yield and related traits in urdbean [*Vigna mungo* (L.) Hepper] genotypes

Ritika, Roshan Parihar, DJ Sharma and AP Agrawal

DOI: <https://doi.org/10.33545/2618060X.2024.v7.i3d.444>

### Abstract

The present study entitled “Correlation and path analysis of yield and related traits in urdbean [*Vigna mungo* (L.) Hepper] genotypes”. Correlation and path analysis were done to study the relationship between yield and its contributing traits in 24 urdbean [*Vigna mungo* (L.) Hepper] genotypes. Significant positive correlations were observed between seed yield and traits like biological yield, harvest index, number of pods per plant. Days to 50% flowering showed significant negative correlation with biological yield. Path analysis revealed that biological yield, harvest index and number of pods per plant had high direct positive effects on seed yield. Days to 50% flowering exhibited high negative direct effect on seed yield. The study concluded that biological yield, harvest index, number of pods per plant and days to 50% flowering were the most important traits influencing seed yield. Significant positive correlations were observed between seed yield and biological yield ( $r = 0.523^{**}$ ), harvest index ( $r = 0.355^*$ ), number of pods per plant ( $r = 0.270^*$ ). Days to 50% flowering showed significant negative correlation with biological yield ( $r = -0.263^*$ ). Path analysis revealed that biological yield ( $0.523^{**}$ ), harvest index ( $0.355^*$ ) and number of pods per plant ( $0.158$ ) had high direct positive effects on seed yield, while days to 50% flowering exhibited a high negative direct effect ( $-0.005$ ). The study concluded that biological yield, harvest index, number of pods per plant and days to 50% flowering were the most important traits influencing seed yield in urdbean. The findings can help in guiding breeding programs aimed at improving yield in urdbean genotypes.

**Keywords:** Tribes, *Vigna mungo*, genotypes, correlation, yield and path analysis

### 1. Introduction

Urdbean [*Vigna mungo* (L.) Hepper]  $2n=2x=22$ ] commonly known as blackgram is a self-pollinating, short duration grain legume belonging to Fabaceae family. It is reported to be originated in India with its secondary centre of origin in Central Asia with *Vigna mungo* var *silvestris* as its wild progenitor. It is consumed in the form of ‘dal’ (whole or split, husked and un-husked) or perched. It is used as nutritive fodder specially for milch animals. It fits well in various multiple cropping and intercropping systems.

Correlation coefficient analysis was used to measure inter relationship among different traits and determine the characters on which selection can be based for genetic progress in the yield, which is not a unitary character however depends on the improvement of diverse plant characters. Involvement of all characters towards increase in yield varies from crop to crop. Therefore, correlation helps in pronouncement out the relationship among different characters and measures the strength of relationship between two variables.

The path analysis helps to partition the correlation coefficient into yield and yield related components with seed yield into direct and indirect effects to indicate the contribution of an individual trait and its influence through other traits as well (Dewey and Lu, 1959) [3]. In situations where multiple characters are implicated in correlation, discerning the traits that significantly contribute to yield becomes challenging. Path analysis proves invaluable in such scenarios by elucidating the direct contributions of all these characters and their indirect impacts mediated through other traits.

### 2. Material and Methods

The experiment was conducted at Instructional Farm of Barrister Thakur Chhedilal College of

Agriculture and Research Station, Bilaspur (Chhattisgarh), during *Zaid* season 2023. The present investigation was undertaken with 24 genotypes including 2 checks (RU-96-3 and Indira-Urd-1). The experiment laid out in Randomized Block Design (RBD) with three replications. The important quantitative traits recorded for study among the genotypes for all characters *viz.*, plant height (cm), branches per plant, pod cluster per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, days to 50% flowering, biological yield (q/ha), seed yield (q/ha) and harvest index (%) indicated the presence of wide range of variability among genotypes for yield and its contributing characters and selection can be effective for another trait in respect of genotypes studied. Observations were conducted on five competing plants from each genotype within randomly labeled. Subsequently, average values were computed, and statistical analysis was conducted.

It is a method for knowing the correlation between two quantitative traits. Association attempts to determine the degree of relation between traits. It is represented by different characters with the help of the formula suggested by Miller *et al.* (1958) [8]. Genotypic correlation coefficient between trait x and y  $r_{xy}(g) = \text{Cov } xy(g) / \sqrt{\text{Var } x(g) \times \text{Var } y(g)}$ , Phenotypic correlation coefficient between trait x and y  $r_{xy}(p) = \text{Cov } xy(p) / \sqrt{\text{Var } x(p) \times \text{Var } y(p)}$ .

The equation shows a basic relationship between correlation coefficient and path coefficient. These equations have been saved by presenting them in matrix notations.  $A = B.C$ . The solution for the vector "C" may be obtained by multiplying both sides by inverse of B matrix *i.e.*,  $B^{-1}$  thus  $B^{-1} A = C$ . After calculations of the values of path coefficient *i.e.* "C" vector, it is possible to obtain the path value for residual (R).

$$R = \sqrt{1 - diXrij}$$

### 3. Result and Discussion

#### 3.1 Correlation coefficient analysis

The correlation analysis, which took into account both genotypic and phenotypic levels, revealed a complex network of relationships between different plant characteristics. The days to 50% flowering showed highly significant and negative correlation with biological yield (-0.263\*) at genotypic levels and significant negative correlation with biological yield (-0.295\*) at phenotypic level similar to Arya *et al.* (2017) [11]. Plant height showed highly significant and positive correlation with branches per plant (0.273\*), pod clusters per plant (0.376\*) and number of seeds per pod (0.281\*) at genotypic levels and significant positive correlation with branches per plant (0.276\*), pod clusters per plant (0.373\*) and number of seeds per pod (0.303\*) at phenotypic level similar to Kavitha *et al.* (2018) [6]. Branches per plant showed highly significant and positive correlation with pod clusters per plant (0.547\*\*), number of pods per plant (0.270\*) and plant height (0.273\*) at genotypic levels and significant positive correlation with pod clusters per plant (0.550\*\*), number of pods per plant (0.272) and plant height (0.276\*) at phenotypic level similar to Panigrahi *et al.*

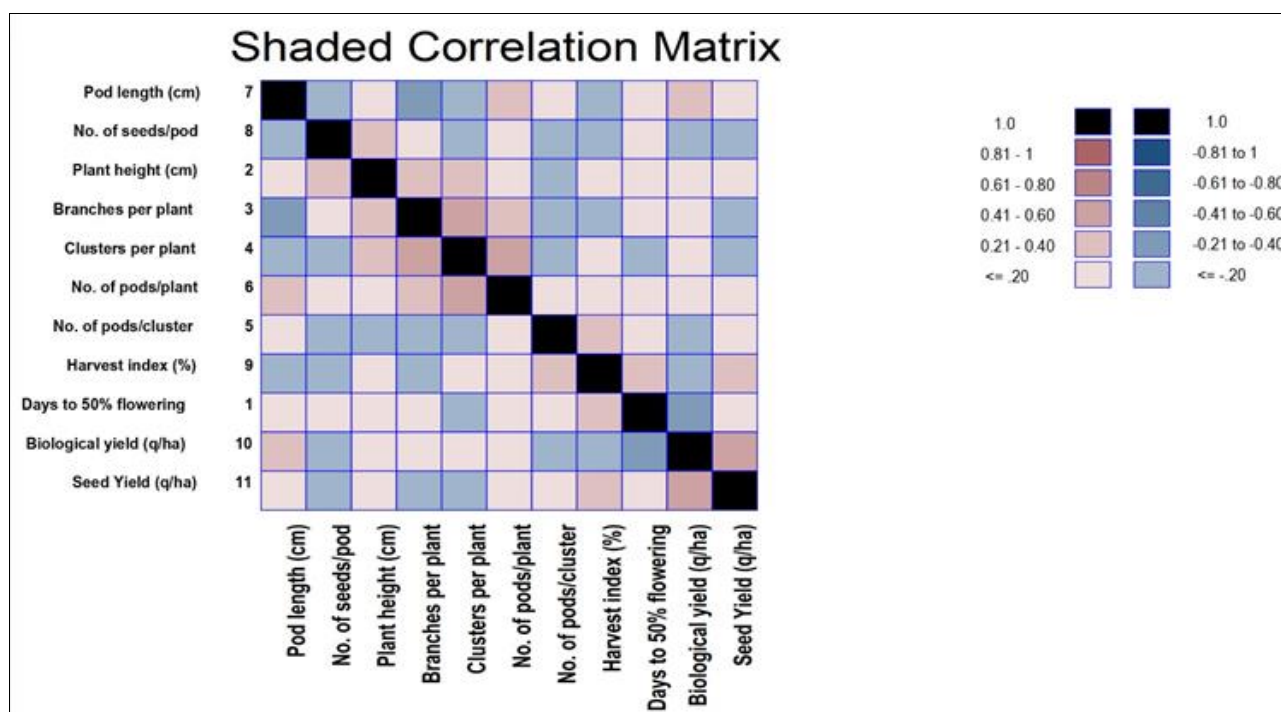
(2014) [9]. Pod clusters per plant showed highly significant and positive correlation with number of pods per plant (0.471\*\*) at genotypic levels and significant positive correlation with number of pods per plant (0.485\*\*) at phenotypic level similar to Sowmini and Jayamani (2013) [10]. Number of pods per cluster showed highly significant and positive correlation with harvest index (0.271\*) at genotypic level and significant and positive correlation with harvest index (0.277\*) at phenotypic level similar to Bharathi *et al.* (2022) [2]. Number of pods per plant showed significant and positive correlation with pod length (0.247\*) at genotypic level and significant and positive correlation with pod length (0.271\*) at phenotypic level similar to Gaibriyal *et al.* (2017) [5]. Biological yield showed highly significant and positive correlation with seed yield (0.523\*\*) at genotypic levels and significant positive correlation with seed yield (0.528\*\*) at phenotypic level similar to Kumar *et al.* (2022) [7]. Seed yield showed highly significant and positive correlation with harvest index (0.355\*) at genotypic levels and significant positive correlation with harvest index (0.358\*) at phenotypic level similar to Bharathi *et al.* (2022) [2]. Harvest index showed highly significant and positive correlation with number of pods per cluster (0.271\*) and seed yield (0.355\*) at genotypic levels and significant positive correlation with number of pods per cluster (0.277\*) and seed yield (0.358\*) at phenotypic level similar to Kumar *et al.* (2022) [7].

#### 3.2 Path coefficient analysis

Path coefficient analysis measures the direct and indirect effects of different independent characters on dependent characters in urdbean genotypes. Dewey and Lu's (1959) [3] used path coefficient analysis to estimate the magnitude and direction of direct and indirect effects of various yield-contributing characters. The genotypic and phenotypic correlation coefficients of various yield-attributing characters for grain yield were further partitioned into direct and indirect effects and is shown in Table 3 & 4 and Fig 3 & 4. The path coefficient analysis of the present characters revealed that at the genotypic level, the highest positive direct effects on seed yield (q/ha) were exhibited by biological yield (q/ha) (0.675), followed by harvest index (%) (0.385), number of pods per plant (0.229), days to 50% flowering (0.087), number of seeds per pod (0.068), number of pods per cluster (0.045) and plant height (cm) (0.043). At the phenotypic level, the highest positive direct effects were exhibited by biological yield (q/ha) (0.683), followed by harvest index (%) (0.373), number of pods per plant (0.199), days to 50% flowering (0.118), number of pods per cluster (0.057), plant height (cm) (0.057), and number of seeds per pod (0.052). The highest direct but negative effects at the genotypic level were exhibited by branches per plant (-0.210), pod clusters per plant (-0.196), and pod length (cm) (-0.119). At the phenotypic level, the highest negative direct effects were exhibited by branches per plant (-0.223), pod clusters per plant (-0.175), and pod length (cm) (-0.111). The results showed varying indirect effects on seed yield of the different genotypes studied. Similar results were observed by Kumar *et al.* (2022) [7], Devi *et al.* (2021) [4], Sowmini and Jayamani, (2016) [10] and Kavitha *et al.* (2018) [6].

**Table 1:** Phenotypic correlation matrix of urbean genotypes

Phenotypic Correlation Matrix											
	Days to 50% flowering	Plant height (cm)	Branches per plant	Pod clusters per plant	No. of pods/cluster	No. of pods/plant	Pod length (cm)	No. of seeds/pod	Harvest index (%)	Biological yield (q/ha)	Seed yield (q/ha)
Days to 50% flowering	1.000	0.124	0.146	-0.082	0.139	0.163	0.026	0.104	0.215	-0.295*	0.029
Plant height (cm)		1.000	0.276*	0.373*	-0.161	0.118	0.069	0.303*	0.177	0.036	0.058
Branches per plant			1.000	0.550**	-0.050	0.272*	-0.219	0.067	-0.042	0.044	-0.193
Pod clusters per plant				1.000	-0.062	0.485**	-0.038	-0.040	0.129	0.156	-0.036
No. of pods/cluster					1.000	0.195	0.164	-0.014	0.277*	-0.186	0.082
No. of pods/plant						1.000	0.271*	0.026	0.146	0.050	0.150
Pod length (cm)							1.000	-0.031	-0.119	0.228	0.125
No. of seeds/pod								1.000	-0.023	-0.142	-0.024
Harvest index (%)									1.000	-0.139	0.358*
Biological yield (q/ha)										1.000	0.528**
Seed Yield (q/ha)											1.000



**Fig 1:** Phenotypic shaded correlation matrix

**Table 2:** Genotypic correlation matrix of urbean genotypes

Genotypic Correlation Matrix											
	Days to 50% flowering	Plant height (cm)	Branches per plant	Pod clusters per plant	No. of pods/cluster	No. of pods/plant	Pod length (cm)	No. of seeds/pod	Harvest index (%)	Biological yield (q/ha)	Seed yield (q/ha)
Days to 50% flowering	1.000	0.147	0.142	-0.070	0.140	0.127	0.046	0.074	0.197	-0.263*	0.011
Plant height (cm)		1.000	0.273*	0.376*	-0.158	0.098	0.085	0.281*	0.168	0.044	0.044
Branches per plant			1.000	0.547**	-0.049	0.270*	-0.216	0.063	-0.042	0.045	-0.190
Pod clusters per plant				1.000	-0.067	0.471**	-0.014	-0.027	0.128	0.146	-0.048
No. of pods/cluster					1.000	0.189	0.142	-0.035	0.271*	-0.168	0.089
No. of pods/plant						1.000	0.247*	0.044	0.153	0.033	0.158
Pod length (cm)							1.000	0.002	-0.115	0.199	0.089
No. of seeds/pod								1.000	-0.009	-0.177	-0.036
Harvest index (%)									1.000	-0.147	0.355*
Biological yield (q/ha)										1.000	0.523**
Seed Yield (q/ha)											1.000

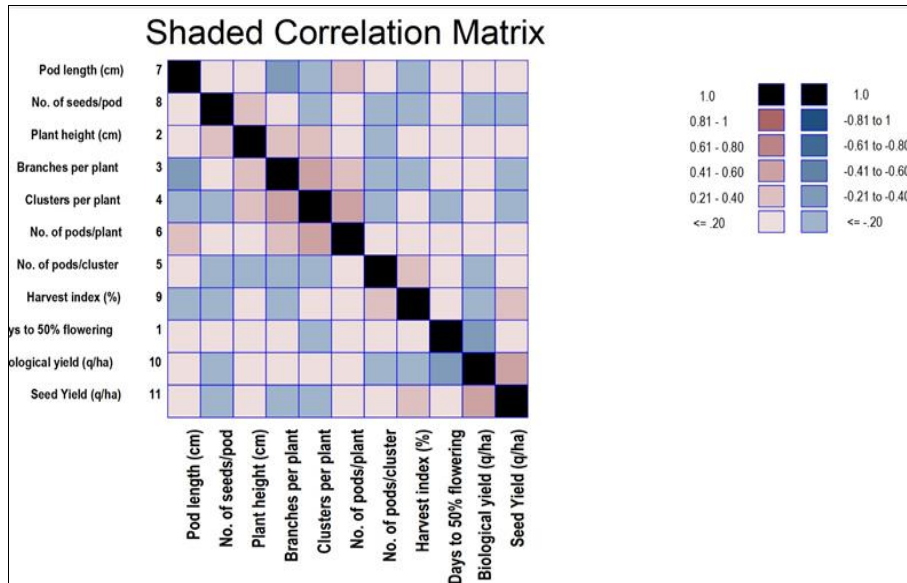


Fig 2: Genotypic shaded correlation matrix

Table 3: Genotypic path coefficients between different traits in elite urdbean genotypes

Genotypic PATH matrix of Seed Yield (q/ha)											
	Days to 50% flowering	Plant height (cm)	Branches per plant	Pod clusters per plant	No. of pods/cluster	No. of pods/plant	Pod length (cm)	No. of seeds/pod	Harvest index (%)	Biological yield (q/ha)	Corr. with seed yield (q/ha)
Days to 50% flowering	0.087	0.013	0.012	-0.006	0.012	0.011	0.004	0.006	0.017	-0.023	0.011
Plant height (cm)	0.006	0.043	0.012	0.016	-0.007	0.004	0.003	0.012	0.007	0.002	0.044
Branches per plant	-0.030	-0.057	-0.210	-0.115	0.010	-0.056	0.045	-0.013	0.008	-0.009	-0.190
Pod clusters per plant	0.013	-0.073	-0.107	-0.196	0.013	-0.092	0.002	0.005	-0.025	-0.028	-0.048
No. of pods/cluster	0.006	-0.007	-0.002	-0.003	0.045	0.008	0.006	-0.001	0.012	-0.007	0.089
No. of pods/plant	0.029	0.022	0.061	0.108	0.043	0.229	0.056	0.010	0.035	0.007	0.158
Pod length (cm)	-0.005	-0.010	0.025	0.001	-0.017	-0.029	-0.119	-0.0003	0.013	-0.023	0.089
No. of seeds/pod	0.005	0.019	0.004	-0.001	-0.002	0.003	0.0002	0.068	-0.0006	-0.012	-0.036
Harvest index (%)	0.076	0.064	-0.016	0.049	0.104	0.059	-0.044	-0.003	0.385	-0.057	0.355*
Biological yield (q/ha)	-0.177	0.030	0.030	0.099	-0.113	0.022	0.134	-0.119	-0.099	0.675	0.523**
Seed Yield (q/ha)	0.011	0.044	-0.190	-0.048	0.089	0.158	0.089	-0.036	0.355*	0.523**	1.000

Diagonal values = Direct effect, off diagonal values = Indirect effect

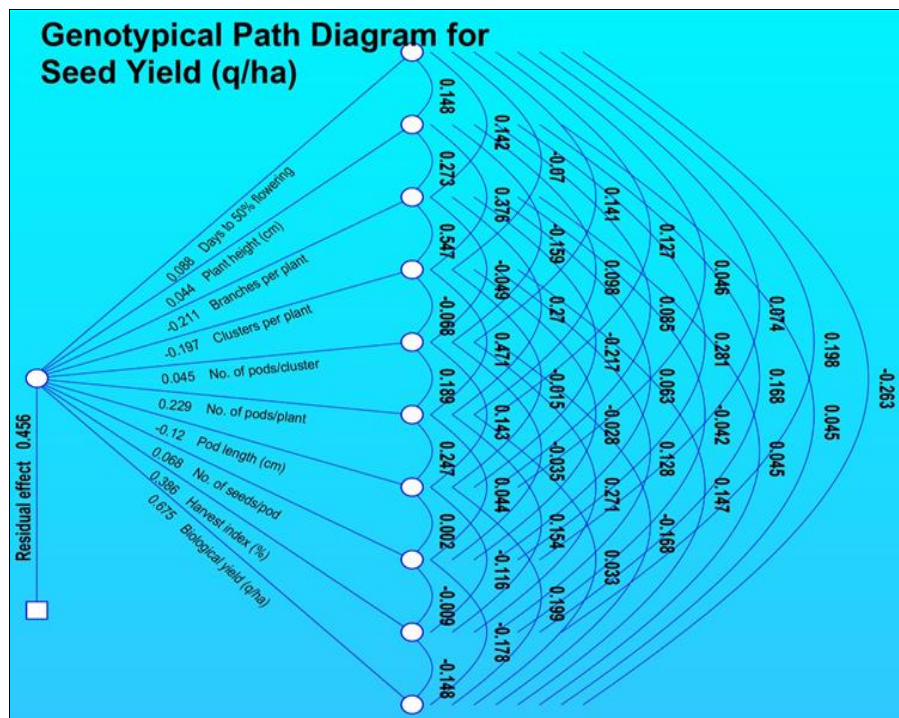
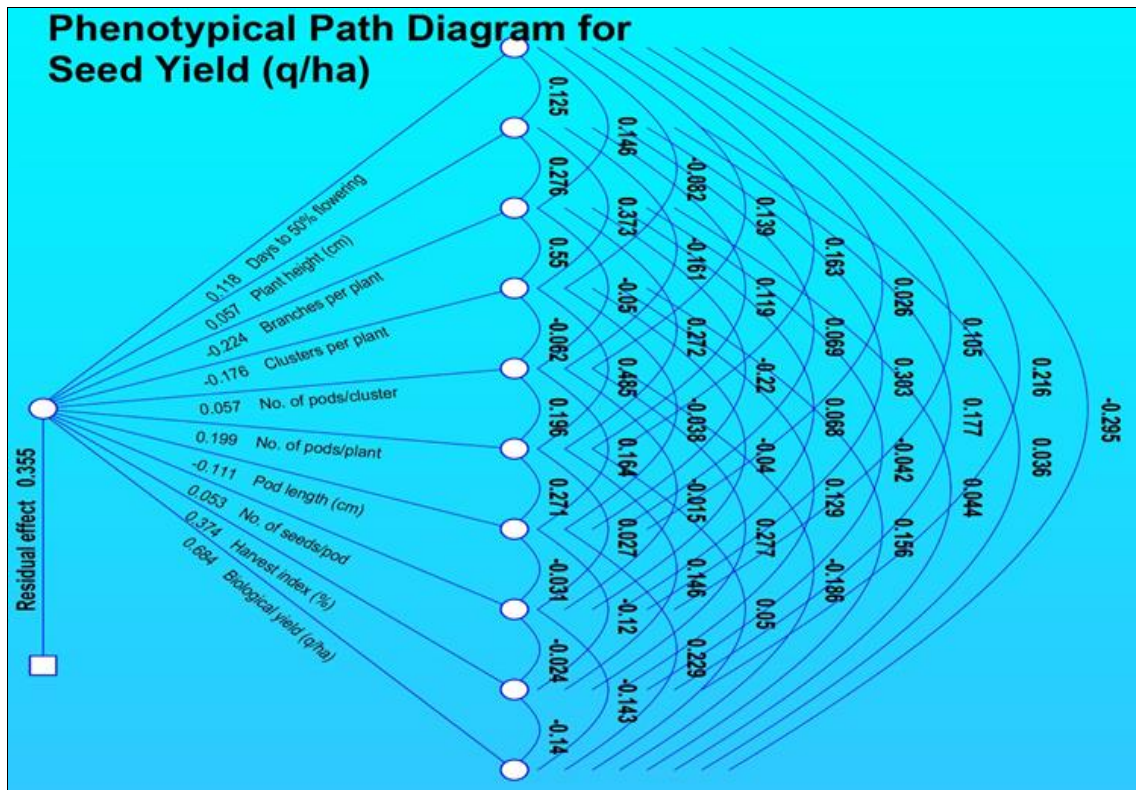


Fig 3: Genotypic Path Diagram for Seed Yield (q/ha)

**Table 4:** Phenotypic path coefficients between different traits in elite urbean genotypes

Phenotypic PATH matrix of Seed Yield (q/ha)											
	Days to 50% flowering	Plant height (cm)	Branches per plant	Pod clusters per plant	No. of pods/cluster	No. of pods/plant	Pod length (cm)	No. of seeds/pod	Harvest index (%)	Biological yield (q/ha)	Corr. with seed yield (q/ha)
Days to 50% flowering	0.118	0.014	0.017	-0.009	0.016	0.019	0.003	0.012	0.025	-0.034	0.029
Plant height (cm)	0.007	0.057	0.015	0.021	-0.009	0.006	0.004	0.017	0.010	0.002	0.058
Branches per plant	-0.032	-0.061	-0.223	-0.123	0.011	-0.060	0.049	-0.015	0.009	-0.009	-0.193
Pod clusters per plant	0.014	-0.065	-0.096	-0.175	0.011	-0.085	0.006	0.007	-0.022	-0.027	-0.036
No. of pods/cluster	0.008	-0.009	-0.002	-0.003	0.057	0.011	0.009	-0.0008	0.015	-0.010	0.082
No. of pods/plant	0.032	0.023	0.054	0.096	0.039	0.199	0.054	0.005	0.029	0.010	0.150
Pod length (cm)	-0.002	-0.007	0.024	0.004	-0.018	-0.030	-0.111	0.003	0.013	-0.025	0.125
No. of seeds/pod	0.005	0.015	0.003	-0.002	-0.0008	0.001	-0.001	0.052	-0.001	-0.007	-0.024
Harvest index (%)	0.080	0.066	-0.015	0.048	0.103	0.054	-0.044	-0.008	0.373	-0.052	0.358*
Biological yield (q/ha)	-0.201	0.024	0.030	0.107	-0.127	0.034	0.156	-0.097	-0.095	0.683	0.528**
Seed Yield (q/ha)	0.029	0.058	-0.193	-0.036	0.082	0.150	0.125	-0.024	0.358*	0.528**	1.000

Diagonal values = Direct effect, off diagonal values = Indirect effect



**Fig 4:** Phenotypic Path Diagram for Seed Yield (q/ha)

**4. Conclusion**

From the correlation and path coefficient analysis it is investigated that biological yield (q/ha), harvest index (%), number of pods per plant and days to 50% flowering were most important traits which should be given proper emphasis during selection program for the improvement of grain yield in long duration urbean genotypes. The study concludes that in urbean crops, earlier flowering reduces yield, while traits like plant height, branches, and pod clusters positively correlate with yield factors. These findings align with prior research, underscoring their potential in guiding breeding programs for yield improvement. The path coefficient analysis further illuminates direct and indirect trait influences, enhancing the understanding of yield determinants.

**5. Research conflict**

While the study presents significant correlations between various phenotypic and genotypic traits with yield in urbean

crops, there exist conflicts within research literature. Some studies may report varying degrees of correlation or even no significant relationship between these traits and yield. Discrepancies can arise from differences in experimental conditions, genetic variability of the urbean populations studied, environmental influences, or the methodologies applied in assessing the traits. Such conflicts highlight the complexity of plant breeding and the need for context-specific research to accurately determine the traits that most effectively predict and enhance yield in urbean crops.

**6. Acknowledgement**

We extend our heartfelt gratitude to all those who have contributed to the successful completion of our research entitled "Correlation and Path Analysis of Yield and Related Traits in urbean [*Vigna mungo* (L.) Hepper] genotypes." We would like to thank the Section of Genetics and Plant Breeding at the BTC College of Agriculture and Research Station, Bilaspur, affiliated

with Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India, for providing the necessary resources and environment to conduct this study.

Special thanks to Dr. Roshan Parihar, Dr. D.J. Sharma, and Dr. A.P. Agrawal for their invaluable guidance, insights, and expertise that significantly contributed to the research. Their mentorship was crucial in interpreting the data and understanding the complex relationships between the traits studied.

We are also thankful to our peers and technical staff for their assistance in the field and laboratory work. Their hard work and meticulous attention to detail have been the backbone of the data collection process.

## 7. References

1. Arya P, Gaibriyal ML, Sapna SL. Correlation and path analysis for yield and yield components in blackgram (*Vigna mungo*). Int. J Adv. Biol. Res. 2017;7(2):382-386.
2. Bharathi D, Hariprasad Reddy K, Mohan Reddy D, Latha P, Ravindra Reddy B. J Res Angra. 2022;50(4):27-36.
3. Dewey DR, Lu KH. A correlation and path analysis of components of wheatgrass seed production. Agron. J. 1959;51:515-51.
4. Devi M, Jayamani P, Kumar M. Genetic Analysis and Seed polymorphism in Inter sub-specific cross of blackgram [*Vigna mungo* (L.) Hepper]. Madras Agric. J. 2021;107:10-12.
5. Gaibriyal ML. Pulses Research at IIPR. Published by: Indian Institute of Pulses Research, Kanpur 208024. India. Available at: <https://www.statista.com/statistics>.
6. Kavitha A, Shanthi Priya M, Mohan Reddy D, Ravindra Reddy B. Genetic variability studies in blackgram. Int. J Chem. Studies. 2018;6(5):2569-2572.
7. Kumar BV, Lal GM, Subba Reddy YV, Kumar S, Bhupal G. Principal component analysis and traits association in blackgram [*Vigna mungo* (L.) Hepper]. Int. J Plt. Soil. Sci. 2022;34(23):37-48.
8. Miller PA, Williams CV, Robinson HF, Comstock RE. Estimates of genotypic and environmental variance and covariance in upland cotton and their implication in selection. Agron. J. 1958;50(3):126-131.
9. Panigrahi KK, Mohanty, Baisakh. Genetic divergence, variability and character association in landraces of blackgram [*Vigna mungo* (L.) Hepper] from Odisha. J Crop. Weed. 2014;10(2):155-165.
10. Sowmini K, Jayamani P. Genetic variability studies for yield and its component traits in RIL population of blackgram [*Vigna mungo* (L.) Hepper]. Elec. J Plt. Breed. 2013;4(1):1050-1055.