

# Assessment of Genetic Variability and Trait Associations for Yield and Yield Components in Urdbean [*Vigna mungo* (L.) Hepper]

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## Abstract

The study encompassed sixty genotypes of urdbean [Vigna mungo (L.) Hepper] and took place at the Agricultural Research Farm, Janta Mahavidyalaya, Ajitmal, Auraiya (U.P.) during the Kharif season of 2021-22. The experiment was designed using a randomized block pattern with three replications. The investigation unveiled notable genotypic distinctions across all examined traits, underscoring a substantial degree of variation among genotypes for each characteristic. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for pods per plant, number of secondary branches per plant, seed yield per plant, plant height, number of primary branches per plant, and pod length. The remaining traits exhibited moderate to low PCV and GCV estimates. High heritability estimates were recorded for the number of primary branches per plant, yield per plant, number of pods per plant, plant height and initial flowering. Moderate to low heritability was observed for 50% flowering, number of seeds per pod and pod length. High heritability coupled with the high genetic advance in per cent of mean was observed for yield per plant, number of pods per plant and number of primary branches per plant. The association study results revealed that grain yield per plant showed a highly significant and positive correlation at the genotypic level with all the traits except initial flowering and 50% flowering, indicating the possibility of simultaneous improvement for these traits. Path analysis indicated that yield per plant was directly influenced by pod length and 100seed weight, 50% flower, number of primary branches per plant, and plant height at the phenotypic level. However, at the genotypic level, plant height, number of primary branches per plant, number of secondary branches per plant, and pod length showed a moderate level of positive indirect effect on yield per plant. Their significant and positive association with grain yield indicated a true and perfect correlation between these traits.

Key words: Genetic variability, Heritability, Genetic advance, Correlation, Path analysis.

## Introduction

Urdbean (*Vigna mungo* (L.) Hepper) plays a crucial role in Indian agriculture as a prominent pulse crop due to its high seed protein content (25-26%), carbohydrates (60%), fat (1.5%), and rich mineral, amino acid, and vitamin composition. It is recommended for medicinal use both externally and internally to address conditions such as paralysis, rheumatism, and nervous system disorders (Singh, 2001). Additionally, its capacity for symbiotic nitrogen fixation contributes to enhancing soil fertility, further highlighting its significance (Malik, 1994). The study of inheritance patterns of various developmental and productive traits through the estimation of genetic parameters such as components of variance, genotypic and phenotypic coefficients of variability, heritability and genetic advance is crucial for devising effective breeding programs. Difficulty in visually discerning subtle differences in quantitative traits among individual plants has led to frequent efforts to identify associated traits that are more easily recognisable for visual selection. Correlation coefficients provide insights into the relationships between traits and indicate the extent to which different crop characteristics are linked to productivity. Selection based on yield components is advantageous when various yield-related traits have been thoroughly documented (Pohelman, 1995; Singh and Singh, 1995). Path coefficient analysis, on the other hand, is a valuable statistical technique specifically designed to quantify the interrelationships among different components and their direct and indirect effects on seed yield. By employing path coefficient analysis, it becomes possible to assign rankings to yield-contributing traits. This statistical technique allows for the identification and prioritization of specific traits that contribute to a given correlation (Rao *et al.*, 2006).

#### **Materials and Methods**

The present investigation was carried out at the Agricultural Research Farm, Janta Mahavidyalaya, Ajitmal, Auraiva (U.P.) using 58 germplasm and 2 check varieties, namely Pratap Urd-1 and Azad, of urdbean [Vigna mungo (L.) Hepper] during the Kharif season of 2021-22. The germplasm lines were sourced from the Indian Institute of Pulse Research, Kanpur, and Chandra Shekhar Azad Seed Processing Centre, Kanpur. The experimental design adopted was a randomized block design with three replications. Each genotype was cultivated in a plot consisting of two rows, each measuring 2.5m in length, with an inter-row spacing of 35 cm and an intra-row spacing of 10 cm. Thinning was performed in the second week after sowing to maintain a distance of 10 cm between plants. All recommended management practices were meticulously followed throughout the crop period. Observations were recorded on various traits including days to initial flowering, days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), and yield per plant (g). Standard statistical procedures were employed for the analysis of variance (Panse and Sukhatme, 1967), calculation of genotypic and phenotypic coefficients of variation (Burton, 1952), estimation of heritability (Hanson et al., 1956), and determination of genetic advance (Johnson et al., 1995). Correlation coefficients were computed following the method outlined by Panse and Sukhatme (1967), while path analysis was conducted based on the procedures described by Wright (1921) and Dewey and Lu (1959).

#### **Results and Discussion**

The analysis of variance results indicated that the variance attributable to treatment was significant for all ten characters under study (Table 1). This provides



evidence of the substantial genetic variability among genotypes, which varied significantly in magnitude. The data on mean, variability, heritability, and genetic advance as a percentage of the mean are presented in Table 2. The maximum range of variation was observed for plant height, followed by days to 50% flowering, days to initial flowering, and number of pods per plant. Additionally, the genotypic coefficients of variation for all characters studied were lower than the phenotypic coefficient of variation, indicating the masking effects of the environment (Table 2). High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for several traits: pods per plant (30.78 and 41.03, respectively), number of secondary branches/plant (16.28 and 38.25), seed yield/ plant (29.87 and 33.02), plant height (20.10 and 27.22), number of primary branches/plant (21.64 and 23.33), and pod length (11.62 and 21.25). Similar results were also reported by Sowmini and Jayamini (2013). In contrast, the remaining traits exhibited moderate to low PCV and GCV estimates.

High heritability estimates were recorded for the number of primary branches/plant (86.04%), seed vield/plant (81.88%), number of pods/plant (56.26%), plant height (54.53%), and initial flowering (48.14%), suggesting that selection would be more effective in improving these traits. Conversely, moderate to low heritability was observed for 50% flowering (40.83%), number of seeds/pod (36.35%), pod length (29.88%), 100-seed weight (21.87%), and number of secondary branches/plant (18.12%), indicating that improvement in these traits could be achieved through selection to some extent. High heritability, coupled with a high genetic advance as a percentage of the mean, was observed for yield/plant (55.69%), followed by the number of pods/ plant and the number of primary branches/plant. The results suggest that these traits are likely controlled by additive gene action, as reported by Johnson et al. (1995), Wright (1921), Dewey and Lu (1959), Panse and Sukhatme (1967), and Panse (1957). Similar findings were also reported by Patel et al. (2014), Gill et al. (2018), Chauhan et al. (2020), and Aman et al. (2022), who observed high heritability coupled with high genetic advance for most of the quantitative characters. The high values of heritability and genetic advance for grain yield, pods per plant, and plant height indicate that these traits are likely controlled by additive gene action, consistent with findings reported by Gowda *et al.* 1997.

The genotypic correlation coefficients between yield and yield components are presented in Table 3. In the current investigation, plant height (cm), number of primary branches/plant, number of secondary branches/plant, pod length (cm), number of seeds/pod, and 100-seed weight (g) exhibited significantly positive correlations with yield per plant (g). This suggests that an increase in growthrelated traits may contribute to higher yields in black gram. Consequently, selecting high-yielding genotypes of black gram necessitates considering these traits with increasing magnitude, facilitating the simultaneous improvement of all positively correlated characters. Similar positive associations of various traits with seed yield have been reported earlier by Chauhan *et al.* (2007), Rao *et al.* (2006), Veeranjaneyulu *et al.* (2007), and Kanimozhi *et al.* (2015). The other traits under study, namely days to initial flowering, days to 50 % flowering and No. of pods/ plant showed a negative and non-significant correlation with yield. The negative and non-significant association among the traits had a complex linkage relation among the pairs of combinations and had a weak association with yield.

<b>Table 1: Analysis of variance</b>	for ten characters in urdbean	[ <i>Vigna mungo</i> (I	L.) Hepper
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Source of variation	d.f.	Days to Initial flowering	Days to 50% flowering	Plant Height (cm)	No. of primary branches /plant	No. of sec- ondary branches /plant	No. of pods/ plant	Pod length (cm)	No. of seeds /pod	100-seed weight (g)	Yield /plant (g)
Replication	2	3.60	1.48	8.58	35.47	0.48	8.86	14.76	79.95	25.63	10.13
Treatment	59	3.79**	3.07**	4.60**	19.49**	1.66**	4.86**	2.29**	2.71**	1.84**	14.55**
Error	118	8.10	9.06	295.92	0.11	0.45	8.60	1.18	0.62	0.21	0.60

\*and\*\* significant level 5% and 1%, respectively.

Table 2: Mean, range, coefficient of variability, heritability (broad sense), genetic advance and	genetic
advance as per cent of the mean in urdbean [ <i>Vigna mungo</i> (L.) Hepper].	

S.N.	Characters	Range			Coefficient of vari- ation %		Heritability (h <sup>2</sup> )	Genetic Ad-	Genetic
		MIN.	MAX.	Mean	GCV	PCV	Broad sense %	vance	% of mean
1	Days to initial flowering	21.86	37.68	32.40	8.46	12.19	48.14	3.9186	12.0929
2	Days to 50% flowering	41.45	57.54	51.86	4.82	7.54	40.83	3.2908	06.3447
3	Plant height (cm)	51.93	136.00	93.71	20.10	27.22	54.53	28.66	30.5844
4	No. of primary branches/plant	1.78	517	3.78	21.64	23.33	86.04	1.5641	41.3546
5	No. of secondary branches/plant	0.83	2.94	1.93	16.28	38.25	18.12	0.2764	14.2754
6	No. of pods/plant	5.51	24.41	10.80	30.78	41.03	56.26	5.1392	47.5665
7	Pod length(cm)	3.97	8.45	6.089	11.62	21.25	29.88	0.7970	13.0871
8	No. of seeds/pod	3.19	6.99	5.27	11.23	18.62	36.35	0.7359	13.9483
9	100-seed weight	3.58	5.30	4.20	5.71	12.22	21.87	0.2316	05.5091
10	Yield/plant(g)	3.15	10.06	5.51	29.87	33.02	81.88	3.0740	55.6945



Traits	Days to Initial flowering	Days to 50% flowering	Plant height (cm)	No. of primary branches/plant	No. of second- ary branches/ plant	No. of pods /plant	Pod length (cm)	No. of seeds/ pod	100- seed weight (g)	Yield/plant (g)
Days to Initial flowering	1.000	0.981**	-0.111	-0.120	-0.313**	0.088	-0.116	0.145	0.311**	-0.055
Days to 50% flow- ering		1.000	-0.065	-0.122	-0.294**	0.120	-0.063	0.199**	0.401**	-0.002
Plant height (cm)			1.000	0.328**	0.501**	-0.070	0.207**	-0.047	0.401**	0.229**
No. of primary branches/plant				1.000	0.957**	0.101	0.748**	0.108	-0.047	0.249**
No. of secondary branches/plant					1.000	0.184*	0.419**	0.018	0.485**	0.263**
No. of pods/plant						1.000	0.017	-0.062	0.541**	-0.120
Pod length (cm)							1.000	0.906**	0.100	0.278**
No. of seeds/pod								1.000	-0.093	0.164*
100-seed weight (g)									1.000	0.187*

# Table 3: Estimate of genotypic correlation between different characters in urdbean [Vigna mungo (L.) Hepper].

\*&\*\* Significant at 5% and 1%, respectively

# Table 4: Direct and indirect effects for different characters on seed yield at a genotypic level in urdbean [Vigna mungo (L.) Hepper].

Traits	Days to Initial flowering	Days to 50% flowering	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	No. of pods /plant	Pod length (cm)	No. of seeds/ pod	100- seed weight (g)	Yield/plant (g)
Days to Initial flowering	-0.927	0.927	0.007	-0.015	0.117	-0.030	-0.117	-0.116	0.098	-0.055
Days to 50% flowering	-0.909	0.945	0.004	-0.015	0.110	-0.041	-0.063	-0.160	0.127	-0.002
Plant height (cm)	0.103	-0.062	-0.063	0.042	-0.187	0.024	0.208	0.038	0.127	0.229**
No. of primary branches/plant	0.111	-0.115	-0.021	0.126	-0.469	-0.034	0.751	-0.087	-0.015	0.249**
No. of secondary branches/plant	0.290	-0.278	-0.032	0.159	-0.373	-0.062	0.421	-0.014	0.153	0.263**
No. of pods/plant	-0.082	0.114	0.004	0.013	-0.069	-0.338	0.017	0.050	0.171	-0.120
Pod length (cm)	0.108	-0.059	-0.013	0.095	-0.157	-0.006	1.004	-0.725	0.032	0.278**
No. of seeds/pod	-0.134	0.188	0.003	0.014	-0.007	0.021	0.909	-0.801	-0.029	0.164*
100 seed weight (g)	-0.288	0.379	-0.025	-0.006	-0.181	-0.183	0.100	0.075	0.316	0.187*

\*&\*\* Significant at 5% & 1%, respectively

Bold values show direct and normal values show indirect effects

Residual Effect = 0.3864

In the study on the interrelation among yieldcontributing characters, days to initial flowering exhibited positive and highly significant interactions with days to 50% flowering (0.981) and 100-seed weight (0.311). Plant height showed positive correlations with the number of primary branches per plant (0.328), the number of secondary branches per plant (0.501), pod length (0.207), and 100-seed weight (0.401). The number of primary branches per plant exhibited positive correlations with the number of secondary branches per plant (0.957) and pod length (0.748). The number of secondary branches per plant showed positive correlations with the number of pods per plant (0.184), pod length (0.419), and 100-seed weight (0.485). The number of pods per plant exhibited a positive correlation with 100-seed weight (0.541), and pod length showed a positive correlation with the number of seeds per pod (0.906). Similar associations were reported by Sohel et al. (2016), Mohanlal et al. (2018), and Sidramappa et al. (2020).

The estimates of correlation coefficients provide insights into the relationships between yield components, but they do not directly show the effects of different traits on yield. This is because the attributes that are associated do not exist independently but are interconnected with other components. However, path coefficient analysis for grain yield and yield components can delineate genotypic correlations into direct and indirect effects. In the present investigation, path coefficient analysis was conducted using correlation coefficients to determine the direct and indirect influence of nine traits on yield (Table 3). It was observed that the highest positive direct effect on grain yield per plant was recorded by pod length (1.004) followed by 50% flowering (0.945) and 100-seed weight (0.316). Hence, selection based on these traits would be effective in increasing the seed yield. These positive direct effects observed with seed yield were in accordance with earlier findings of Hakim (2008), Kanimozhi et al. (2015) and Gill et al. (2018). Days to initial flowering, days to 50% flowering, and number of pods per plant exhibited a negative and indirect effect on yield per plant. This suggests that early maturing genotypes with a longer reproductive phase are more conducive to obtaining high seed yield per plant. Similar findings have also been supported by Kumar and Sharma (2019).

In the present study, the residual effect was determined to be 0.3864, indicating that the characters included in the path analysis accounted for 61.36% of the variability in grain yield, while the remaining 38.64% requires additional characterization for future breeding programs. The partitioning of correlation values revealed that some traits did not exhibit significant correlations with single plant yield, possibly due to very high negative direct effects. Considering the nature and magnitude of trait associations and their direct and indirect effects, it can be inferred that simultaneous improvement of grain yield is achievable through the enhancement of pod length, days to 50% flowering, and 100-seed weight. Therefore, emphasizing these traits in selection programs for increasing grain yield would be rewarding. Selection for these traits could lead to improvements in both yield and yield components.

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