Character Association and Path Analysis for Yield and its Attributing Traits in Urdbean Genotypes and its Triple Test Cross F_1 Hybrids

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ABSTRACT

This research delves into the association and path coefficient analysis between yield and its attributing traits among 111 diverse lines of urdbean. 27 lines, three testers, and Eighty-one F_1 hybrids were grown in a Randomized Block Design (RBD) with three replications during Kharif 2023 at the Crop Experimental Research Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kalyanpur, Kanpur (U.P.). The analysis of variance for parents (27 lines and three testers) and their 81 triple test cross hybrids indicated highly significant genotypic differences across all 12 quantitative traits under study *viz.,* days to 50% flowering (DFF), days to 75% maturity (DM), plant height (cm) (PH), number of primary branches per plant (NPB), pods per plant (NPP), pod length (cm) (PL), seeds per pod (NSP), biological yield per plant (g) (BYPP), seed yield per plant (g) (SYPP), harvest index (%),(HI), 100-seed weight (HSW), and protein content (%) (PC). All the traits studied showed a significant positive correlation with seed yield, except for days to 50% flowering, and days to 75 % maturity at phenotypic and genotypic levels. Path analysis revealed that all the traits had high direct positive effects on seed yield except for days to 50% flowering and days to 75 % maturity at phenotypic and genotypic levels. Therefore, these traits should be the primary focus in black gram breeding programs aimed at yield improvement.

Keywords: Correlation; genotypic; path coefficient; phenotypic; urdbean.

1. INTRODUCTION

“Urdbean [*Vigna mungo* (L.) Hepper], commonly known as blackgram, "mash kalai," urd, or urad, is a self-pollinated diploid grain legume (2n=2x=22) from the family Fabaceae (Leguminosae) and subfamily Faboideae (Papilionoideae or Papilionaceae). It has a small genome size of 0.56 g/PC or 574 Mbp” [1,2]. “The wild progenitor of blackgram domesticated in India is believed to be *Vigna mungo var. silvestris”* [3,4]. “Being a leguminous crop, it enhances soil fertility by fixing atmospheric nitrogen, thereby preventing soil erosion. It is widely consumed as dry whole grain or split grain known as daal and as unfermented and fermented flour” [5]. “Urdbean is a nutritious pulse crop that possesses approximately 24%–26% protein, 60% carbohydrates, 1.3% fats, phosphorus (345 mg/100 g), potassium, iron (8.7 mg/100 g), and calcium (185 mg/100 g) along with several essential amino acids (arginine, phenylalanine, leucine, lysine, valine, and isoleucine, etc.), vitamins such as vitamin B_3 (niacin; 2 mg/100 g), vitamin A (23 IU/100 g), vitamin B_1 (thiamine; 0.42 mg/100 g), and vitamin B_2 (riboflavin; 0.37 mg/100 g)” (USDA National Nutrient Database, [6]. “In India, about 92 % (percent) of urdbean production comes from 9 states Madhya Pradesh, Rajasthan, Uttar Pradesh, Tamil Nadu, Andhra Pradesh, Maharashtra, Jharkhand, Gujarat, and Karnataka. The urdbean production of India was 2.78 million tonnes from the acreage of 4.63 million hectares with a productivity of 600 Kg/ha. (Agricultural Statistics Division”, DES, MoAF&W, [7]. “Despite its great importance, the productivity of urdbean in India continues to be low due to several factors including limited genetic diversity for developing high-yielding varieties, lack of variability, inadequate plant ideotype, suboptimal crop management, weed infestation, and vulnerability to both biotic and abiotic stresses" [8]. "The repeated use of a limited number of parents with a high degree of similarity in crossing programs" [9]. "To increase the productivity and production of this crop, developing new high-yielding genotypes is a prime goal of urdbean breeding" [10]. "The correlation coefficient estimates, which indicate the degree and direction of association between pairs of traits, have proven useful for the simultaneous improvement of correlated traits through selection" [11,12]. "Path coefficient analysis, conversely, is an effective statistical method specifically designed to quantify the interrelationships among various components and their direct and indirect effects on seed yield" [13]. Correlation studies, combined with path analysis, can provide a better understanding of the interrelationships between different traits and seed yield, benefiting breeders during the selection process. Therefore, the current study focused on correlation and path coefficient analysis to identify superior black gram genotypes and F_1 TTC hybrids for future application in breeding programs.

2. MATERIALS AND METHODS

The present investigation was conducted during *Kharif,* 2023 at the Crop Experimental Research Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kalyanpur, Kanpur (U.P.). The material for the investigation comprised 111 diverse lines of urdbean, namely; Shekhar-1, Shekhar-2, KU-14-1, KU-16- 4, KU 17-4, KU-17-9, KU-19-10, KU-20-12, KU-48, KU-88-1, KU-88-31-2, KU-99-12, KU-99-19, KU-96-05, KU-321, KU-333, KU-717, KUG-818, KPU-1720-140, Azad-2, IPU-17-1, IPU-12-5, IPU-13-3, PU-13-15, Pant-431, SBC-50, and VBG-13-003. These lines were crossed with three testers *viz.,* KU-96-7 (L_1), Azad-3 (L_2)**,** and F_1 of KU-96-7 × Azad-3 i.e., L_3, to produce 81 triple test cross (TTC) progenies. TTC progenies in the form of 54 single crosses and 27 three-way crosses. Therefore, 27 lines, three testers, and Eighty-one F_1 hybrids were grown in a Randomized Block Design (RBD) with three replications respectively. Standard production techniques were followed to get a healthy crop. The data on 12 quantitative traits *viz.,* days to 50% flowering (DFF), days to 75% maturity(DM), plant height (cm) (PH), number of primary branches per plant (NPB), pods per plant (NPP), pod length (cm) (PL), seeds per pod (NSP), seed yield per plant (g) (SYPP), biological yield per plant (g) (BYPP), harvest index (%),(HI), 100-seed weight (HSW), and protein content (%) (PC) were recorded. The seed protein content was estimated by using [14].

2.1 Analysis of Variance for Randomized Block Design

The data for the various characters were analyzed according to Panse and Sukhatme [15]. The analysis of variance followed the linear model proposed by Fisher [16].

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = phenotypic observation of the i^{th} genotype in the j^{th} replication.
μ = general population mean
g_i = effect of i^{th} genotype.
r_j = effect of j^{th} replication.
e_{ij} = random error (error associated with i^{th} genotype in the j^{th} replication).

2.2 Estimation of Correlation Coefficient

2.2.1 Genotypic and phenotypic correlation coefficient

The genotypic and phenotypic correlation coefficient was calculated by the formulae given by Robinson et al. [17];

a. Genotypic Correlation Coefficient between characters x and y: rg (xy) $=\frac{\mathrm{CoV.(g)xy}}{\sqrt{[\mathrm{Var(g)x \times Var(g)y}]}}$
b. Phenotype correlation coefficient between characters x and y: rp (xy) $=\frac{\mathrm{CoV.(p)xy}}{\sqrt{[\mathrm{Var(p)x \times Var(p)y}]}}$

Where,

r_{xy} = Correlation coefficient between characters x and y.
CoV.xy = Covariance between characters x and y.
Var. x = Variance for x character.
Var. y = Variance for y character.

2.2.2 Estimation of path coefficient

Path analysis was also performed to determine the direct and indirect effects of various components on yield, following the procedure outlined by Dewey and Lu **[**18].

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

The analysis of variance revealed significant differences in the 27 parents, 3 Testers, and the 81 cross combinations for all the traits, indicating that the parents were genetically diverse and sufficient variability was generated through hybridization *i.e.,* sufficient genetic variability among crosses for all the traits, *viz.,* DFF, DM, PH, NPB, NPP, PL, NSP, SYPP, BYPP), HI, HSW, and PC indicated ample genetic variability in the existing genetic materials. Earlier [19,12] also had similar findings about significant genetic variability for all the characters. Thereby justifying the selection of the experimental materials. Understanding the extent of variability within crop species is crucial as it forms the foundation for the effective selection of desired traits [20].

3.2 Correlation Coefficient Analysis

Correlation coefficients were calculated to evaluate the strength of the association between seed yield and other contributing traits. The Genotypic and phenotypic correlations between yield and its components in blackgram are depicted in Table 1. Generally, the genotypic correlation coefficient estimates were higher than their corresponding phenotypic values except for biological yield per plant, implying an inherent association among the studied traits.

In the current investigation, seed yield per plant showed a highly significant and positive correlation with pods per plant (NPP) (0.778**, 0.744**), followed by biological yield per plant (g) (BYPP) (0.604**, 0.618**), harvest index (%),(HI) (0.475**, 0.473**), **), number of primary branches per plant (NPB) (0.372**, 0.349**), plant height (cm) (PH) (0.366**, 0.347), pod length (cm) (PL) (0.233**, 0.216**), 100-seed weight (HSW) (0.229**, 0.228**), seeds per pod (NSP) (0.193**, 0.160**), and protein content (%) (PC) (0.115*, 0.112*) at genotypic and phenotypic levels respectively. These results are consistent with Saran et al. [19], and Chauhan et al. [21]. Similarly, the association pattern of seed yield showed a significant and positive correlation with plant height [21,22,23] and the number of pods per plant [12,19,24]. Meanwhile, [25] also observed a positive significant correlation of primary branches, pods per plant, seed index, and harvest index with the seed yield per plant at both genotypic and phenotypic levels. It suggested that an increase in growth-related traits, such as plant height and pod characteristics, might contribute to higher yields in black gram. The other traits studied, namely days to 50% flowering and days to 75% maturity, showed positive but non-significant correlations with yield, indicating a weak association with seed yield. Similar findings were reported by Gnanasekaran et al. [23] for days to maturity.

From the inter-correlation studies, days to 50 % flowering had a negative significant association with plant height, number of primary branches per plant, biological yield per plant, and hundred seed weight. Plant height had a positive significance with the number of primary branches per plant (0.416**, 0.394**), pod length (0.133**, 0.123**), number of pods per plant (0.457**, 0.428**), biological yield per plant (0.336**, 0.316**),100 seed weight (0.138**, 0.129**) and protein content (0.181**, 0.169**). The number of primary branches per plant had a positive significance with pod length (0.264**, 0.244**), number of pods per plant (0.396**, 0.383**), seeds per pod (0.245**, 0.218**), biological yield per plant (0.370**, 0.350**), 100 seed weight (0.141**, 0.115**) and protein content (0.148**, 0.137**). Pod length had a positive significant association with the number of pods per plant (0.159**, 0.155**), seeds per pod (0.420**, 0.342**), biological yield per plant (0.181**, 0.168**), and protein content (0.249**, 0.232**). The number of pods per plant had a positive significance with seeds per pod (0.117**, NS), biological yield per plant (0.513**, 0.489**), harvest index (0.267**, 0.263**), and 100 seed weight (0.267**, 0.239**). The number of seeds per pod had a positive significance with a harvest index (0.231**, 0.196**). Biological yield per plant had positive significance with 100-seed weight (0.153**, 0.153**). The results of inter-correlation studies were closely in harmony with the results of Sathees et al. [26,27] observed that the number of primary branches per plant had a positive significance with the number of pods per plant, number of seeds per pod, and the hundred seed weight from 120 germplasm lines.

From these facts, it is evident that the yield component traits *viz.,* pods per plant, seeds per pod, plant height, pod length, number of primary branches per plant, biological yield per plant, harvest index, and 100-seed weight, are highly correlated with seed yield per plant and with each other. Therefore, simultaneous selection for these traits will be more effective in improving black gram breeding.

3.3 Path Coefficient Analysis

The correlation coefficient estimates only indicated the relationships between yield components, without showing the direct and indirect effects of different traits on seed yield. This is because the associated attributes are not independent but are linked to other components. However, path coefficient analysis for grain yield and its contributing components can elucidate genotypic and phenotypic correlations in terms of direct and indirect effects.

In this study, path coefficient analysis was conducted using correlation coefficients to determine the direct and indirect effects of 11 traits on seed yield (Table 2). The results showed that biological yield per plant (0.7219, 0.7455), harvest index (0.6963, 0.6743), and number of pods per plant (0.2289, 0.2070) had the strongest positive direct effects on seed yield per plant at genotypic and phenotypic levels. Therefore, selecting these traits would be effective in increasing seed yield. Additionally, primary branches per plant, pod length, 100-seed weight, and protein content also had direct positive effects on seed yield. These results were in harmony with the findings of Shanthi et al. [28,12,19,24,25]. Plant height, number of primary branches per plant, and pod length positively indirectly affected yield through the number of pods per plant and biological yield per plant. The number of pods per plant positively influenced yield indirectly via biological yield per plant and harvest index. Similarly, seeds per pod had a positive indirect effect on yield through the harvest index. The remaining traits, particularly days to 50% flowering and days to 75% maturity, have a negligible impact on seed yield per plant.

Table 1. Genotypic and phenotypic correlation coefficient among 12 quantitative traits of Urdbean genotypes.

Traits ↓		Days to 50% flowering	Days to 75% Maturity	Plant Height (cm)	Primary Branches Per Plant	Pod Length (cm)	No. of Pods Per Plant	Seeds Per Pod	Biological Yield Per Plant (g)	Harvest Index (%)	100-Seed Weight (gm)	Protein Content (%)	Seed Yield / Plant (gm)
Days to 50% flowering	G	1	0.994**	-0.221**	-0.117*	0.077	-0.041	0.161**	-0.179**	0.173**	-0.187**	-0.068	0.002
	P	1	0.831**	-0.187**	-0.108*	0.06	-0.039	0.109*	-0.154**	0.160**	-0.135*	-0.055	0.004
Days to 75% Maturity	G		1	-0.164**	-0.091	0.059	-0.03	0.142**	-0.214**	0.238**	-0.262**	-0.142**	0.017
	P		1	-0.138*	-0.073	0.041	-0.024	0.119*	-0.192**	0.221**	-0.207**	-0.127*	0.016
Plant Height (cm)	G			1	0.416**	0.133*	0.457**	0.043	0.336**	0.075	0.138*	0.181**	0.366**
	P			1	0.394**	0.123*	0.428**	0.028	0.316**	0.073	0.129*	0.169**	0.347**
Primary Branches Per Plant	G				1	0.264**	0.396**	0.245**	0.370**	0.001	0.141**	0.148**	0.372**
	P				1	0.244**	0.383**	0.218**	0.350**	-0.004	0.115*	0.137*	0.349**
Pod Length (cm)	G					1	0.159**	0.420**	0.181**	0.067	-0.022	0.249**	0.233**
	P					1	0.155**	0.342**	0.168**	0.066	0.004	0.232**	0.216**
No. of Pods Per Plant	G						1	0.117*	0.513**	0.267**	0.267**	0.025	0.778**
	P						1	0.099	0.489**	0.263**	0.239**	0.023	0.744**
Seeds Per Pod	G							1	0.065	0.231**	-0.073	0.104	0.193**
	P							1	0.054	0.196**	-0.056	0.081	0.160**
Biological Yield Per Plant (g)	G								1	-0.352**	0.153**	0.082	0.604**
	P								1	-0.337**	0.153**	0.079	0.618**
Harvest Index (%)	G									1	0.051	0.015	0.475**
	P									1	0.064	0.016	0.473**
100-Seed Weight(gm)	G										1	0.104	0.229**
	P										1	0.103	0.228**
Protein Content (%)	G											1	0.115*
	P											1	0.112*
Seed Yield / Plant(g)	G												1
	P												1

*G = Genotypic correlation coefficient. P = Phenotypic correlation coefficient. *Significant at 5% level, **Significant at 1% level*

Table 2. Path coefficients of yield and its components of black gram genotypes

Parent/Hybrids		Days to 50% flowering	Days to 75% Maturity	Plant Height (cm)	Primary Branches Per Plant	Pod Length (cm)	No. of Pods Per Plant	Seeds Per Pod	Biological Yield Per Plant (g)	Harvest Index (%)	100-Seed Weight(gm)	Protein Content (%)	Seed Yield / Plant(gm)
Days to 50% flowering	G	0.2522	-0.2259	0.0086	-0.0053	0.0025	-0.0095	-0.0121	-0.1295	0.1207	-0.0002	-0.0017	0.0000
	P	0.0078	0.0163	0.0082	-0.0032	0.0011	-0.0082	-0.0055	-0.1150	0.1080	-0.0030	-0.0022	0.0040
Days to 75% Maturity	G	0.2506	-0.2273	0.0064	-0.0041	0.0019	-0.0069	-0.0107	-0.1543	0.1657	-0.0003	-0.0035	0.0170
	P	0.0065	0.0196	0.0060	-0.0022	0.0008	-0.0051	-0.0060	-0.1428	0.1488	-0.0046	-0.0052	0.0160
Plant Height (cm)	G	-0.0557	0.0372	-0.0390	0.0187	0.0042	0.1046	-0.0032	0.2426	0.0520	0.0002	0.0045	0.366**
	P	-0.0015	-0.0027	-0.0438	0.0115	0.0023	0.0886	-0.0014	0.2355	0.0489	0.0028	0.0069	0.347**
Primary Branches Per Plant	G	-0.0294	0.0207	-0.0162	0.0450	0.0084	0.0906	-0.0184	0.2671	0.0002	0.0002	0.0037	0.372**
	P	-0.0008	-0.0014	-0.0173	0.0293	0.0046	0.0792	-0.0109	0.2611	-0.0024	0.0025	0.0056	0.349**
Pod Length (cm)	G	0.0193	-0.0134	-0.0052	0.0119	0.0320	0.0365	-0.0316	0.1303	0.0469	0.0000	0.0062	0.233**
	P	0.0005	0.0008	-0.0054	0.0072	0.0187	0.0320	-0.0171	0.1254	0.0448	0.0001	0.0095	0.216**
No. of Pods Per Plant	G	-0.0104	0.0069	-0.0178	0.0178	0.0051	0.2289	-0.0088	0.3700	0.1860	0.0003	0.0006	0.778**
	P	-0.0003	-0.0005	-0.0188	0.0112	0.0029	0.2070	-0.0050	0.3643	0.1770	0.0052	0.0010	0.744**
Seeds Per Pod	G	0.0406	-0.0324	-0.0017	0.0110	0.0134	0.0268	-0.0752	0.0469	0.1611	-0.0001	0.0026	0.193**
	P	0.0009	0.0024	-0.0012	0.0064	0.0064	0.0205	-0.0500	0.0405	0.1323	-0.0012	0.0033	0.160**
Biological Yield Per Plant (g)	G	-0.0452	0.0486	-0.0131	0.0167	0.0058	0.1173	-0.0049	0.7219	-0.2448	0.0002	0.0021	0.604**
	P	-0.0012	-0.0038	-0.0138	0.0103	0.0031	0.1012	-0.0027	0.7455	-0.2273	0.0034	0.0032	0.618**
Harvest Index (%)	G	0.0437	-0.0541	-0.0029	0.0000	0.0022	0.0611	-0.0174	-0.2538	0.6962	0.0001	0.0004	0.475**
	P	0.0012	0.0043	-0.0032	-0.0001	0.0012	0.0543	-0.0098	-0.2513	0.6743	0.0014	0.0007	0.473**
100-Seed Weight(gm)	G	-0.0472	0.0597	-0.0054	0.0064	-0.0007	0.0612	0.0055	0.1104	0.0355	0.0011	0.0026	0.229**
	P	-0.0011	-0.0041	-0.0057	0.0034	0.0001	0.0495	0.0028	0.1140	0.0432	0.0219	0.0042	0.228**
Protein Content (%)	G	-0.0172	0.0322	-0.0071	0.0067	0.0080	0.0057	-0.0078	0.0593	0.0104	0.0001	0.0250	0.115*
	P	-0.0004	-0.0025	-0.0074	0.0040	0.0043	0.0049	-0.0040	0.0589	0.0109	0.0023	0.0409	0.112*

*Bold are direct effects***, G:** *Genotypic path coefficient, Residual effects (G): 0.0601; P: Phenotypic path coefficient, Residual effects (P): 0.655.*
**, ** significant at 5% and 1% level, respectively*

The number of pods per plant alone showed a high positive indirect effect on seed yield among all the characters. The residual effect values of 0.0601 and 0.655 suggest that there may be other secondary components that should not be overlooked, traits included in the path analysis explained approximately 75% of the total variation in the dependent variable, namely seed yield. These findings are consistent with those of Gomathi [12,23,29].

4. CONCLUSION

In the present investigation, association analysis revealed that generally, the genotypic correlation coefficient estimates were higher than their corresponding phenotypic values except for biological yield per plant. Analysis of correlation shows PH, NPB, NPP, PL, NSP, BYPP, HI, HSW, and PC were significantly and positively correlated with seed yield per plant (SYPP) except, days to 50% flowering (DFF), days to 75% maturity (DM). Path coefficient analysis revealed that among the yield contributing characters, biological yield per plant, harvest index, and number of pods per plant, had the strongest positive direct effects on seed yield per plant at genotypic and phenotypic levels. Therefore, considering the nature and magnitude of correlation coefficients, and their direct and indirect effects, it can be concluded that the enhancement of black gram seed yield is achieved through the simultaneous selection of plant height, primary branches per plant, number of pods per plant, biological yield, and harvest index. Henceforth, the selection based on these traits will help the improvement of seed yield in blackgram and further study.

DISCLAIMER (ARTIFICIAL INTELLIGENCE):

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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