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Genetic variability and character association studies in Urdbean (*Vigna mungo* L.) under irrigated and rainfed conditions of Jammu region

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Abstract

The present investigation was carried out during *Kharif* 2020 at three locations viz. SKUAST-J, Chatha, Arid Centre for Rainfed Agriculture, Rakhdhiansar and Pulses Research Sub-Station, Samba for estimating genetic variability parameters and to outline the association of grain yield with yield contributing traits. The presence of significant genetic variation was revealed by analysis of variance among urdbean genotypes in each environment as well as on pooled basis.Pooled estimates of components of genetic variance revealed that phenotypic variance was relatively higher than genotypic variance for all the morpho-physiological traits implying the role of the environment in the expression of such traits. High heritability coupled with high genetic advance as percentage of mean was observed for number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 1000 grain weight,grain yield per plant, biological yield per plant and harvest index indicating that these parameters are governed by additive-gene action and direct selection is effective for improving such traits. Grain yield per plant was found positively and significantly correlated with number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length, test weight, biological yield and harvest index which revealed the importance of these characters indetermining the grain yield per plant.

Key words: Urdbean, variance, heritability, genetic advance, correlation, path analysis

Urdbean [*Vigna mungo* (L.) Hepper], commonly known as Urd/ Biri/ Mashis one of the important nutritious grain legumes of the Indian subcontinent that is utilized in the diet, green fodder, soil conservation, integrated farming systems, reclaiming of degraded pastures and symbiotic nitrogen fixation. It is said to have originated in the Indian subcontinent (Vavilov, 1926) and was domesticated from *Vignamungovar.sylvestris* (Lukoki *et al*., 1982). Being the third important pulse crop in India, it was cultivated over an area of 5.44 Mha (*Kharif*+*Rabi*) and recorded a production of 3.56 Mt at a productivity level of 655 kg/ ha (Singh *et al*., 2021). It has a distinct prominence in rainfed agriculture due to its significant soil binding ability. This is a major pulse crop in

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Jammu region after Rajamash. It was cultivated over an acreage of 12.955 thousand hectares in the Jammu division of the UT of Jammu and Kashmir during 2016-17, yielding 57.077 thousand quintals (Anonymous, 2017). The study of genetic architecture is a fundamental need to intensify the productivity of a specific crop. Understanding the inheritance pattern of yield and yield contributing traits is a precondition in yield enhancement breeding programmes and it is estimated through the computation of genetic variability parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance. Yield is the end product of interaction among different attributing traits and selection is practiced on these characters to increase the grain yield in urdbean. The genetically inherited fraction of variations is crucial for improvement of economically important traits like yield and it is estimated throughparameters such as heritability and genetic advance. Heritability in broad sense offers insights into the additive and non-additive genetic effects on the manifestation of characters. However, heritability coupled with genetic advance are more considerable than genetic advance alone to comprehend the ultimate effect of the best individuals (Johnson *et al*., 1955). Grain yield is a complex biometrical trait which is driven by polygenes and affected by a number of yield attributing variables, either directly or indirectly. The trait association studies demonstrate how different yield attributes influence grain yield. The correlation of coefficient evinces the link between traits, but does not provide the extent of alteration in both. The degree of influence of one variable on the other is determined by path analysis. Therefore, rapid improvement in grain yield is expected to result if selection is practiced for its component traits. In order to formulate selection criteria to enhance the grain yield of urdbean genotypes, the present study was executed to assess the important tools *viz*., genetic variability parameters, correlation coefficients and path analysis.

Material and Method

The present research was carried out during *Kharif* season of 2020 at three different localities of Jammu division, namely Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Main Campus,Chatha, Jammu, Advanced Centre for Rainfed Agriculture (ACRA), Rakh Dhiansar and Pulse Research Sub-Station, Samba. Twenty urdbean genotypes namely DUS19, PGRU99022, Mash 479, PLU499-52, Mash 338, UH82 14, PL4158, PU19, No. 40, IPU02-43, T9, UH86-4, STTZ834, Mash 114, SPS38, NKD4-2, IPU96-16, IPB96-6, PU 31 (C) and Uttara (C) constituted the experimental material that originated from diverse locations of the country. This experimental material was received from the ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh and maintained at PRSS, Samba. Genotypes Mash 479, Mash 338 and Mash 114 were developed by PAU, Ludhiana, IPU02-43, IPU96-16 and Uttara were developed by IIPR, Kanpur, PU 19 and PU 31 developed at GBPUA&T, Pantnagar. The experimental material was set up in Randomized Complete Block Design and replicated three times with plot size of 2 x 1.20 m^2. Each plot was divided into four rows. The spacing of 30 cm between lines and 10 cm between plants was maintained. The seeds were placed by hand at a depth of around 5 cm beneath the soil surface. A consistent set of cultural and agronomic practices was put in place to ensure a healthy crop. Thirteen morphological and physiological traits *viz*., days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 1000 grain weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%) were taken into consideration for the present study. Data were collected forsuch traits on five plants chosen at random in each plot of each replication as well as observations on days to 50 per cent flowering and days to maturity on a plot-by-plot basis. The data were statistically interpreted using the mean values.The coefficients of variation as well as heritability were computed as per Burton's (1952) formulae. Expected genetic advancewas assessed using a formula purposed by Johnson *et al*. (1955). Correlation coefficients attributed to genotype, phenotype and environment were derived using the corresponding constituents of variances and co-variances as per the approach introduced by Fisher in 1954 and Al-Jibouri *et al*., in 1958 as well as the equation proposed by Singh and Chaudhary in 1977. The coefficients of path were computedusingthe series of algorithm proposed by Dewey and Lu (1959).

Results and Discussion

Results revealed that mean sum of squares due to replication were non-significant, although sum of squares due to genotype were highly significant for all the traits considered, indicating that genotypes varied significantly and could be exploited in future breeding programmes through selection for traits under study (Table 1). These findings are in consonance with those described inmungbean (Ramkisanrao, 2017) and green gram (Desai *et al.,* 2020). The success of any breeding programme depends upon the extent of genetic variability present in the base population and it is essential to subject a population to selection for improving a particular trait.

The estimates of genetic variability parameters for all thirteen traits are illustrated in Table 2. With the exception of days to 50 percent flowering and days to maturity, the present investigation found a high to moderate magnitude of coefficients of variation due to genotype and phenotype for the majority of the yield attributes considered. The highest genotypic and phenotypic coefficients of variation were observed for number of primary branches per plant followed by number of pods per plant, number of clusters per plant, number of pods per cluster and number of seeds per pod;suggesting possibility of improvement in these traits through direct selection. These outcomes are in close agreement with the study of Kumar *et al*. (2014). Traits such as 1000 grain weight, grain yield per plant, pod length and biological yield per plant exhibited moderate range (10-20%) whereas days to 50 per cent flowering and days to maturity had low (<10%) estimates for genotypic and phenotypic coefficients of variation.

The computed coefficients due to phenotype were observed to be higher than genotypic coefficients (Figure 1). On the basis of this result, it is concluded that the environment had an impact on the expression of these traits, but the deviations were non-significantfor most of the traits studied, inferring that the environment had the modest impact on the manifestation of these variables and, therefore, selection for improvement of certain characters relying on phenotype would be beneficial to improve the urdbean genotypes studied. Kumar *et al*. (2014); Yashoda *et al*. (2016); and Kumar *et al*. (2020) have previously published analogous studies in urdbean. Days to 50 per cent flowering and days to maturity had the smallest magnitudes of both coefficients of variation. Plant height exhibited lower magnitude while grain yield per plant showed moderate magnitude of genetic coefficient of variation. Desai *et al*. (2020) reported results which substantiate the outcomes of present study for these traits.

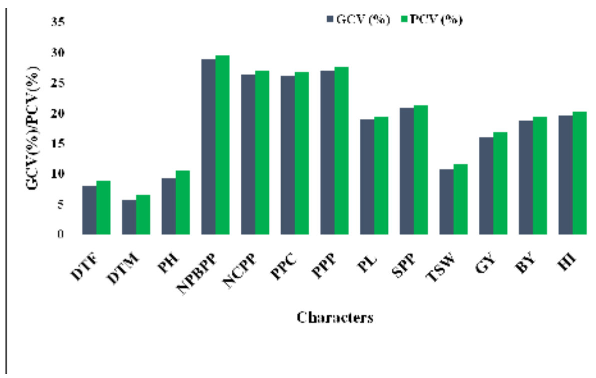

Fig. 1. Estimates of genotypic and phenotypic coefficient of variation

High heritability (broad sense) estimates were recorded for majority of quantitative traits studied with heritability percentage exceeding seventy five as illustrated in the Figure 2. These results are in agreement with those of Kumar *et al*. (2014), Priya *et al*. (2018) and Chowdhury *et al.* (2020) for majority of the morpho-physiological traits. The maximum heritability was estimated for number of pods per plant (96.38 %) preceded by number of primary branches per plant (96.30 %), number of pods per cluster (96.13 %), number of clusters per plant (96.08 %), number of seeds per pod (94.73 %), pod length (93.91 %), harvest index (93.79 %), biological yield per plant (93.51 %), grain yield per plant (92.25 %) and 1000 grain weight (84.88 %), indicating that selection for these traits may be useful for achieving higher genetic

Table 1. Environment wise analysis of variance for different morpho-physiological traits in Urdbean (*Vigna mungo* L.)

Env.	Source	d.f.	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	1000 grain weight (cm)	Grain yield/ plant (g)	Biological yield/ plant (g)	Harvest index (%)
Research Farm, Chatha, SKUAST-Jammu (Irrigated)															
E I	Replication	2	0.17	30.22	38.93	0.03	0.36	0.03	1.36	0.10	0.18	0.69	0.02	0.20	0.76
	Genotype	19	51.46**	43.41**	107.74**	5.55**	15.66**	3.89**	306.93**	2.11**	2.24**	44.79**	1.57**	38.22**	36.04**
	Error	38	6.34	9.56	13.75	0.09	0.18	0.04	4.70	0.05	0.07	2.95	0.03	0.79	0.84
Experimental Farm, Advance Centre for Rainfed Agriculture, Dhiansar (Rainfed)															
E II	Replication	2	1.70	0.84	0.66	0.02	0.02	0.03	8.61	0.06	0.01	0.24	0.01	1.05	4.33
	Genotype	19	52.18**	84.13**	132.94**	5.19**	11.67**	4.27**	331.09**	2.03**	2.57**	41.84**	1.68**	41.00**	59.58**
	Error	38	3.70	6.96	10.84	0.05	0.17	0.05	4.53	0.05	0.05	2.27	0.05	1.07	1.48
Pulses Research Sub-Station, Samba (Rainfed)															
E III	Replication	2	3.16	0.98	25.13	0.09	0.96	0.16	5.50	0.02	0.02	1.69	0.07	2.36	1.80
	Genotype	19	76.79**	104.13**	112.66**	5.22**	14.04**	3.97**	331.05**	2.13**	2.56**	39.11**	1.60**	39.04**	51.03**
	Error	38	1.53	5.37	11.56	0.05	0.24	0.05	6.02	0.03	0.04	3.40	0.06	1.20	1.45

*, ** significant at 5 percent and 1 percent level, respectively

Table 2. Pooled analysis of variance for different morpho-physiological traits in Urdbean (*Vigna mungo* L.) across the environments

Source of variation	**d.f.**	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	No. of cluster per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	1000 grain weight (cm)	Grain yield/ plant (g)	Biological yield/ plant (g)	Harvest Index (%)
Replication	6	0.19	18.23	48.78	0.12	0.97	0.05	13.85	0.16	0.08	2.33	0.04	1.48	6.81
Genotypes	19	364.02**	415.71**	420.97**	24.28**	39.56**	12.60**	1079.75**	8.19**	9.04**	79.36**	8.99**	122.23**	112.88**
Environments	2	114.01*	156.55*	239.00*	9.55	29.57*	7.38	792.58**	4.16**	5.61**	96.43**	3.38*	89.18**	112.73**
Genotype XEnvironment	38	33.21**	37.56**	57.16**	3.21**	5.90**	2.38**	88.25**	1.06**	0.88**	14.65**	0.74**	14.54**	16.96**
Pooled error	114	3.81	7.29	11.91	0.06	0.20	0.05	4.94	0.04	0.05	2.78	0.05	1.02	1.23
Total	177	25.73	34.24	50.60	2.01	4.98	1.46	118.34	0.79	0.92	16.09	0.65	14.61	17.71

*, ** significant at 5 percent and 1 percent level, respectively

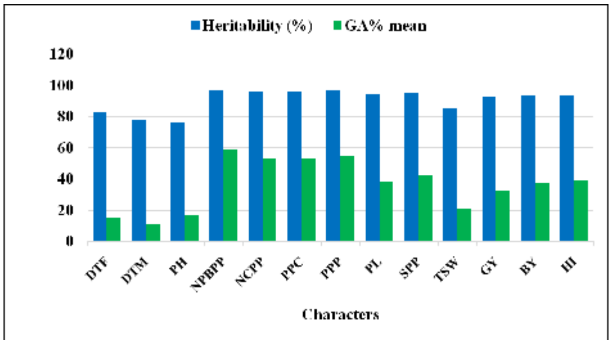

Fig. 2. Estimates of heritability and genetic advance as percentage of mean

gains. Johnson *et al*. (1955) found that estimate of heritability value together with genetic advance are more important in predicting the expected progress to be achieved through selection. With the exception of days to 50 percent flowering, days to maturity and plant height, rest of the traits in the current research had high estimates of heritability associated with high genetic advance as percentage of mean, showing additive gene effect and simple selection will be effective for their improvement. Kumar *et al*. (2014); Priya *et al*. (2018) and Kumar *et al*. (2020) found comparable results. Days to 50 per cent flowering, days to maturity and plant height demonstrated high heritability coupled with moderate genetic advance as percentage of mean. Ozukum and Sharma (2017) and Aftab *et al*. (2018) came up with the similar conclusions with respect to all these traits.

Table 3 depicts the genotypic and phenotypic coefficients of correlation for thirteen morpho-physiological traits across the environments. Estimates of correlation due to genotype were generally higher than phenotype, yet both were in the same direction. In present study, majority of morpho-physiological traits exhibited positive and significant correlation with grain yield per plant at both levels. It suggested that selection for increase in growth related traits viz. pod characters and seed characters might lead to high grain yield in urdbean. Equivalent findings were proposed by Sivade *et al*. (2011),Gowsalya *et al.* (2016), Sathvik and Lal (2018) and Sridhar *et al*. (2020). Apart from plant height, all of the other twelve yield attributing variables had positive and significant interactions with each other. At the phenotypic level, plant height had positive but non-significant correlation with number of pods per cluster and number of pods per plant. These findings are in line with the research findings of Shivade *et al*.(2011), Gowsalya *et al*. (2016) and Tank and Sharma (2019) in various pulse crops.

On the basis of correlation studies, more emphasis needs to be given on number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod, 1000 grain weight and harvest index as yield contributing characters based on their strong correlation with seed yield per plant.

Table 3. Pooled estimates of genetic parameters for different morpho-physiological traits in Urdbean (*Vigna mungo* L.) across the environments

Genetic Parameters	Mean	Range		P.C.V.	G.C.V.	Heritability	Genetic	Genetic
		Min.	Max.			(%)	advance	advance
				(%)				(%) Mean
Days to 50% flowering	52.7	46.22	60.66	8.94	8.13	82.84	8.04	15.25
Days to maturity	85.54	79.78	92.78	6.63	5.83	77.35	9.04	10.56
Plant height (cm)	66.42	57.52	73.99	10.62	9.26	76.06	11.05	16.64
No. of branches per plant	4.35	2.87	6.25	29.47	28.92	96.30	2.54	58.46
No. of clusters per plant	8.38	6.00	11.64	26.95	26.42	96.08	4.47	53.34
No. of pods per cluster	4.21	2.84	5.94	26.78	26.26	96.13	2.23	53.03
No. of pods per plant	42.31	23.45	57.07	27.58	27.08	96.38	23.17	54.76
Pod length (cm)	4.37	3.37	5.65	19.54	18.93	93.91	1.65	37.79
No. of seeds per pod	4.61	3.43	5.67	21.45	20.88	94.73	1.93	41.87
1000 grain weight (g)	36.52	31.6	42.71	11.74	10.82	84.88	7.50	20.53
Grain yield/ plant (g)	4.61	3.53	5.71	16.84	16.17	92.25	1.47	32.00
Biological yield/plant (g)	20.37	15.48	26.00	19.46	18.82	93.51	7.64	37.49
Harvest index (%)	22.03	17.72	29.43	20.21	19.57	93.79	8.6	39.04

The coefficients of correlation must be partitioned into the indirect and direct effects in order to assess the extent of influence of explanatory or predictor attributes on the dependent or response variable, grain yield per plant in this instance (Table 4). Path analysis study revealed that days to 50 per cent flowering, plant height, number of clusters per plant, number of seeds per pod and harvest index exhibited positive direct effect on grain yield per plant at genotypic level whereas 1000 grain weight showed positive direct effect on grain yield per plant at genotypic and phenotypic level. These findings are in line with the work of Shivade *et al*. (2011); Arya *et al.* (2017); Rajasekhar *et al*. (2017), Partap *et al.* (2019), Saran *et al.* (2020) and Shuban *et al.* (2020). This suggests a true relationship between these traits with seed yield per plant and direct selection for these traits would be rewarding for grain yield improvement in urdbean.

Days to 50 percent flowering was positive and significantly correlated with grain yield per plant as well as it had positive genotypic direct effect. Large positive association was reinforced by its indirect influences *via* number of primary

Table 4. Pooled Phenotypic (r_p) and Genotypic (r_g) correlation coefficient analysis for grain yield with other morpho-physiological traits across the environments

Characters		Days to	Plant maturity (cm)	No. of height branches per plant	No. of primary per plant	No. of clusters per cluster	No. of pods per plant	Pod pods (cm)	No. of length per pod	1000 grain seeds weight (g)	Biological Yield/ plant (g)	Harvest Index (%)	Grain yield/ plant (g)
Days to 50% flowering	r_g	0.890**	0.645**	0.827**	0.807**	0.968**	0.690**	0.938**	0.913**	0.752**	0.760**	0.943**	0.711**
	r_p	0.754**	0.188	0.649**	0.726**	0.738**	0.555**	0.746**	0.647**	0.590**	0.432**	0.741**	0.569**
Days to maturity	r_g		0.585**	0.993**	0.875**	0.802**	0.908**	0.997**	0.866**	0.819**	0.927**	0.729**	0.864**
	r_p		0.411**	0.689**	0.676**	0.679**	0.570**	0.712**	0.742**	0.725**	0.394**	0.607**	0.636**
Plant height (cm)	r_g			0.531**	0.385**	0.319*	0.303*	0.535**	0.406**	0.421**	0.631**	0.514**	0.454**
	r_p			0.496**	0.306*	0.22	0.22	0.392**	0.352**	0.414**	0.484**	0.330*	0.426**
No. of primary branches per plant	r_g				0.957**	0.927**	0.718**	0.970**	0.942**	0.996**	0.702**	0.926**	0.962**
	r_p				0.935**	0.863**	0.662**	0.895**	0.863**	0.863**	0.673**	0.864**	0.924**
No. of clusters per plant	r_g					0.962**	0.798**	0.966**	0.964**	0.729**	0.731**	0.950**	0.976**
	r_p					0.929**	0.757**	0.908**	0.895**	0.871**	0.706**	0.922**	0.904**
No. of pods per cluster	r_g						0.734**	0.911**	0.930**	0.995**	0.681**	0.927**	0.931**
	r_p						0.717**	0.832**	0.826**	0.808**	0.650**	0.907**	0.820**
No. of pods per plant	r_g							0.834**	0.868**	0.923**	0.630**	0.814**	0.895**
	r_p							0.797**	0.781**	0.725**	0.579**	0.787**	0.786**
Pod length (cm)	r_g								0.958**	0.848**	0.745**	0.971**	0.835**
	r_p								0.913**	0.847**	0.640**	0.888**	0.885**
No. of seeds per pod	r_g									0.998**	0.805**	0.976**	0.992**
	r_p									0.907**	0.660**	0.845**	0.857**
1000 grain weight (g)	r_g										0.814**	0.845**	0.934**
	r_p										0.638**	0.811**	0.917**
Biological Yield/ plant (g)	r_g											0.858**	0.720**
	r_p											0.809**	0.693**
Harvest Index (%)	r_g												0.989**
	r_p												**0.854****

*, ** significant at 5 per cent and 1 per cent level, respectively

branches per plant, 1000 grain weight and number of pods per plant. Large and significant positive association of days to maturity with grain yield resulted due to its indirect influences through days to 50 percent flowering, number of clusters per plant, 1000 grain weight, number of seeds per pod, plant height and harvest index at genotypic level as it had negative direct effect. The direct positive effect of plant height and its indirect influence *via* number of seeds per pod, days to 50 per cent flowering, number of clusters per plant, harvest index and 1000 grain weight resulted in positive correlation with grain yield per plant. The negative direct effect of number of primary branches per plant was nullified through its indirect impacts *via* days to 50 per cent flowering, number of seeds per pod, number of clusters per plant, harvest index and plant height which resulted in the positively significant association.

Large positive association of number of clusters per plant with grain yield per plant appearedto be due its indirect influences through days to 50 per cent flowering, harvest index, number of seeds per pod, 1000 grain weight and plant height. Number of pods per cluster had negative direct effect but large and positive correlation with grain yield per plant that was accompanied by its indirect influences through days to 50 per cent flowering,

Table 5. Pooled analysis of path coefficients of different morpho-physiological traits on grain yield at genotypic and phenotypic levelacross the environments

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	1000 grain weight (g)	Biological Yield/ plant (g)	Harvest Index (%)	Correlation coefficient with Grain yield/ plant
Days to 50% flowering	G	0.939	-0.195	0.304	-0.346	0.450	-0.795	-0.104	-0.817	0.504	0.347	-0.060	0.486	0.711**
	P	-0.065	-0.024	-0.022	0.4514	-0.045	-0.057	0.162	0.174	-0.263	0.322	0.072	-0.136	0.569**
Days to maturity	G	0.823	-0.179	0.275	-0.402	0.692	-0.183	-0.136	-0.464	0.317	0.369	-0.513	0.264	0.864**
	P	-0.049	-0.032	-0.047	0.479	-0.042	-0.053	0.167	0.166	-0.302	0.395	0.066	-0.111	0.636**
Plant height (cm)	G	0.606	-0.104	0.471	-0.179	0.554	-0.920	-0.045	-0.176	0.669	0.139	-0.710	0.151	0.454**
	P	-0.012	-0.013	-0.115	0.345	-0.019	-0.017	0.064	0.091	-0.143	0.226	0.081	-0.06	0.426**
No. of primary branches	G	0.964	-0.213	0.250	-0.337	0.377	-0.677	-0.108	-0.750	0.551	0.329	-0.104	0.681	0.962**
per plant	P	-0.042	-0.0223	-0.057	0.695	-0.058	-0.067	0.194	0.208	-0.352	0.471	0.112	-0.158	0.924**
No. of clusters per plant	G	0.945	-0.210	0.181	-0.322	0.440	-0.778	-0.120	-0.631	0.587	0.340	-0.282	0.827	0.976**
	P	-0.047	-0.022	-0.035	0.650	-0.062	-0.072	0.221	0.211	-0.365	0.475	0.118	-0.169	0.904**
No. of pods per cluster	G	0.908	-0.197	0.150	-0.313	0.385	-0.801	-0.110	-0.074	0.531	0.328	-0.167	0.289	0.931**
	P	-0.048	-0.022	-0.025	0.600	-0.058	-0.078	0.210	0.194	-0.336	0.441	0.108	-0.166	0.820**
No. of pods per plant	G	0.648	-0.162	0.142	-0.242	0.148	-0.120	-0.150	-0.394	0.429	0.305	-0.707	0.997	0.895**
	P	-0.036	-0.019	-0.025	0.460	-0.047	-0.056	0.293	0.185	-0.318	0.395	0.097	-0.144	0.786**
Pod length (cm)	G	0.880	-0.196	0.252	-0.327	0.29	-0.630	-0.125	-0.071	0.177	0.346	-0.018	0.257	0.835**
	P	-0.048	-0.023	-0.045	0.622	-0.056	-0.065	0.233	0.233	-0.372	0.462	0.107	-0.163	0.885**
No. of seeds per pod	G	0.857	-0.190	0.191	-0.318	0.388	-0.69	-0.131	-0.899	0.646	0.330	-0.183	0.987	0.992**
	P	-0.042	-0.024	-0.041	0.600	-0.056	-0.064	0.228	0.212	-0.407	0.494	0.110	-0.155	0.857**
1000 grain weight (g)	G	0.987	-0.200	0.198	-0.336	0.481	-0.873	-0.139	-0.265	0.544	0.330	-0.205	0.411	0.934**
	P	-0.038	-0.024	-0.048	0.600	-0.054	-0.063	0.212	0.197	-0.369	0.545	0.106	-0.149	0.917**
Biological Yield/ plant (g)	G	0.713	-0.166	0.297	-0.237	0.053	-0.467	-0.095	-0.031	0.326	0.269	-0.210	0.268	0.720**
	P	-0.028	-0.013	-0.056	0.468	-0.044	-0.050	0.170	0.149	-0.269	0.348	0.167	-0.148	0.693**
Harvest Index (%)	G	0.885	-0.202	0.242	-0.312	0.367	-0.677	-0.122	-0.952	0.606	0.645	-0.327	0.836	0.989**
	P	-0.048	-0.020	-0.038	0.601	-0.057	-0.070	0.230	0.207	-0.344	0.442	0.135	-0.183	0.854**

Genotypic Residual effect = 0.0950 Phenotypic Residual effect = 0.0385 *, ** significant at 5 per cent and 1 per cent level, respectively number of seeds per pod, number of clusters per plant, 1000 grain weight, harvest index and plant height. Number of pods per plant had positive significant association with grain yield per plant due to its indirect influences through harvest index, days to 50 per cent flowering, number of seeds per pod, 1000 grain weight, number of clusters per plant and plant height, although it had negative direct effect. Pod length and grain yield per plant had positive significant correlation but it implied negative genotypic direct effectat genotypic level that was nullified by its indirect impacts through days to 50 per cent flowering, 1000 grain weight, number of clusters per plant, plant height, harvest index and number of seeds per pod.

Number of seeds per pod had positive genotypic direct effect with grain yield per plant and its indirect influences through harvest index, days to 50 per cent flowering, number of clusters per plant, 1000 grain weight and plant height played a key role along with direct effect to create positive association. 1000 grain weight had positive and significant correlation with grain yield per plant combined with positive direct effect. Negative direct effect of biological yield per plant was negated by its indirect influence through days to 50 per cent flowering, number of seeds per pod, plant height, 1000 grain weight and harvest index which appeared to have positive significant correlation with grain yield per plant. Harvest index had positive and significant association with grain yield per plant that was mainly due to its direct effect as well as its indirect influence through days to 50 per cent flowering, 1000 grain weight, number of seeds per pod, number of clusters per plant and plant height. These results are supported by the findings of Arya *et al.* (2017), Partap *et al*. (2019), Chowdhary *et al*. (2020), Desai *et al*. (2020) and Subhan *et al.* (2020)

Conclusion

The variations owing to genotypes were highly significant for all the yield attributes in environment wise variance analysis, illustrating that there was a significant variability among them. For number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod, high estimates of coefficient of variation owing to genotype and phenotype were enumerated. With the exception of days to 50 per cent flowering, days to maturity and plant height, the remaining characters signified high heritability paired with high genetic advance as percentage of mean. The analysis of coefficients of correlation showed that grain yield per plant had a positively significant association with all twelve yield contributing traits considered. These findings emphasized the usefulness of these characteristics in assessing the grain yield per plant of urdbean genotypes. Path analysis studies revealed that some traits *viz*., days to 50 per cent flowering, plant height, number of clusters per plant, number of seeds per pod, weight of 1000 grains and harvest index were key features to enhance grain yield per plant of urdbean genotypes as they had significant positive genotypic direct effect on grain yield.

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