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Genetic Association and Assessment of Genetic Variability of Urdbean [*Vigna mungo* (L.) Hepper] Genotypes based on Morphological Traits

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ABSTRACT

Background: The present investigation was undertaken to examine the genetic variability and association between morphological traits among the 22 advanced lines including 3 checks of urdbean diverse collections. Genetic variability and association studies play an important role in developing a new genotype. The urdbean productivity remains low in India because of the low genetic base for yield improvement, limited amount of variability for yield traits, poor ideotype of urdbean plant, inadequate management of the crop, weed infestation and susceptibility to abiotic and biotic stresses. Genetic variability is the most important factor in the success of any crop improvement programme.

Methods: An experiment was laid out in a completely randomized block design with three replications at Regional Agricultural Research Station, Sagar, Madhya Pradesh in high productive black cotton soils during *Kharif* 2014 on 22 advance lines including 3 checks. Each plot comprised 6 rows of 4 meter length with 30 cm distance between rows and 10 cm between plants.

Result: The study found that the mean amounts of squares due to the genotype were very significant for all morphological characteristics except 100 seed weight. High estimates of heritability and genetic advance were recorded for seed yield, days to maturity and plant height indicating the role of additive gene effects with little environmental influence in determining these traits and simple phenotypic selection can be effective. The results also indicated improvement through direct selection for these traits can increase directly the grain yield in Urdbean.

Key words: Association, GCV, Genetic variability, Germplasm, PCV, Urdbean.

INTRODUCTION

Urdbean is one of the important ancient pulse crop. Archaeological surveys have studied that it was grown domestically since 2200 BC. It is a nutritious, short-duration crop with wide adaptability extensively cultivated in India. In India, the Urdbean is grown on 56.02 lakh hectares with a production of 30.56 lakh tonnes. But the productivity in India is 546 kg per hectare (Source: DES, Ministry of Agri and FW, DAC and FW, Govt. of India 2018-19) which is very low when compared with other pulses. To increase productivity and production of this crop, the development of new high yielding genotypes is a prime goal of urdbean breeding. It is a good source of digestive protein (25-28%), 1-1.5% oil, 3.5-4.5% fiber, 4.5- 5.5 ash and 62-65% carbohydrate on dry basis. It is a rich in phosphoric acid. Therefore, urdbean is suitable for alleviating malnutrition in India. The grains of Urdbean (whole or split) are used as dal or made into flour. Various preparations are made from its flour, *e.g.* papad, barian, dosa, vada *etc.* Urdbean is low need for inputs and have the capacity to improve soil fertility by fixing atmospheric nitrogen. It will be increase fertility level of soil, production and economic returns of farmers. urdbean productivity remains low in India because of its low genetic base for improvement of high yielding genotypes, absence of variability, poor ideotype of urdbean plant, poor management of crop, weed infestation and susceptibility to biotic and abiotic stresses (Souframanien and Gopalakrishnan 2004). Genetic variability is most important factor of success of any crop improvement programme. The study of genetic variability present in different characters and their nature of heritability are the pre-requisites for an efficient crop improvement programme. Therefore, the present study was attempted to assess the genetic variability,

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heritability, genetic advance, GCV, PCV and correlation in morphological characters in 22 Urdbean genotypes.

MATERIALS AND METHODS

An experiment was conducted in a completely randomized block design with three replications at Regional Agricultural Research Station, Sagar, Madhya Pradesh in black cotton soils during *kharif* 2014. Each plot comprised 6 rows of 4 meter length with 30 cm distance between rows and 10 cm between plants. The all good agronomic practices for crop management were applied. Twenty Two Urdbean Advance lines with 2 national checks were used in the experiment obtained from Indian Institute of Pulses Research, Kanpur (U.P.). These lines were developed at different part of India for the cultivation (Table 1).

The data on eight morphological characters *viz*., days to 50% flowering, days to maturity, plant height (cm), plant stand, no. of branches/plant, no. of pods/plant, 100 seed weight (g) and seed yield/plot were recorded.

Analysis of variance and correlation coefficients for the observations were calculated by web agri state package 2.0 online data analysis software developed by ICAR-Central Coastal Agricultural Research Institute. The estimation PCV and GCV were calculated according to the formula given by Burton and De Vane (1953) and Singh and Choudhary (1985)-

$$PCV = \frac{\sqrt{\sigma_P^2}}{X} \times 100 \quad GCV = \frac{\sqrt{\sigma_g^2}}{X} \times 100$$

The genetic advance (GA) was estimated by following Robinson *et al.* (1949) equation.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance for different quantitative traits of twenty two urdbean advance lines along with the checks revealed that the component of variance with the genotypes was significant at 1% level of probability in all the traits namely seed yield/plot (g), days to 50% flowering, maturity, plant stand, plant height (cm), number of branches/plant and number of pods/plant presented in Table 2. The variation among these traits can be utilized in further breeding programme for improvement and selection of traits. Whereas, 100 seed weight (g) showed less variance and improvement for such trait through simple selection may be limited in the present investigation. Therefore, genes for such important trait may be utilized from other source such as from germplasm and other diverse genotypes. Similar results were reported by Punia *et al.,* (2013) and Ghafoor *et al.* (2001).

Study of mean and range

The Mean values of all eight quantitative traits were presented in Table 3. The range of all the traits representing maximum and minimum values of quantitative traits were as brief below :

Seed yield g/plot were ranged from 885.7 to 268.3, days to 50% flowering were ranged from 42.3 to 34.3 days, days to maturity were ranged from 80.3 to 68.3, plant stand were ranged from 95.3 to 59.7, plant height (cm) were ranged from 57.9 to 26.7 cm, number of branches/plant ranged from 5.7 to 3.7, number of pods/plant showed range from 28.2 to 10.3 whereas 100 seed weight (g) were ranged from 5.7 to 4.7.

Estimates of PCV and GCV

Generally, the phenotypic coefficients of variability were higher than corresponding genotypic coefficients of variability for the observed traits which indicates the impact of environment upon the traits (Table 3). The higher estimate of phenotypic and genotypic coefficient of variation (PCV and GCV *i.e*., more than 20%) were observed for number of pods per plant (37.5 and 30.0), followed by seed yield g/plot (31.7 and 30.1), plant height (cm) (19.1 and 17.1), with less difference between observed PCV and GCV estimates, indicating presence of exploitable genetic variance for these traits and suggested possible improvement through direct selection. Moderate phenotypic and genotypic coefficient of variation (10 to 19%) was observed for number of branches/plant (18.9 and 10.4) and plant stand (18.8 and 13.4), which suggested that there is considerable scope of improvement in these traits in desired direction through a selection processes. The low estimates of phenotypic and genotypic coefficient of variation were observed for the parameters 100 seed weight (g) (8.5 and 0.02), days to 50% flowering (8.0 and 7.4) and days to maturity (7.1 and 0.30), indicating the major role of genetic factors changing the expression of these traits. The above findings were accordance with the findings of Punia *et al*., (2013), Panigrahi *et al.,* (2014), Deepshika *et al.,* (2014), Babu *et al*., (2016), Singh *et al.,* (2016), Priyanka *et al*., (2016) and Hemalatha *et al.,* (2017), Chaithanya *et. al.,* (2019).

Heritability and genetic advance as a % of mean

Heritability estimates along with genetic advance were more helpful than heritability alone in predicting the resultant gain under selection of best individual. Heritability and genetic advance as percent of mean were estimated to get a clear picture for improvement in various traits through selection. In the results of the present investigation, high heritability were observed for the traits (>70%) for days to maturity (91%), followed by seed yield g/plot (90%), days to 50% flowering (87%) and plant height (cm) (79%). the high value of heritability indicates that though the trait is least influenced by environmental effect, the selection for such character may not be useful because heritability is the estimate of both fixable and non-fixable variances. Whereas, moderate heritability (50-70%) were observed in plant stand (51%) and number of pods/plant (50%). The lowest estimates of heritability were observed in number of branches/plant (31%) and 100 seed weight (g) (5%) this reveals that character is

Table: 1 List of Urdbean lines selected for experiment.

Genotypes	Pedigree	Source
KU 96-3 (Ch)	PU 19 × NP 21	CSAUT, Kanpur
NUL 7(Ch)	NULS 11-2 × NULS 86-2-1	Nirmal Seeds, Pachora
NDUK 13-4	NDU 25-4 × Azad 1	NDUAT, Faizabad
PU 11-14	PU 19 × KU303	GBPUAT, Pantnagar
IU 02-1-3	KU 96-3 × TRU 05-2	IGKVV, Raipur
TU 67	TAU 1 × KU 96-3	BARC, Trombay Mumbai
DKU 11	KU 59 × UL 338	RWRC, Malan, HP
NDUK 13-6	Pant U 31 × NDU 1	NDUAT, Faizabad
PU 09-37	PU 19 × KU 96-3	GBPUAT, Pantnagar
NUL 244	NUL 7 × NUL 138	Nirmal Seeds, Pachora
AKU 11-8	TAU 1 × Mash 1008	PDKV, Akola
MU 44	Biswas × BDU 1	MSS Ltd, Akola
KU 13-01	Shekhar 3 × Azad 2	CSAUT, Kanpur
AKU 10-6	TAU 1 × Pant U 31	PDKV, Akola
LBG 791	Pure line sel. From Pant U 31	ANGRAU, Hyderabad
MU 06	Local Sel. × T 9	MSS Ltd, Akola
VBG 11-31	ADT 5 × *Vigna syl.*	TNAU, Coimbatore
VBG 11-016	VBN 5 × VBG 04-001	TNAU, Coimbatore
COBG 10-06	COBG 67 × ADT 5	TNAU, Coimbatore
SBG 47	UG 157 × PDB 88-31	ARS, Shillongani
KUG 715	KUG 50 × KUG 15-1	PAU, Ludhiana
KU 96-7	PU 35 × Azad 1	CSAUT, Kanpur

Ch: check.

Table 2: Analysis of variance for 8 different quantitative traits of 22 Urdbean advance lines with checks.

Source of variation	Degree of freedom	Mean sum of squares							
		Seed yield g/plot	Days to 50% glowering	Maturity	Plant stand	Plant height(cm)	No. of branches/ plant	No. of pods/ plant	100 Seed weight (g)
Replications	2	4707.0	0.5	1.8	627.7	6.8	1.5	7.3	0.1
Genotypes	21	81529.7**	16.9**	52.0**	338.4**	143.7**	1.0*	68.4**	0.2
Error	42	4386.2	1.2	2.4	108.7	16.4	0.5	22.7	0.2
Sem±		38.2	0.6	0.9	6.0	2.3	0.4	2.7	0.2
CD (P=0.05%)		108.7	1.8	2.6	17.1	6.7	1.2	7.8	0.7
CV		10.1	2.9	2.1	13.1	8.7	15.8	26.5	8.3

**Highly significant at 1% and * significant at 5% level of significance.

Table 3: Descriptive statistics for 8 quantitative traits among 22 Urdbean advance lines with checks.

Character	Mean	Range		PCV	GCV	Heritability	GA %
		Min.	Max.	%	%	%	over mean
Seed yield g/plot	653.20	268.3	885.7	31.7	30.1	90	58.7
Days to 50% flowering	37.73	34.3	42.3	8.0	7.4	87	14.3
Maturity	73.58	68.3	80.3	7.1	6.8	91	13.3
Plant stand	79.70	59.7	95.3	18.8	13.4	51	19.8
Plant height (cm)	46.77	26.7	57.9	19.1	17.1	79	31.3
No. of branches/plant	4.71	3.7	5.7	18.9	10.4	31	11.9
No. of pods/plant	17.99	10.3	28.2	37.5	30.0	50	38.8
100 seed weight (g)	5.12	4.7	5.7	8.5	0.02	.05	0.8

Table 4: Estimate of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for quantitative traits in Urdbean advance lines with checks.

Character	Seed yield/ plot(g)	Days to 50% flowering	Maturity	Plant stand	Plant height (cm)	No. of branches/ plant	No. of pods/ plant	100 Seed weight (g)
Seed yield/plot (g)	1	-0.661**	-0.463	0.297	-0.460**	0.381	0.427	0.013
Days to 50% flowering	-0.804**	1	0.210	-0.195	0.464**	-0.169	-0.408	0.057**
Maturity	-0.536	0.302	1	-0.232	0.149	-0.207**	-0.040**	-0.166**
Plant stand	0.561	-0.375	-0.234	1	0.192	0.011	-0.138	-0.137
Plant height (cm)	-0.572**	0.582**	0.235	0.346	1	-0.146	-0.241	0.278
No. of branches/plant	0.829	-0.427	-0.392**	-0.433	-0.635	1	0.414	0.003
No. of pods/plant	0.560	-0.813	-0.043**	0.052	-0.357	0.879	1	0.060
100 seed weight (g)	-0.055	0.565**	-0.570**	0.267	0.925	0.167	-0.458	1

**Highly significant at 1% and 5% level of significance.

highly influenced by environmental effect and genetic improvement through selection will be difficult due to masking effect of environment. Similar results were reported by Pushparani *et al.* (2013) and Hemalatha *et al*., (2017)

Higher estimates of genetic advance as a % over mean (*i.e*., >15%) were observed in seed yield g/plot (58.7%), followed by number of pods/plant (38.8%), plant height (31.3%) and plant stand (19.8%) this showed that character is governed by additive genes and selection will be rewarding. Moderate value of genetic advance as % over mean (10-15%) were observed in days to 50% flowering (14.3%), followed by days to maturity (13.3%) and number of branches/plant (11.9 %) and lowest value was observed in 100 seed weight (g) (0.80%). The lowest value suggestion utilization heterosis breeding for improvement of this trait as it is governed by non-additive genes. The results were in accordance with Usharani and Ananda kumar (2015) and Duddukur *et al*. (2017).

Hence, The high heritability and along with higher estimates of genetic advance over percentage of mean will be rewarding as likely it is governed by additive genes and selection will be effective for such observed traits *viz*., seed yield plot, number of pods/plant and plant height (cm). These findings were supported by Rolaniya *et al*., (2017). Although low estimates heritability and genetic advance over percentage of mean of were observed for 100 seed weight (g) indicates that selection will be ineffective as the trait is under high influence of environment.

Correlations with seed yield per plot

Genotypic correlation coefficients were higher than the phenotypic correlation coefficient for most of the traits. This indicates relatively less influence of environment in modifying the total expression of the genotypes, thus changes the phenotypic expression. The associations among seed yield-related traits and the pattern of influence on urd grain yield were investigated. At genotypic level seed yield per plot reported positive correlation with number of pods/plant (0.427), number of branches/plant (0.381), plant stand (0.297) and 100 seed weight (g) (0.013). Whereas, seed yield/plot (g) had significant negative correlation with days to 50% flowering (-0.661), days to maturity (-0.463) and plant height (cm) (-0.460) presented in Table 4. This suggesting that increasing in number of pods per plant and number of branches per plant will leads to increase in seed yield.

Whereas at phenotypic level seed yield per plot (g) were significantly positively correlated with number of branches per plant (0.829), plant stand (0.561), number of pods per plant (0.560) and it is significantly negatively correlated with days to 50% flowering (-0.804), plant height (cm) (-0.572), days to maturity (-0.536) and 100 seed weight (-0.055). Inter-correlation among other important traits *i.e.* days to 50% flowering had significant positive correlation with plant height (cm) (0.464) and days to maturity (0.210) and it had significant negative correlation with number of pods per plant (-0.408). The maturity in days had significant negative correlation with number of branches per plant (-0.207) and 100 seed weight (g) (-0.166). Plant height had positive association with 100 seed weight (g) (0.278) and it had negative association with number of pods per plant (-0.241). Whereas, number of branches per plant had significant positive association number of pods/plant (0.414). No. of pods per plant had significant and negatively correlated with days to flowering, while, 100 seed weight significant and positive correlation with days to flowering and negative correlation with maturity. Similar correlations were reported by Parveen *et al.,* (2011); Makeen *et al.,* (2009); Chauhan *et al.,* (2007) and Gupta *et al.,* (2001).

CONCLUSION

The above experimentation concludes that the higher estimate of phenotypic and genotypic coefficient of variation for number of pods per plant, seed yield/plot (g) and plant height (cm), revealed presence of exploitable genetic variance which can be improved through direct selection. Also the above traits reported high heritability coupled with high genetic advance over percentage of mean reporting selection will be rewarding and effective as traits were likely to governed by additive genes. The seed yield per plot has high significant and positive correlation with number of pods per plant and number of branches per plant suggesting that by selection and increasing number of these traits will directly increase the yield. Knowledge of the correlation assists a plant breeder in determining the methodology for improving a particular trait that is not readily suitable for direct selection. It also provides information on the correlated response to directional selection to predict genetic advancements and so, can be used as selection indices for the functioning of a more efficient selection program. Also, the above study was very useful for breeder in order to increase yield *per se* performance.

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