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Variability and Character Association in M_3 generation of Urdbean [*Vigna mungo* (L.) Hepper]

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ABSTRACT: Urdbean is an important pulse crop produced in all seasons but due to its cleistogamous nature creation of variability through artificial hybridization is difficult so mutation breeding occurs as the cleanest approach to induce desirable changes in the crop. Present study was undertaken to study genetic variability and character association in M_3 generation of Urdbean and to find out promising mutant lines for yield and protein content. Gamma rays irradiated 72 mutants from parent varieties PU 1 and CO 6 were evaluated in kharif, 2019 in Augmented design in four blocks along with five check varieties including parental varieties viz., PU 1, CO 6, MU 2, TPU-4, KU 96-3 in Research farm, Sri Karan Narendra Agriculture University, Jobner, Jaipur. Analysis of variance depicted sufficient genetic variability for most of the characters. Mutations were induced in both the directions. Heritability and Genetic advance were high for the characters seed yield per plant and pods per plant. GCV and PCV was highest for seed yield per plant. Most of the characters exhibited positive and significant correlation with seed yield per plant. Among the 72 mutants, five M_3 treatments were found to be best i.e. T2-19, T1-6, T1-1, T2-14 and T6-67 on the basis of seed yield per plant.

Keywords: Urdbean, Mutation, Variability, Character Association.

INTRODUCTION

Urdbean is an important annual pulse crop (2n=2x=22) which is native to Central Asia and belongs to family Leguminosae also known as black gram, urd or mash. It is rich in protein (25-28%) and also helps in improving soil fertility (Rao *et al*., 2021). The productivity of this crop is less due to narrow genetic diversity which hinders it in achieving raised yield levels. Influence of any character depends upon the extent of genetic variability present in a breeding population. Major research concern for urdbean in India involves development of high yielding, early maturing and MYMV resistance.

Creation of variability through pollination and artificial hybridization is very difficult in this crop as the flowers are cleistogamous and delicate to handle. But, artificial induction of variability by mutation breeding can be effectively utilized to generate new variability and it has been recognized as a valuable supplement to conventional breeding in crop improvement (Singh *et al.,* 2000; Deepalakshmi and Anandakumar, 2004; Wani and Khan, 2006 and Selvam *et al*., 2010).

Induced mutagenesis is an important tool in the hands of plant breeder to create variation in breeding material of a particular crop. A mutation is a sudden heritable change in the DNA in a living cell, not caused by genetic segregation or genetic recombination. Mutation induction coupled with selection remains the cleanest and most inexpensive way to create varieties by changing single characters without affecting the overall phenotype. When desired variation is available in different cultivars of a crop, its breeding objectives may be achieved through crossbreeding. Therefore, the present study was undertaken on urdbean mutants to study genetic variability, character association in M_3 generation of urdbean and to identify promising mutants.

MATERIAL AND METHODS

The experimental material consisted of 72 mutant lines of urdbean variety Pratap Urd 1 and CO 6 collected from BRNS project, ARS, Kota, Agriculture University, Kota. The progenies employed in the present investigation were derived from three dose of physical mutagen (gamma rays) *viz*., 200 Gy, 400 Gy and 600 Gy. The experiment was conducted at the experimental farm, Department of Plant Breeding & Genetics, Sri Karan Narendra College of Agriculture, Jobner (SKNAU, Jobner-Jaipur). It consists 72 M_2 lines and check varieties *viz.*, PU1, CO6, MU 2, TPU 4, KU 96-3 evaluated in Augmented Design during *kharif*, 2019.

Each genotype was sown in a plot of single row of 4-meter length. Row to row and plant to plant distance was maintained as 30 and 10 cm, respectively. All the agronomical practices were followed to raise a good and healthy crop. Observations were recorded for twelve quantitative traits *viz*., days to 50 per cent flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100 seed weight, seed yield per plant and protein content. Data were recorded on randomly selected five plants from each mutant line per replication and mean value was used for analysis. Data on days to 50 per cent flowering, days to maturity and 100-seed weight were however recorded on whole plot basis. The mean data were subjected to analysis of variance as per the method suggested by (Federer, 1956) calculated using statistical software, INDOSTAT. GCV and PCV values calculated by Burton (1952) and Johnson *et al.* (1955), heritability by Hanson *et al.* (1956), genetic advance by Johnson *et al*. (1955) and protein analysis by Micro-Kjaldahl method.

RESULTS AND DISCUSSION

A. Genetic variability studies

The analysis of variance revealed significant difference among the genotypes, indicating the presence of genetic variability for almost all the traits studied and further possibility of exercising selection (Table 1). Presence of narrow gap between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) but greater values of PCV for all the characters studied as in agreement with Gill *et al.* (2017) indicates that there is role of limited influence of environment in expression of these traits (Table 2). High values of GCV and PCV were visible for seed yield per plant and pods per plant indicates the presence of high genetic variability present in the population for the traits and direct selection will be effective for these traits. Whereas, moderate GCV and PCV values were observed for plant height (cm), branches per plant, seeds per pod, pods per cluster and cluster per plant. Low GCV and PCV were recorded in pod length, 100-seed weight and protein content. The findings were in consonance with Thamodharan *et al*. (2017), Priya *et al*. (2018), Usharani and Kumar (2016), Meshram *et al*. (2013), Mahesha and Lal (2017), Gill *et al*. (2017), Meshram *et al*. (2013), Kuralarasan *et al*., (2017), Asari *et al.,* (2019), Senthamizhselvi *et al*., (2019), Ramya *et al*., (2018), Partap *et al*. (2019), Pavan *et al*., (2019) and Ankur *et al*., (2019). Heritability (in broad sense) was high for all the characters (>60%) indicating that characters were least influenced by environment and selection of such characters may be useful. High heritability (in broad sense) interfused with high genetic advance was observed in seed yield per plant, pods per plant, seeds per pod, plant height, clusters per plant, pods per cluster and branches per plant. The above estimates offer the most favorable situations for further selection. It also indicates that the presence of additive gene action in the traits and further suggest reliable improvement in urdbean through selection for such traits.

Table 1: Analysis of variances in respect of different quantitative characters observed in M_3 progenies of urdbean.

Characters	D.F.	Plant height (cm)	Branches per Plant	Pods per Plant	Pod length (cm)	100-seed weight (g)	Seeds per pod	Seed yield per plant (g)	Pods per cluster	Clusters per plant	Protein (%)
Block	3	127.42**	0.03	01.78	0.01	0.22	0.10	0.07	0.05	0.05	00.29
Treatment	76	33.47*	0.33**	07.46**	0.14**	0.39*	1.31**	0.80**	0.23**	0.45**	03.78**
Check	4	71.05*	0.17**	05.68*	0.14**	1.09**	0.87*	0.86**	0.17**	0.28*	00.70*
Progenies	71	31.25	0.34**	07.55**	0.14**	0.36*	1.35**	0.79**	0.24**	0.46**	03.88**
Families	5	27.19	0.74**	20.98**	0.67**	0.45*	2.86**	5.36**	0.58**	1.86**	30.43**
Prog/Fam 1	11	15.19	0.33**	07.06**	0.06**	0.16	0.65*	0.65**	0.19**	0.45**	03.43**
Prog/Fam 2	11	16.08	0.33**	04.87**	0.08**	0.17	0.46	1.12**	0.12*	0.24*	01.22**
Prog/Fam 3	11	07.93	0.09**	03.29*	0.10**	0.31	0.77*	0.35**	0.15**	0.34**	01.34**
Prog/Fam 4	11	07.90	0.22**	04.02*	0.12**	0.33	0.40	0.25**	0.23**	0.32*	01.42**
Prog/Fam 5	11	17.29	0.38**	08.10**	0.11**	0.56*	4.29**	0.57**	0.18**	0.54**	03.22**
Prog/Fam 6	11	03.87	0.42**	07.14**	0.06**	0.12	0.59*	0.34**	0.16**	0.38**	03.13**
C v/s G	1	40.70	0.01	07.95*	0.01	0.03	0.01	0.91**	0.06	0.16	09.09**
Error	12	13.62	0.02	01.10	0.01	0.14	0.20	0.06	0.03	0.08	00.21

Table 2: Different variability parameters for different quantitative characters in M_3 generation of urdbean.

Sr. No.	Characters	Mean	Range	GCV	PCV	$h^2_{(bs)}$	GA	GA %
1.	Plant height (cm)	27.28	15.4-39.7	15.39	20.49	56.42	6.50	23.81
2.	Branches per plant	3.02	1.8-4.8	18.78	19.38	93.88	1.13	37.49
3.	Clusters per plant	3.09	1.3-4.53	20.08	22.02	83.19	1.17	37.73
4.	Pods per cluster	2.84	2.0-4.0	16.25	17.18	89.47	0.90	31.67
5.	Pods per plant	8.59	2.6-17	29.55	31.97	85.46	4.84	56.27
6.	Pod length (cm)	4.19	3.22-4.88	8.49	8.91	90.79	0.70	16.66
7.	Seeds per pod	4.60	2.74-11.28	23.27	25.24	85.03	2.04	44.21
8.	100-seed weight (g)	4.84	3.14-6.52	9.54	12.36	59.60	0.74	15.17
9.	Seed yield per plant	1.93	0.35-5.24	44.20	46.05	92.11	1.69	87.38
10.	Protein %	22.99	19.22-28.60	8.33	8.57	94.51	3.84	16.69

GCV = Genetic coefficients of variation; GA = Genetic advance; PCV = Phenotypic coefficients of variation; GA% = Genetic advance as % mean; $h^2_{(bs)}$ = Heritability (broad sense)

High heritability (in broad sense) coupled with moderate genetic advance was observed for pod length, 100-seed weight showing medium heritability with moderate genetic advance, and protein content was in agreement with Asari *et al*., (2019).

B. Association analysis

Selection cannot be relied on single character because most of the characters are polygenic in nature and they having the effects on each other. Correlation gives knowledge about magnitude and direction of association between two characters. It has been observed that phenotypic correlation coefficient was higher than their genotypic correlation coefficient counterparts in most of the characters (Table 3 and 4). This implies that the genetic causes affect the values of correlation. Most of the characters studied *viz.,* plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod and 100 seed weight were positively significant with seed yield per plant indicates that the selection based on these characters may result in high seed yield, which was in accordance with Sathees *et al*. (2019), Partap *et al*. (2019). On the other hand, the trait protein content is not significant with seed yield per plant which was in agreement with Asari *et al.* (2019).

Table 3: Correlation coefficients between different characters in M_3 generation of urdbean at phenotypic level.

	Plant height (cm)	Branches per plant	Cluster per plant	Pod per cluster	Pods per plant	Pod length (cm)	Seed per pod	100 Seed Weight (g)	Protein content	Seed yield per plant (g)
Plant height (cm)	1	0.221^{NS}	0.413**	0.291*	0.403**	0.553**	0.351**	0.480**	0.549**	0.622**
Branches per plant	0.221^{NS}	1	0.631**	0.670**	0.767**	0.001^{NS}	0.225^{NS}	0.019^{NS}	-0.071^{NS}	0.604**
Clusters per plant	0.413**	0.631**	1	0.511**	0.864**	0.211^{NS}	0.165^{NS}	0.143^{NS}	0.077^{NS}	0.728**
Pods per cluster	0.291*	0.670**	0.511**	1	0.845**	0.038^{NS}	0.254*	0.046^{NS}	-0.177^{NS}	0.623**
Pods per plant	0.403**	0.767**	0.864**	0.845**	1	0.146^{NS}	0.208^{NS}	0.109^{NS}	-0.019^{NS}	0.776**
Pod length (cm)	0.553**	0.001^{NS}	0.211^{NS}	0.038^{NS}	0.146^{NS}	1	0.380**	0.485**	0.226^{NS}	0.473**
Seeds per pod	0.351**	0.225^{NS}	0.165^{NS}	0.254*	0.208^{NS}	0.380**	1	0.298*	0.029^{NS}	0.546**
100 Seed Weight (g)	0.480**	0.019^{NS}	0.143^{NS}	0.046^{NS}	0.109^{NS}	0.485**	0.298*	1	0.254*	0.411**
Protein content	0.549**	-0.071^{NS}	0.077^{NS}	-0.177^{NS}	-0.019^{NS}	0.226^{NS}	0.029^{NS}	0.254*	1	0.105^{NS}
Seed yield per plant (g)	0.622**	0.604**	0.728**	0.623**	0.776**	0.473**	0.546**	0.411**	0.105^{NS}	1

* Significant at p = 0.05, ** Significant at = 0.01 and NS = Non-Significant

Table 4: Correlation coefficients between different characters in M_3 generation of urdbean at genotypic level.

	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm)	Seeds per pod	100 Seed Weight (g)	Protein content	Seed yield per plant (g)
Plant height (cm)	1	0.143^{NS}	0.246*	0.119^{NS}	0.171^{NS}	0.417**	0.239*	0.329**	0.453**	0.477**
Branches per plant	0.143^{NS}	1	0.635**	0.635**	0.754**	-0.022^{NS}	0.157^{NS}	0.037^{NS}	-0.104^{NS}	0.528**
Clusters per plant	0.246*	0.635**	1	0.567**	0.880**	0.179^{NS}	0.158^{NS}	0.039^{NS}	0.075^{NS}	0.731**
Pods per cluster	0.119^{NS}	0.635**	0.567**	1	0.858**	0.057^{NS}	0.192^{NS}	0.022^{NS}	-0.161^{NS}	0.622**
Pods per plant	0.171^{NS}	0.754**	0.880**	0.858**	1	0.101^{NS}	0.149^{NS}	0.018^{NS}	-0.045^{NS}	0.740**
Pod length (cm)	0.417**	-0.022^{NS}	0.179^{NS}	0.057^{NS}	0.101^{NS}	1	0.398**	0.343**	0.211^{NS}	0.492**
Seeds per pod	0.239*	0.157^{NS}	0.158^{NS}	0.192^{NS}	0.149^{NS}	0.398**	1	0.273*	0.063^{NS}	0.533**
100 Seed Weight (g)	0.329**	0.037^{NS}	0.039^{NS}	0.022^{NS}	0.018^{NS}	0.343**	0.273*	1	0.183^{NS}	0.312**
Protein content	0.453**	-0.104^{NS}	0.075^{NS}	-0.161^{NS}	-0.045^{NS}	0.211^{NS}	0.063^{NS}	0.183^{NS}	1	0.162^{NS}
Seed yield per plant (g)	0.477**	0.528**	0.731**	0.622**	0.740**	0.492**	0.533**	0.312**	0.162^{NS}	1

* Significant at p = 0.05, ** Significant at = 0.01 and NS = Non-Significant

CONCLUSIONS AND FUTURE SCOPE

Physical mutagens may effectively be used to induce desirable mutants for improvement of yield potential in urdbean. Variable frequencies of mutants were induced in response to different dose of mutagen (200 Gy, 400 Gy and 600 Gy) and such frequencies were more in PU 1 as compared to CO 6 indicating diverse genetic base and higher sensitivity of PU 1 to gamma irradiation. 200 & 400 Gy dose was found to be the most effective in parent variety PU 1 whereas in case of CO 6, 600 Gy dose was the most effective. After finding out the results it was concluded that M_3 progenies showing best yielding ability were T_2-19, T_1-6, T_1-1, T_2-14 and T_6-67 indicates lower concentrations (200 Gy & 400 Gy) of mutagen were prominent, therefore further breeding may concentrate on these mutagen doses.

Conflict of Interest: The authors declare no conflict of interest exist for the present research paper

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