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Research Article

Genetic variability and diversity analyses in Electron Beam and Gamma Ray induced mutants for yield attributing traits in urdbean [*Vigna mungo* (L.)]

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Abstract
An investigation was carried out in Electron Beam and Gamma Ray induced thirty eight Urdbean mutants with two checks to explore the genetic variability and diversity. Based on the overall performance of yield attributing traits, mutants *viz*., ACM-014-021, ACM-015-015, ACM-015-011, ACM-015-025, ACM-015-026 and ACM-014-007 were found to be superior and could be used in breeding programme for advancing yield coupled with batter quality. High phenotypic and genotypic coefficients of variation were recorded towards single plant yield and peduncle length. High heritability along with high genetic advance was noticed for base length, peduncle length, clusters count per plant, pods count per plant and seed yield per plant. The experiment on correlation showed that seed yield per plant recorded high positive correlation with pods count per plant, pod length, clusters count per plant and seeds per pod. Genetic diversity analysis resulted in grouping of forty genotypes *viz.,* 38 mutants and two varieties into two clusters. Cluster I had 16 mutant lines along with VBN (Bg) 4 variety and cluster II had 22 mutant lines along with MDU1 variety. D^2 cluster analysis based on eleven quantitative characters resulted in five groups with cluster V containing maximum of sixteen mutants along with two check varieties followed by clusters I with 15 mutants, cluster IV with three mutants and cluster II and III with two mutants each. The cluster *per se* performance revealed that cluster III recorded the maximum mean values for branches per plant, clusters, pod numbers per plant, quantity of seeds per pod, test weight, seed yield per plant and plant height. Cluster IV had the highest mean value for base length and pod length. Cluster I had the maximum peduncle length. As the mutants falling between cluster IV and V exhibited maximum inter-cluster distance, selection of parents could be made from these clusters for future breeding program.

Key words: Variability, Association analysis, Diversity, Urdbean.

INTRODUCTION

Generation of genetic material, selecting superior genotypes from the variable genetic materials and developing superior varieties are all part of the urdbean breeding approach. As a result, artificial induction of variability by mutation breeding could be used to generate novel variability and it has been regarded as a significant addition to traditional breeding in crop improvement (Deepalakshmi and Anandakumar, 2004; Anbu Selvam *et al*., 2010; Ali *et al*., 2011). The genotypes with high mean performance could be useful for breeding programme leading to the identification of a good number of potential genotypes. Exploitation of the genetic variability in the breeding lines holds promise for producing high yielding good varieties. The broad sense heritability estimates help to determine the heritable variation for that character. The genotypes selected for breeding based on the diversity among the yield related characters might be highly useful and efficient. Mutation is a classical and oldest breeding technique which contributed much in crop improvement. Besides electromagnetic radiations such as X-ray and γ-ray, electron beams are now being used to induce mutations. In the present study, variability and genetic diversity was assessed using induced mutants.

MATERIALS AND METHODS

Materials subjected for experiment comprised of 38 mutants and two varieties *viz.,* MDU1 released from AC&RI, Madurai and VBN (Bg)4 released from NPRC, Vamban. Among them, thirty genotypes were selected from M5 generation and remaining eight genotypes were selected from M6 generation. The details of the mutant lines used under this study are presented in **Table 1**.

The mutagens *viz.,* gamma rays and electron beam were employed for treating the seeds. Well filled, sun dried seed materials were exposed to gamma rays in the

Table 1. Parentage details of 38 Urdbean mutant lines

S.No	Lines	Parentage	Treatment	Generation
1	ACM-014-003	MDU 1	300 Gy (GAMMA RAY)	M_5
2	ACM-014-006	MDU 1	200 Gy (GAMMA RAY)	
3	ACM-014-007	MDU 1	400Gy (GAMMA RAY)	
4	ACM-014-008	MDU 1	200Gy (GAMMA RAY)	
5	ACM-014-019	MDU 1	200 Gy (GAMMA RAY)	
6	ACM-014-021	MDU 1	300 Gy (GAMMA RAY)	
7	ACM-014-024	MDU 1	200Gy (GAMMA RAY)	
8	ACM- 015-001	VBN (Bg) 4	400 Gy (ELECTRON BEAM)	
9	ACM -015- 002	VBN (Bg) 4	400 Gy (ELECTRON BEAM)	
10	ACM -015- 003	MDU 1	200 Gy (ELECTRON BEAM)	
11	ACM- 015- 004	VBN (Bg) 4	400 Gy (ELECTRON BEAM)	
12	ACM -015 -005	VBN (Bg) 4	300Gy (ELECTRON BEAM)	
13	ACM- 015 -006	VBN (Bg) 4	100 Gy (GAMMA RAY)	
14	ACM- 015- 007	VBN (Bg) 4	100 Gy (GAMMA RAY)	
15	ACM -015- 008	VBN (Bg) 4	300 Gy (GAMMA RAY)	
16	ACM- 015- 009	VBN (Bg) 4	300 Gy (GAMMA RAY)	
17	ACM- 015-010	VBN (Bg) 4	300 Gy (GAMMA RAY)	
18	ACM- 015 -011	MDU 1	400 Gy (GAMMA RAY)	
19	ACM -015-012	MDU 1	200 Gy (ELECTRON BEAM)	
20	ACM -015-013	MDU 1	100 Gy (GAMMA RAY)	
21	ACM -015-014	MDU 1	400 Gy (GAMMA RAY)	
22	ACM -015 -015	MDU 1	200 Gy (ELECTRON BEAM)	
23	ACM- 015-016	VBN (Bg) 4	400 Gy (GAMMA RAY)	
24	ACM- 015-017	MDU 1	500 Gy (GAMMA RAY)	
25	ACM -015-018	MDU 1	500 Gy (GAMMA RAY)	
26	ACM- 015-019	MDU 1	500 Gy (GAMMA RAY)	
27	ACM -015-020	MDU 1	500 Gy (ELECTRON BEAM)	
28	ACM- 015-021	VBN (Bg) 4	200 Gy (ELECTRON BEAM)	
29	ACM- 015-022	VBN (Bg) 4	600 Gy (ELECTRON BEAM)	
30	ACM- 015-023	VBN (Bg) 4	400 Gy (ELECTRON BEAM)	
31	ACM- 015-024	VBN (Bg) 4	600 Gy (ELECTRON BEAM)	M_6
32	ACM- 015-025	VBN (Bg) 4	400 Gy (ELECTRON BEAM)	
33	ACM- 015-026	MDU 1	500 Gy (ELECTRON BEAM)	
34	ACM- 015-027	VBN (Bg) 4	200 Gy (GAMMA RAY)	
35	ACM- 015-028	MDU 1	400 Gy (ELECTRON BEAM)	
36	ACM- 015-029	MDU 1	300 Gy (GAMMA RAY)	
37	ACM- 015-030	MDU 1	300 Gy (ELECTRON BEAM)	
38	ACM- 016-001	MDU 1	200 Gy (ELECTRON BEAM)	

Gamma chamber maintained at the Directorate of Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The seeds were treated with 10 MeV electron beam from electron accelerator facility at Bhabha Atomic Research Centre (BARC), Navi Mumbai, India. Forty Urdbean genotypes (thirty eight mutants and two varieties) were evaluated in Randomized Block Design (RBD) with two replications under irrigated condition at Agricultural College and Research Institute, Madurai, during *kharif,* 2017. Each genotype was raised in three rows of 2.5 meter length with spacing of 30×10 cm in every replication. Biometric observation on yield contributing traits *viz.,* days taken for 50% flowering, height of the plant (cm), base length (cm), peduncle length (cm), pod length (cm), clusters per plant, pods per plant, seeds per pod, 100 seed weight (g) and plant yield (g) were recorded.

The analysis of variance was conducted based on the procedure suggested by Panse and Sukhatme (1961) using the mean values of ten individual plants in every replication. Method suggested by Lush (1940) was used to calculate phenotypic and genotypic variances. As per the protocol followed by Sivasubramanian and Madhava Menon, (1973), phenotypic and genotypic coefficients of variation were studied. Following the formula given by Lush (1940), heritability in broad sense (h^2) was calculated for each trait. Genetic Advance as per mean (GAM) was arrived as per the formula stated by Johnson *et al*. (1955). The quantitative characters were taken into consideration for divergence studies and analyzed using D^2 method by Mahalanobis (1936). Simple criterion given by Rao (1952) was followed for formulating the group constellation. According to Al-Jibouri *et al.* (1958), the genotypic correlation coefficients between yield and yield components were calculated and path coefficient analysis was done by the method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Among the 38 mutants studied, mutant entries *viz.,* ACM -014-019 and ACM -015-027 showed earliness in flowering and plant height (short plant stature) coupled with higher grain yield as compared to the general mean. Similar report for earliness in flowering was made by Usharani and Ananda Kumar (2016) in barnyard millet. This can be considered as a valuable trait for the development of short stature plant type with early maturing and high yielding genotypes in the breeding programme.

Based on the overall *per se* performance for major yield attributing traits *viz.,* length of the pod, pods per plant, clusters per plant, seeds per pod, test weight and yield per plant, the mutants namely ACM -014-021, ACM -015-015, ACM -015-011, ACM -015-025, ACM -015-026, ACM -014-007 were found to be superior. Mutant lines *viz.,* ACM -014-021, ACM -015-015, ACM -015-011, ACM -015-013, ACM -015-025, ACM -015-026 and ACM -014-007 had higher single plant yield along with clusters and pods per plant, seeds per pod and test weight. It indicated that the highest clusters and pods per plant, seeds per pod and test weight could lead to enhanced plant yield. Hence, these mutant lines might be exploited for improving yield attributing characters in Urdbean.

The variability observed among different characters was compared by the phenotypic and genotypic coefficients of variation (**Table 2**). Besides, high heritability along with high genetic advance would be trustworthy in formulating a selection scheme for crop improvement. High phenotypic and genotypic coefficients of variation were recorded for single plant yield and peduncle length. This showed that the variations observed in these characters contributed markedly to the total variability. Similar results were supported by Punia *et al.* (2014), Ramya *et al.* (2014), Usharani and Ananda Kumar (2016) in Urdbean, Rukmini *et al.* (2016) in rice for seed yield, Suresh *et al.* (2010) for single plant yield in greengram and Tushar Choudhury (2020) in Urdbean. High heritability with high genetic advance was observed for base length, peduncle length, clusters and pods per plant and single plant yield. Similar results were also supported by Suresh *et al*. (2010), Rahim *et al*. (2010) and Lovejit Singh *et al*. (2020) for different yield contributing traits in Urdbean. Considering, GCV, PCV, h^2 and GAM, significant yield attributing characters *viz.*, pods per plant, pod length, clusters per plant, seeds per pod were found to be given importance for further improvement of the Urdbean mutants.

Seed yield had significantly positive correlation with pods number, pod length, clusters number and seeds per pod (**Table 3**). This was corroborated by the findings of Punia *et al.* (2014), Kanimoli mathivathana *et al.* (2015) and Jyothsna *et al.* (2016) for the same characters in Urdbean. Hence, those characters should be considered for crop improvement in Urdbean. Number of branches had registered positive association with pod length, clusters and pods per plant and test weight. Number of clusters per plant exhibited high positive association with number of pods per plant, test weight. Seeds per pod and test weight showed positively significant correlation with pods count. Similar results were reported by Kanimoli mathivathana *et al.* (2015) in Urdbean. Hence, selection criteria should include all the essential characters in Urdbean improvement. Among the different characters studied, length of the pod, pods per plant, days to 50% flowering, plant height, clusters and pods per plant showed high positive direct effect on seed yield. This result was similar to the findings reported by Tushar Chowdhury *et al.* (2020) in Urdbean. It may be concluded that the selection for these important traits must be given priority for enhanced seed yield in Urdbean.

Based on the cluster analysis, 38 mutants were distributed into five clusters. Among them, V cluster had the highest number of sixteen mutants along with two controls followed

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Table 2. Analysis of Variance for quantitative traits in advanced generation of Urdbean mutants along with parents

S.No.	Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	Genetic advance	GA as % of mean
1	Days to 50% flowering	32.26	37.00-28.50	7.04	5.75	66.71	3.12	9.67
2	Plant height (cm)	49.29	58.20-37.85	10.30	9.66	87.95	9.19	18.65
3	Base length (cm)	5.63	8.26-4.05	15.50	14.80	91.18	1.64	29.12
4	Number of branches per plant	3.63	4.83-2.70	20.67	15.08	53.21	0.82	22.66
5	Peduncle length	12.97	18.76-8.36	22.28	21.38	92.08	5.48	42.27
6	Pod length (cm)	4.27	4.90-3.78	6.80	5.44	63.93	0.38	8.96
7	Number of clusters per plant	22.12	33.40-13.58	18.08	16.39	82.17	6.77	30.60
8	Number of pods per plant	53.26	75.90-33.80	18.20	17.72	94.78	18.93	35.54
9	Number of seeds per pod	6.88	7.95-4.49	11.18	10.36	85.92	1.36	19.79
10	Test weight (g)	5.11	6.07-4.47	6.14	5.95	93.99	0.61	11.88
11	Single plant yield (g)	12.80	19.76-7.74	22.48	20.35	81.93	4.86	37.94

Table 3.Correlation among yield and yield influencing quantitative traits in advanced generation of Urdbean mutants along with parents

Characters		DFF	PH	BL	NOB	PED LEN	POD LEN	NCP	NPP	NSP	100 SW	SPY
Days to 50% flowering	G	1.000	0.100	-0.106	0.312*	-0.008	0.057	-0.177	-0.209	-0.300	0.145	0.195
	P	1.000	0.138	-0.061	0.082	-0.015	0.026	-0.116	-0.197	-0.273	0.154	0.136
Plant height	G		1.000	0.006	-0.335*	0.516*	-0.213	0.054	-0.062	0.057	-0.066	-0.060
	P		1.000	0.050	-0.272	0.470*	-0.200	0.083	-0.050	-0.050	-0.043	-0.023
Base length	G			1.000	-0.174	-0.399*	0.493*	-0.001	0.244	0.198	0.031	0.159
	P			1.000	-0.125	-0.360*	0.361*	-0.030	0.227	0.122	0.053	0.107
Number of branches per plant	G				1.000	-0.042	0.422*	0.021	0.049	-0.102	0.187	0.029
	P				1.000	-0.025	0.186	0.067	0.019	-0.054	0.065	-0.043
Peduncle length	G					1.000	-0.271	-0.031	0.015	0.104	-0.201	-0.214
	P					1.000	-0.210	-0.037	0.031	0.097	-0.187	-0.197
Pod length	G						1.000	0.374*	0.525*	0.266	0.006	0.675*
	P						1.000	0.214	0.436*	0.211	-0.004	0.479*
Number of clusters per plant	G							1.000	0.347*	0.574*	0.451*	0.515*
	P							1.000	0.297	0.530*	0.388*	0.412*
Number of pods per plant	G								1.000	0.503*	0.127	0.705*
	P								1.000	0.444*	0.135	0.617*
Number of seeds per pod	G									1.000	0.220	0.390*
	P									1.000	0.172	0.367*
Test weight	G										1.000	0.173
	P											0.145
Single plant yield	G											1.000
	P											1.000

*Significance at 5% level

by clusters I with 15 mutants, cluster IV with three mutants and cluster II and III with two mutants each (**Table 4**). Cluster IV had the greatest intra cluster distance, followed by cluster V and cluster I, showed genetic variations within clusters (**Table 5**). Mutants in clusters IV and V had the greatest inter-cluster distances, indicating a high degree of genetic diversity. This finding of the genetic diversity analysis was consistent with those of Senapati and Misha (2010) and Panigrahi *et al*. (2014) in Urdbean. As a result, genotypes from the most diversified cluster could be employed as parents in hybridization programmes to create high-yielding cultivars.

Number of branches, clusters and pods per plant, seeds per pod, test weight, and seed yield were maximum in cluster III. For length of the pod, cluster IV had the highest mean value (**Table 6**). Cluster III had the highest mean value for branches per plant, clusters and pods per plant, the seeds per pod, test weight and plant yield. The mutants in these clusters had all of the desirable features that could be directly selected and used to increase yield. The traits *viz.,* clusters and pods per plant, test weight and plant yield possessed high heritability and generated the most genetic divergence. As a result, these traits could be used to improve phenotypic selection in the future.

The mutant lines v*iz*., ACM -014-021, ACM -015-015, ACM -015-011, ACM -015-013, ACM -014-006 registered superior mean value for many quantitative traits. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and high heritability with high genetic advance as per cent of mean values were

Table 4. D^2 clusters for quantitative traits in advanced generation of Urdbean mutants along with parents

Cluster Number	Number of genotype	Name of the genotypes
I	15	ACM-015-001, ACM-015-002,ACM-015-003, ACM-015-004, ACM-015-005, ACM-015-006, ACM-015-007, ACM-015-008, ACM-015-009, ACM-015-010, ACM-015-011, ACM-015-012, ACM-015-013, ACM-015-014, ACM-015-017
II	2	ACM-015-020,ACM-014-019
III	2	ACM-015-030, ACM-014-006
IV	3	ACM-015-015, ACM-015-019, ACM-015-021
V	18	ACM-015-016, ACM-015-018, ACM-015-021,ACM-015-022, ACM-015-023, ACM-015-025, ACM-015-026, ACM-015-027, ACM-015-028, ACM-015-029, ACM-014-003, ACM-014-007, ACM-014-008, ACM-014-021, ACM-014-024, ACM-016-001, MDU1, VBN(Bg) 4

Table 5.Average of intra and inter cluster D^2 distance for quantitative traits in advanced generation of Urdbean mutants along with parents

Cluster	I	II	III	IV	V
I	13.55	12.10	16.97	19.96	14.60
II	12.10	4.82	10.00	17.93	12.22
III	16.97	10.00	6.48	18.61	15.86
IV	19.96	17.93	18.61	19.37	20.12
V	14.60	12.22	15.86	20.12	15.64

Table 6.Cluster mean values of quantitative traits in advanced generation of Urdbean mutants along with parents

Cluster	Days to 50% flowering	Plant height (cm)	Base length (cm)	Number of branches per plant	Peduncle length (cm)	Pod length (cm)	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	Test weight (g)	Single plant yield (g)
I	32.43	50.44	5.43	3.51	14.19	4.22	21.65	49.75	6.91	5.02	12.10
II	31.00	44.88	5.15	3.32	11.61	4.17	20.04	56.30	7.10	5.23	12.91
III	32.50	42.73	5.30	4.28	12.10	4.41	24.95	68.45	7.40	5.27	14.41
IV	32.63	50.25	7.38	3.42	9.42	4.48	21.40	56.85	7.14	5.12	14.01
V	32.15	49.34	5.48	3.74	12.99	4.26	22.62	53.36	6.71	5.14	12.94

recorded for peduncle length, clusters and pods per plant and single plant yield. Correlation analysis clearly indicated that the traits *viz.,* clusters and pods per plant, pod length and number of seeds per pod had direct effect on yield. Path analysis for the quantitative traits revealed that the traits *viz.,* days to 50% flowering, plant height, pod length, clusters and pods per plant, seeds per pod and test weight showed high positive direct effect on seed yield. Based on the divergence studies, the highest intra cluster distance was observed in cluster IV followed by cluster V. Mutants falling between cluster IV and V exhibited maximum inter-cluster distances could be widely exploited in Urdbean breeding to develop high promising genotypes.

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