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Genetic and Biochemical Characterization of Electron Beam and Gamma Ray Induced Mutants for Superior Battering Quality Trait and MYMV in Urdbean [*Vigna mungo* (L.)]

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ABSTRACT

Background: A systematic investigation of the induced mutagenesis in Urdbean was attempted with cultivars *viz.,* MDU 1 and VBN (Bg) 4 to generate superior battering quality varieties. Induced mutation is proven as an applicable breeding method to build variation in plant materials. In this study, 40 Urdbean genotypes including thirty eight mutants of two promising Urdbean varieties namely MDU1 and VBN (Bg) 4 and two parental genotypes were involved for quality analysis. One of the most dangerous diseases in legumes is Mungbean Yellow Mosaic Virus (MYMV). In legume, this virus causes enormous losses in the areas of Urdbean cultivation. The prevailing varieties are partially resistant to this virus. Hence, the paramount approach to control this disease is breeding for resistance or tolerance to this disease. There is a necessity of searching the sources of disease resistance. In this study, screening of the mutants was conducted to make out the source of resistance to this disease.

Methods: The nutritional characters *viz*., albumin, globulin and total soluble protein along with biochemical analysis of battering quality through Arabinose estimation were analyzed to find out the quality characters of the mutants. Batter volume analysis from idli batter was conducted conducted. Scoring of disease severity was done for all the plants on 50th day on the basis of visual scoring. The disease was scored on a 1-9 arbitrary scale. For biochemical characterization for this disease estimation of total phenol content, total sugars and phytic acid was executed.

Result: Based on the general performance of albumin content, globulin content, total soluble protein, arabinose content, 100 seed weight and seed yield per plant, the mutant lines *viz.,* ACM-014-021, ACM-015-015, ACM-15-023, ACM-015-013, ACM-015-003, ACM-015-030, ACM-014-006, ACM-014-007 were recognized as the best. Hence these mutant lines could be exploited directly in the breeding programme to develop superior battering quality Urdbean varieties. Based on over all mean performance of important batter volume characters *viz*., initial batter volume analysis, final batter volume, improved batter volume, arabinose content and single plant yield the mutant lines ACM-15-015, ACM-015-030, ACM-015-003, ACM-015-023 were identified to be superior in terms of yield, arabinose content and batter volume. The mutant lines *viz.,* ACM-014-021, ACM-015-025, ACM-014-006, ACM-015-022, ACM -015-023, ACM-014-019, ACM-014-007, ACM-015-017, ACM-014- 003 and VBN (Bg) 4 were recognized as resistant to MYMV. These lines had higher total phenol, phytic acid content and less total sugar content in the leaves when compared with the highly susceptible mutant lines. The present study indicated that phytic acid content recorded highly significant positive correlation with total phenol. Based on the *per se* performance for all the characters studied *viz.,* seed batter analysis, seed volume analysis and MYMV scoring, the mutant lines *viz.,* ACM-014-021, ACM-015-23, ACM-015-030, were judged as the best and could be exploited directly or in breeding experiments for improving yield along with batter quality.

Key words: Battering quality, Characterization, Induced mutants, MYMV, Urdbean.

INTRODUCTION

Two components, namely surface active protein (globulin) and an arabinogalactan (polysaccharide) present in idli batter are responsible for the soft spongy texture observed in the leavened steamed idli made out of Urdbean. In this study, two cultivars *viz.,* MDU 1 and VBN (Bg) 4 were involved to synthesize superior battering quality varieties through mutation breeding. Mungbean Yellow Mosaic Virus (MYMV) disease is one of the most dangerous diseases of legumes. A group of gemini viruses belonging to the genus, *begomovirus* of the family, *Geminiviridae* is the causal organism for this disease. Whitefly is the vector for transmission of this disease. The best method to control this disease is to find out the source of resistance to the disease by screening the available breeding stocks of

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urdbean. In this study, the mutants were subjected to screening at field level to categorize the source of resistance to Mungbean Yellow Mosaic Virus (MYMV).

MATERIALS AND METHODS

Thirty eight black gram mutants of promising varieties *viz.,* MDU 1 and VBN (Bg) 4 and the same parents as checks were taken as materials for this study. The details of the mutant lines used under this study were given in Table 1. The physical mutagens *viz*., gamma rays and electron beam were employed for treating the seeds. The good quality seeds were subjected for treatment with gamma rays in the Gamma chamber installed at the Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore where Cobalt-60 served as the source of gamma rays. With 10 MeV electron beam from electron accelerator facility at Electron Beam Centre, Bhabha Atomic Research Centre, Kharghar, Navi Mumbai, India, the seeds were irradiated. Forty black gram genotypes were raised in randomized block design with two replications under irrigated condition at Agricultural College and Research Institute, Madurai, during *kharif* 2016. Every entry was raised in 2.5 meter length of three rows with spacing of 30 × 10 cm in each replication.

Table 1: Parentage details of 40 mutant lines.

Lines	Parentage	Treatment
ACM-014-003	MDU 1	300 Gy (GAMMA RAY)
ACM-014-006	MDU 1	200 Gy (GAMMA RAY)
ACM-014-007	MDU 1	400 Gy (GAMMA RAY)
ACM-014-008	MDU 1	200 Gy (GAMMA RAY)
ACM-014-019	MDU 1	200 Gy (GAMMA RAY)
ACM-014-021	MDU 1	300 Gy (GAMMA RAY)
ACM-014-024	MDU 1	200 Gy (GAMMA RAY)
ACM-015-001	VBN (Bg) 4	400 Gy (ELECTRON BEAM)
ACM-015-002	VBN (Bg) 4	400 Gy (ELECTRON BEAM)
ACM-015-003	MDU 1	200 Gy (ELECTRON BEAM)
ACM-015-004	VBN (Bg) 4	400 Gy (ELECTRON BEAM)
ACM-015-005	VBN (Bg) 4	300 Gy (ELECTRON BEAM)
ACM-015-006	VBN (Bg) 4	100 Gy (GAMMA RAY)
ACM-015-007	VBN (Bg) 4	100 Gy (GAMMA RAY)
ACM-015-008	VBN (Bg) 4	300 Gy (GAMMA RAY)
ACM-015-009	VBN (Bg) 4	300 Gy (GAMMA RAY)
ACM-015-010	VBN (Bg) 4	300 Gy (GAMMA RAY)
ACM-015-011	MDU 1	400 Gy (GAMMA RAY)
ACM-015-012	MDU 1	200 Gy (ELECTRON BEAM)
ACM-015-013	MDU 1	100 Gy (GAMMA RAY)
ACM-015-014	MDU 1	400 Gy (GAMMA RAY)
ACM-015-015	MDU 1	200 Gy (ELECTRON BEAM)
ACM-015-016	VBN (Bg) 4	400 Gy (GAMMA RAY)
ACM-015-017	MDU 1	500 Gy (GAMMA RAY)
ACM-015-018	MDU 1	500 Gy (GAMMA RAY)
ACM-015-019	MDU 1	500 Gy (GAMMA RAY)
ACM-015-020	MDU 1	500 Gy (ELECTRON BEAM)
ACM-015-021	VBN (Bg) 4	200 Gy (ELECTRON BEAM)
ACM-015-022	VBN (Bg) 4	600 Gy (ELECTRON BEAM)
ACM-015-023	VBN (Bg) 4	400 Gy (ELECTRON BEAM)
ACM-015-024	VBN (Bg) 4	600 Gy (ELECTRON BEAM)
ACM-015-025	VBN (Bg) 4	400 Gy (ELECTRON BEAM)
ACM-015-026	MDU 1	500 Gy (ELECTRON BEAM)
ACM-015-027	VBN (Bg) 4	200 Gy (GAMMA RAY)
ACM-015-028	MDU 1	400 Gy (ELECTRON BEAM)
ACM-015-029	MDU 1	300 Gy (GAMMA RAY)
ACM-015-030	MDU 1	300 Gy (ELECTRON BEAM)
ACM-016-001	MDU 1	200 Gy (ELECTRON BEAM)

Gy-Gamma Ray.

Estimation on nutritional properties *viz.,* albumin, globulin and total soluble protein was carried out by Lowrey's Method (1951) and biochemical analysis of battering quality through Arabinose estimation as Bial (1902). Batter volume analysis and enumeration of microorganism (*Lactobacillus sp.,* bacteria and fungi) from idli batter were estimated. The disease was scored on a 1-9 arbitrary scale according to Alice and Nadarajan (2007). By visual scoring, the incidence of this disease was scored in all plants on 50th day. The check MDU 1 recorded scale 9. Biochemical characterization for this disease was carried out through estimation of total phenol content, total sugars and phytic acid.

RESULTS AND DISCUSSION

To identify the genotypes, qualitative characters exhibiting stable and discrete inheritance are normally used as plant descriptors. In this study, to characterize the mutant lines, fifteen qualitative characters were used. Among them, there was no variations for the characters such as hypocotyl colour, growth habit, raceme position, attachment of pod to peduncle, immature pod colour, seed shape and hilum colour among the lines. Hence, these traits could not be used to distinguish these mutants. The same report was suggested by Joshi *et al.* (2014) in kodo millet land races whcih had erect (62.9%) growth habit and all the land races showed sheath base pigmentation, internode pigmentation, flag leaf at the second primary axis node, panicle exertion and spikelet arrangement on rachis which had no variations among them. This result was similar to the study of Jayamani *et al.* (2014) who reported no variation for the characters like corolla colour and lusture on seed surface. The traits *viz.,* primary leaf colour, terminal leaf colour, leaf pubescence, petiole colour, stem colour, mature pod colour, seed colour and seed lusture showed frequency distribution and thus for identifying the genotypes, these characters might be considered for selection.

Based on 15 qualitative characters, cluster analysis based on similarity matrix and similarity coefficients at 0.75 grouped 40 Urdbean genotypes into 2 clusters. Cluster I had 16 mutant lines along with VBN (Bg) 4 variety and cluster II comprised of 22 mutant lines along with MDU1 variety. From the cluster diagram it was inferred that, morphological features related to MDU1 variety formed one cluster and morphological features related to VBN (Bg) 4 formed another cluster. Among the 40 mutants studied, superior twenty

mutants were selected based on single plant yield and biochemical works were carried out on those mutants. Analysis of variance of the seed quality characters *viz.,* albumin content, globulin content, total soluble protein, arabinose content, hundred seed weight and single plant yield indicated the existence of considerable differences among the mutant lines for those characters (Table 2). This result was supported by the findings of Veni *et al*. (2016).

Albumin protein fraction content varied from 6.08 to 8.94 per cent and the mutant line ACM-014-007 recorded the maximum albumin content followed by ACM-014-019 and ACM-014-021. Globulin protein fraction of the mutant lines ranged from 9.81 to 16.39 per cent and the mutant line ACM-014-021 recorded the maximum globulin content followed by ACM-015-024 and ACM -014-019. Total soluble protein of the mutant lines ranged from 18.31 to 30.14 per cent. The mutant line ACM-015-017 recorded the maximum protein content followed by ACM-014-019 and ACM-014-021.

Arabinose content of the mutant lines ranged from 5.88 to 11.03 per cent. The mutant line ACM-15-023 recorded the maximum arabinose content followed by ACM-015-030 and ACM-015-003 (Table 3). High amount of albumin, globulin total soluble protein content, hundred seed weight and single plant yield was recorded in the line ACM -014-021. More values of albumin, globulin, total soluble protein and hundred seed weight were recorded by ACM-014-019. Albumin content and hundred seed weight were high in the line ACM-014-007. Globulin content, total soluble protein content, arabinose content and hundred seed weight showed high positive association with seed yield per plant. Hence, to improve the battering quality along with yield these characters might be given importance.

Globulin, total soluble protein, arabinose content and hundred seed weight exhibited positive and significant correlation with albumin content. Total soluble protein content exhibited positive and significant correlation with globulin and arabinose content. The results revealed the traits albumin, globulin, total soluble protein, arabinose, hundred seed weight had strong inter correlation with battering quality which might lead to the improvement of battering quality in Urdbean (Table 4). These results were in conformity with finding of Veni (2015).

Based on the general performance of albumin content, globulin content, total soluble protein, arabinose content, hundred seed weight and single plant yield the mutant lines *viz.,*ACM-014-021, ACM-015-015, ACM-15-023, ACM-015-013, ACM-015-003, ACM-015-030, ACM-014-006, ACM-014-007 were identified as the best. Hence to develop high yielding, good battering quality Urdbean varieties, these mutant lines could be utilized directly in the breeding plans. Four mutants *viz.,* ACM-015-023, ACM-015-030, ACM-015-003, ACM-015-015 with higher arabinose content (higher than 10%) along with two controls were selected and batter volume analysis was assessed. Analysis of variance of the batter volume traits *viz.,* initial batter volume, final batter volume, increased batter volume, arabinose content and single plant yield exhibited the existence of significant differences among the mutant lines for these characters (Table 5a). The mutant line ACM- 015-030 recorded the maximum final batter volume followed by ACM-015-003 and ACM-015-015. Increased batter volume (IBV) ranged from 79 ml to 120 ml. Maximum protein content was recorded by the mutant line ACM-015-030 followed by ACM-015-003 and ACM-015-015. Arabinose content ranged from 7.38 to 11.03 per cent. Maximum arabinose content was recorded by the mutant line ACM-15-023 followed by ACM-015-030 and ACM-015-003 (Table 5b).

The mutant lines ACM-15-015, ACM-015-030, ACM-015-003, ACM-015-023 were found to be superior based on over all mean performance of important batter volume traits *viz*., initial batter volume analysis, final batter volume, increased batter volume, arabinose content and single plant yield. Twenty mutants along with two controls (MDU 1, VBN (Bg) 4) were screened against MYMV to identify the source of resistance by using 1-9 arbitrary scale as per the method suggested by Alice and Nadarajan (2007). Among them, nine mutant lines have been identified exhibiting promising resistant reaction to MYMV resistance. The mutant lines *viz.,* ACM-014-021, ACM-015-025, ACM-014-006, ACM-015-022, ACM -015-023, ACM-014-019, ACM-014-007, ACM-015-017, ACM-014- 003 and VBN (Bg) 4 were found to be resistance. Peerajade *et al*. (2004), Pathak and Jhamaria, (2004) and Vanniarajan *et al*. (2019) also confirmed the results through similar type of genotype evaluations. These mutants could be used directly as a variety or in the breeding plan to generate MYMV resistance or tolerant lines.

Table 2: Analysis of variance for battering quality traits in Urdbean mutants.

Characters	Grand mean	Range	SD	SED	CD (5%)
Albumin content (%)	7.45	6.08-8.94	0.77	0.38	0.79
Globulin content (%)	11.81	9.81-16.39	2.10	0.31	0.65
Total soluble protein content (%)	24.82	18.31-30.14	3.74	0.25	0.52
Arabinose content (%)	8.06	5.88-11.03	1.48	0.52	1.09
Hundred seed weight (g)	5.19	4.47-6.07	0.33	0.09	0.19
Single plant yield (g)	14.59	11.12-19.76	2.32	1.19	2.48

SD- Standard deviation; SED- Standard error of difference; CD- Critical difference.

In the present investigation, phytic acid content (mg/g), total phenol (mg/g) and total sugar content (mg/g) and MYMV disease score in 20 mutant lines of Urdbean were correlated. It was noted that the Urdbean mutant lines exhibited dissimilar level of total phenol and total sugar content to altering degree of MYMV disease resistance. The highly resistant mutant lines to MYMV *viz*., ACM-014-021, ACM-015-025, ACM-014-006, ACM-015-022, ACM -015-023,

Table 3: Mean performance of battering quality traits in Urdbean mutants.

Genotypes	ALB (%)	GLO (%)	TSP (%)	ARA (%)	HSW (g)	SPY (g)
ACM-014-021	8.48*	16.39*	28.95*	6.89	5.32*	19.76*
ACM-015-015	6.85	11.97*	27.52*	9.58*	4.47	19.13*
ACM-015-011	6.96	10.84	25.64*	7.83	5.11	18.30*
ACM-015-025	7.29	9.81	18.31	5.94	4.81	17.02*
ACM-015-026	7.08	10.03	19.43	5.88	6.07*	16.99*
ACM-015-013	7.28	14.59*	27.53*	8.36	4.91	16.05*
ACM-015-014	6.93	11.94*	24.68	9.59*	5.30*	15.09*
ACM-015-030	6.98	10.98	23.99	10.79*	5.25	14.74*
ACM-014-006	8.14*	11.69*	28.94*	8.28	5.30*	14.07
ACM-015-003	8.54*	14.65*	29.98*	6.83	5.44*	13.96
ACM-015-024	8.50*	15.94*	21.68	6.74	5.20*	13.77
ACM-015-022	7.03	10.94	25.49	7.96	4.99	13.76
ACM-015-023	8.02*	9.97	22.73	11.03*	5.39*	13.75
ACM-014-019	7.03	13.84*	22.5	6.83	5.20	13.64
ACM-015-012	6.54	10.11	26.23*	7.29	5.24	13.14
ACM-014-007	8.94*	12.23*	27.94*	8.14*	5.47*	13.13
ACM-015-019	8.39*	10.06	28.76*	8.39*	5.47*	12.98
ACM-015-017	7.79*	13.64*	30.14*	8.98*	5.29*	12.92
ACM-014-03	6.74	9.94	19.06	7.17	4.98	12.65
ACM-015-27	6.08	10.09	18.94	6.03	4.76	12.60
MDU1	6.98	9.94	24.13	8.08	5.25	12.38
VBN(Bg)4	7.28	10.25	23.54	7.38	4.86	11.12
MEAN	7.45	11.81	24.82	8.06	5.19	14.59
CD (5%)	0.794	0.651	0.519	1.087	0.188	2.482
SE	0.16	0.44	0.80	0.32	0.07	0.49

ALB- Albumin content (%); ARA- Arabinose content (%); GLO- Globulin (%); HSW- Hundred seed weight (g); TSP- Total soluble protein (%); SPY- Single plant yield (g); SE- Standard error; CD- Critical difference; *- Significant at 5% level.

Table 4: Correlation studies for battering quality traits in Urdbean mutants with hundred seed weight and single plant yield.

Characters		ALB	GLO	TSP	ARA	HSW	SPY
Albumin content (%)	G	1.000	0.559*	0.562*	0.048	0.480*	-0.015
	P	1.000	0.489*	0.486*	-0.018	0.398*	-0.016
Globulin content (%)	G		1.000	0.4578	0.002	0.060	-0.420*
	P		1.000	0.452*	0.009	0.043	-0.370*
Protein content (%)	G			1.000	0.302	0.130	0.213
	P			1.000	0.284	0.127	0.101
Arabinose content (%)	G				1.000	-0.024	0.071
	P				1.000	-0.036	0.069
Hundred seed weight (g)	G					1.000	0.054
	P					1.000	0.040
Single plant yield (g)	G						1.000
	P						1.000

* - Significant at 5% level.

ACM-014-019, ACM-014-007, ACM-015-017, ACM-014-003 and VBN (Bg) 4 had reasonably higher total phenol, phytic acid content and lower total sugar content than the susceptible mutant lines (Table 6). In this study, high significant positive correlation was observed between total phenol and phytic acid content (Table 7). Earlier studies reported that resistance to *B. tabaci* in had been imparted through higher quantities of total phenols many crops such as cotton (Balakrishnan, 2006; Acharya and Singh, 2008) and in brinjal (Soundarajan and Bhaskaran, 2001). Sujithra *et al.* (2012) studied the morphological and biochemical factors influencing plant resistance to pod borer on field bean in 84 entries and the results revealed that tolerant cultivars possessed lower amount of reducing sugars than susceptible cultivars. Like that resistance was imparted due to the presence of higher quantities of phytic acid in crops which was reported by earlier workers *viz.,* Srinivasan and Durairaj (2017) in rice bean, Dhole and Reddy (2016) in 94 green gram germplasm. In resistant lines, resistance was intensified due to the rapid accumulation of phenols and lesser accumulation of total sugar content compared to susceptible ones for this disease. This process rendered a viable approach on plant resistance in insect plant interaction. This mechanism paved a way to understand the biochemical basis responsible for plant resistance to pest and for comparison between resistant and susceptible genotypes for this disease. These findings were supported by the findings of many researchers *viz*., Acharya and Singh, (2008) in cotton.

Table 5a: Analysis of variance for batter volume analysis in of Urdbean mutants.

Characters	Grand Mean	Range	SE	SD	CV
Initial batter volume (ml)	50	-	0.31	1.04	2.08
Final batter volume (ml)	138	129-170	0.96	1.76	10.25
Increased batter volume (ml)	83	79 -120	0.87	2.03	14.60
Arabinose (%)	9.49	7.38-11.03	0.41	1.41	14.94
Single plant yield (g)	13.96	11.12- 19.13	0.84	2.90	19.98

SE- Standard error; SD- Standard deviation; CV- Coefficient of variation.

Table 5b: Mean performance of batter volume analysis in isolated mutants based on arabinose content.

Mutant lines	Initial batter volume (ml)	Final batter volume (ml)	Increased batter volume (ml)	Arabinose content (%)	Single plant yield (g)
ACM-015-023 (V)	50	136	86*	11.03*	13.75
ACM-015-030 (M)	50	170*	120*	10.79*	14.74
ACM-015-003 (M)	50	158*	108*	10.08*	12.65
ACM-015-015 (M)	50	149*	99*	9.58*	19.13*
MDU1	50	146*	96*	8.08	12.38
VBN (Bg)4	50	129	79	7.38	11.12
MEAN	50	138	83	9.49	13.96
SE	0.31	0.96	0.87	0.41	0.84

* - Significant at 5% level; SE - Standard error.

Table 6: Grouping of mutant lines against MYMV scoring in Urdbean mutants at field level screening.

Rating	Reaction	Genotypes
1.0-2.0	Resistant (R)	ACM-014-021, ACM-015-025, ACM-014-006, ACM-015-022, ACM-015-023, ACM-014-019, ACM-014-007, ACM-015-017, ACM-014-003, VBN (Bg)4.
2.1-4.0	Moderately resistant (MR)	ACM-015-015, ACM-015-011, ACM-015-014, ACM-015-030, ACM-015-012, ACM-015-019.
4.10-5.00	Moderately susceptible (MS)	ACM-015-003, ACM-015-027, ACM-015-024
5.1-7.00	Susceptible (S)	ACM-015-026, MDU1.
7.1-9.0	Highly susceptible (HS)	ACM-015-013.

Table 7: Screening of Urdbean mutants against Mungbean Yellow Mosaiv Virus (MYMV) with biochemical traits.

Mutant Lines	Phytic Acid (mg/g)	Phenols (mg/g)	Sugars (mg/g)	MYMV scoring (mg/g)
ACM-014-21	7.21	3.25*	28.25*	2
ACM-015-15	8.04	1.50	26.75*	3
ACM-015-11	9.77*	1.25	27.5*	3
ACM-015-25	11.18*	5.00*	17.25	1
ACM-015-26	9.13	1.50	31.38*	6
ACM-015-13	8.68	2.25	35.75*	7
ACM-015-14	9.90*	3.25*	26.25*	3
ACM-015-30	9.32	2.75	20.88	3
ACM-014-06	8.68	3.50*	19.75	1
ACM-015-03	6.26	3.25*	21.38	5
ACM-015-24	8.42	2.00	21.25	5
ACM-015-22	8.42	2.25	22.38	2
ACM-015-23	11.24*	4.75*	16.38	1
ACM-014-19	10.22*	2.50	29.75*	2
ACM-015-12	8.87	1.50	30.63*	4
ACM-014-07	9.83*	2.75	31.63*	2
ACM-015-19	9.06	1.38	21.75	4
ACM-015-17	11.24*	5.25*	15.13	1
ACM-014-03	7.21	2.50	17.88	1
ACM-015-27	8.68	1.50	31.13*	5
MDU1	8.04	1.50	32.25*	7
VBN (Bg) 4	10.54*	2.75	14.75	1
MEAN	9.09	2.64	24.55	
CD (5%)	0.44	0.55	2.39	
SE	0.28	0.24	1.35	

* - Significant at 5% level; SE- Standard error; CD- Critical difference.

CONCLUSION

The present investigation in mutant population of Urdbean led to the following conclusion. Based on the cluster analysis, fifteen qualitative traits were grouped into 2 clusters. Cluster I had 16 mutant lines along with VBN (Bg) 4 variety and cluster II contained 22 mutant lines along with MDU1 variety. The mutant lines *viz.,* ACM-014-021, ACM-015-015, ACM-15-023, ACM-015-013, ACM-015-003, ACM-015-030, ACM-014-006 and ACM-014-007 were found to be superior for albumin, globulin, total soluble protein and arabinose content. Seed volume analysis recorded that the mutant lines *viz.,* ACM-15-015, ACM-015-030, ACM-015-003 and ACM-015-023 were found to be superior in terms of yield, arabinose content and batter volume. Based on MYMV screening, the mutant lines *viz.,* ACM-014-021, ACM-015-025, ACM-014-006, ACM-015-022, ACM -015-023, ACM-014-019, ACM-014-007, ACM-015-017 and ACM-014-003 were found to be superior. Overall mean performance for all the traits *viz.,* quantitative traits, seed batter analysis, seed volume analysis, MYMV scoring revealed that the mutant lines *viz.,* ACM-014-021, ACM-015-015, ACM-015-23, ACM-015-030, ACM-014-006, ACM-014-007, ACM-015-025 and ACM-015-026 were judged as the best and could be used directly or in breeding programme for improving yield along with batter quality.

Conflict of interest

All authors declared that there is no conflict of interest.

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