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Research Article

DUS characterization and genetic variability studies of rice mutants

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Abstract

Forty five mutant lines developed using gamma rays and electron beam irradiation in the background of ADT 37 and ADT (R) 45 were characterized for twenty four DUS characters. Out of the twelve visually assessed qualitative traits, shape of ligule, colour of ligule, stigma colour, sterile lemma colour, panicle secondary branching and panicle attitude were monomorphic, culm attitude, panicle exertion, flag leaf attitude, presence of awns and distribution of awns were dimorphic and the grain shape was polymorphic. The analysis of variance revealed the existence of significant differences among genotypes for six characters *viz.,* days to 50% flowering, plant height, number of productive tillers, number of filled grains per panicle, single plant yield and panicle length. The traits *viz.,* number of productive tillers, number of filled grains per panicle, 1000 grain weight, leaf blade width, LB ratio and single plant yield had high heritability along with genetic advance as percent of mean. These characters are governed by additive gene action and improvement in these characters would be possible through direct selection. The diversity analysis of both qualitative and quantitative characters grouped the mutant lines into seven clusters. Among the seven clusters, the maximum number of genotypes (27) present in cluster IV. The intra cluster distance was maximum in cluster I and the highest inter-cluster distance was recorded between cluster I and cluster VI. Five mutant lines *viz.,* M6, M66, M79, M85 and M88 of ADT (R) 45 were identified as desirable lines based on non-lodging habit and increase in 1000 grain weight and six mutant lines *viz.,* M69, M71, M78, M79, M85 and M88 of ADT 37 with medium slender grain type were selected as novel mutants. These selected lines will be promoted to yield trials. Two unique mutant lines M 37 and M 39 of ADT (R) 45 with distinct culm and flag leaf attitude were selected as desirable mutants and these will be registered under PPV&FR Act for obtaining plant breeder's rights.

Keywords
DUS characterization, Diversity, Genetic variability, Mutants, Rice

Introduction

Rice is one of the most important food crops grown worldwide. It is the staple food crop for more than 60% of the population and provides 20% of calories and 15% of protein. Although it is a chief source of carbohydrates and protein in Asia, it also provides minerals and fibers. In ancient days farmers grows only landraces and which gives limited yield. After green revolution, the high yielding fertilizer responsive and short statured rice varieties introduced in the country, this event helped in attaining self-sufficiency in grain production at the cost of loss of conventional varieties (Chakrapathy *et al.,* 2012). Apart from yield, people preferring varieties with acceptable grain qualities.

The Government of India enacted a legislation on the "Protection of Plant Varieties and Farmers Act" (PPV&FRA) in 2001 for providing protection to plant varieties based on distinctiveness, uniformity, and stability (DUS) test apart from novelty. This is a unique and model act which gives equal importance to the farmers and breeders and treats them as partners in their efforts for sustainable food security (Patra, 2000). The concept of DUS is thus, fundamental to the characterization of a variety as a unique creation. Characterization is essential for identifying and avoiding the duplication of a variety. Characterization should eventually lead to the system of recording and storing the useful data that can be readily retrieved and made available to others and helps in planning breeding programme (Dabas *et al*., 1994).A major objective of varietal characterization is to establish the distinctiveness among the varieties.

Registration is allowed for three types of plant varieties that is new varieties bred by breeders, extant varieties and farmer's varieties subject to their fulfilling the conditions of DUS in case of breeder's variety (Rawte and Saxena, 2018). The uniqueness of a particular variety is to be established by the DUS test. For all major crop species, morphological and physiological descriptors are available to establish the uniqueness of a variety (Moukoumbi *et al.,* 2011). Hence, characterization and registration of rice cultivars are crucial for the genetic improvement, release

and seed production programs. The identity profiles of rice varieties were established by using set of morphological characteristics prescribed in the DUS test guidelines of rice. Thus, characterization of mutant lines will further contribute towards creating a genetic database for breeding programs.
A critical analysis of the genetic variability is a prerequisite for any crop improvement programme and for adopting of appropriate selection techniques (Dhanwani *et al*., 2013). Mutation breeding is one of the tool for inducing desired attributes or variability. Induced mutation (physical or chemical) has been documented as an effective method to improve food production in rice, sunflower, wheat, and many other crop varieties (Riaz and Gul, 2015). More than 3000 mutant varieties have been developed in 200 plant species over the past six decades (Kurowska *et al*., 2012). Many mutant varieties have been developed by radiation, as direct mutants, with gamma rays, x-rays, fast neutrons and other radiation sources (Maluszynski *et al.*, 2001). Many characteristics of 828 rice cultivars have been improved by mutation, resulting in a high yield, colored grain rice, culinary quality, disease resistance, drought tolerance, a shorter duration, a shorter height, and being slightly aromatic (Xuan *et al*., 2019).

Mutation breeding can be used to alter a specific character without altering the genetic makeup of the cultivar. Keeping this in view, a research work on development of mutants was undertaken during 2013-16 involving two high yielding rice varieties *viz.*, ADT 37 and ADT (R) 45. These two varieties are popular among the farmers of Tamil Nadu because of its high yield potential. The variety ADT (R) 45 is considered as one of the best variety with good grain quality and fetches high price in the market due to its medium slender grain type, but the only lacuna is its less 1000 grain weight (17.50 g) and susceptibility to lodging. The another variety ADT 37 is used for *idli* making due to its short bold grain type, but it is less preferred for cooked rice. In order to improve these traits, it was programmed to isolate mutants with non-lodging and increased 1000 grain weight in ADT (R) 45 and medium slender grain type in ADT 37. The present study was conducted to characterize 45 mutant line generated from these varieties and also to identify the desirable mutants.

Materials and Methods

The materials comprised of 45 M_5 mutant lines which were developed using gamma and electron beam radiation. The mutant lines include nine mutants of ADT 37 and 36 mutants of ADT (R) 45 (Table 1). These were raised at Agricultural College & Research Institute, Madurai during *kharif*, 2018 in a plot size of 4 sqm (4 m×1m) with a plant spacing of 20 cm × 20 cm. Five plants were selected randomly from each mutant line to record the observations on plant characters. National DUS guidelines on rice were followed to characterize the rice mutant lines. Twelve morphological characters and twelve quantitative characters were recorded at different stages of crop growth.

The plants were examined for different morphological characters during different growth stages in field. Leaf blade length, leaf blade width, ligule shape, ligule colour and culm attitude were recorded at booting stage. Days to 50 % flowering, flag leaf attitude and colour of stigma were observed at flowering stage. At the time of maturity, plant height, panicle numbers per plant, panicle length, panicle exertion, panicle attitude, presence of secondary branching, presence of awns, awn distribution and sterile lemma colour were recorded. The characters *viz.*, number of filled grains per panicle, single plant yield, 1000 grain weight, grain length , grain width, LB ratio and seed shape were recorded after harvest.

The diversity analysis was performed on twelve quantitative characters. Hierachial classification was done using ward's method based on square Enclidaen D^2 technique through $SPSS_{16.0}$. The genetic divergence between two genotypes was calculated using the formula proposed by Mahalanobis (1936).The quantitative data were statistically analysed by the analysis of variance (ANOVA) method to find the significant differences between the mutant lines for each character. Analysis of variance worked out by the method suggested by Panse and Sukhatme (1961) and the genotypic and phenotypic and environmental coefficient of variances was estimated by the method suggested by Burton, 1952).

The GCV and PCV are classified as low (< 10%), medium (10-20%) and high (> 20%) suggested by Sivasubramanian and Madhavamenon (1973). Heritability was estimated by the formula given by Johnson *et al.* (1955) and they classified the heritability as low (below 30%), medium (30-60%) and high (above 60%).

The expected genetic advance as percent of mean for different traits under study was estimated using formula suggested by Comstock and Robinson (1952). The range of genetic advance as percent of mean was classified as low (0-10%), moderate (10-20%) and high (>20%) suggested by Johnson *et al.* (1955).

Results and Discussion

A total of 45 M_5 mutant lines along with two parental varieties *viz.,* ADT 37 and ADT (R) 45 were taken for characterization using 24 DUS characters. Out of the twelve visually assessed DUS characters studied, six were found monomorphic (shape of ligule, colour of ligule, stigma colour, sterile lemma colour, panicle secondary branching, and panicle attitude), five were dimorphic (Culm attitude, panicle exertion, flag leaf attitude, Presence of awns and distribution of awns) and the grain shape was polymorphic *i.e*. medium slender (24 lines), short bold (5 lines) and long slender (18 lines) (Table 2 & 3). Two mutant lines M 37 and M 39 were distinct from the parental variety ADT (R) 45 for culm attitude and flag leaf attitude (Table 2). With respect to mutant lines of ADT 37, six were identified with desirable medium slender grain type.

Chakrabarthy *et al.* (2012) has recorded 44 plant and grain qualitative characters in 91 farmer's varieties. Among these characters, eight showed only single state of expression, eight were dimorphic, thirteen trimorphic and remaining fifteen showed more than three states of expression. Manjunatha *et al*. (2018) has recorded 25 qualitative and quantitative characters in sixty landraces of rice collected from Wayanad. Among this, three were monomorphic, seven were dimorphic, six were trimorphic, seven were tetramorphic and grain shape showed five state of expression.

The mean performance for various quantitative traits is presented in Table 4. Among the 36 mutant lines of ADT (R) 45, seven lines *viz,* M6, M55, M66, M78, M79, M85 and M88 had significant reduction in plant height compared to the parental variety ADT (R) 45. Of these seven lines, M6, M66, M79, M85 and M88 were identified as desirable mutant lines since these lines also had significant increase in hundred grain weight compared to ADT (R) 45. In the case of mutant lines of ADT 37, six mutant lines *viz.,* M69, M71, M78, M79, M85 and M88 had recorded significant increase in LB ratio in comparison with the parental check ADT 37.

The analysis of variance revealed the existence of significant differences among the genotypes for six characters *viz.*, days to 50% flowering, plant height, number of productive tillers, number of filled grains per panicle, single plant yield and panicle length (Table 5). The mean, variability estimates *ie*., Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation(PCV), Heritability (%) and Genetic advance as percent of means are presented in Table 6. The traits *viz*., leaf blade length, days to 50 % flowering, plant height, panicle length, kernel length and kernel breadth had high low GCV indicating that the mutant lines had attained homozygosity for these characters. High GCV and PCV were observed for number of productive tillers (23.19%) and single plant yield (21.07%), hence these characters can be improved through selection. Genotypic coefficient of variation measures the extent of genetic variability per cent for a trait but does not asses the amount of genetic variation which is heritable (Manjunatha *et al*., 2018).

The estimates of heritability act as the predictive instrument in expressing the reliability of phenotypic value (Nuruzzaman *et al*., 2016). The traits expressed moderate to high heritability estimates ranging from 34.80% to 99.93%. Heritability estimates were high for 100 grain weight (99.93%), kernel breadth (99.43%), leaf blade width (95.31%), LB ratio (95.31%), kernel length (91.67%), leaf blade length (79.52%), single plant yield (74.97%) and number of productive tillers (63.45%) (Table.6). High heritability indicates that the traits under study are less influenced by environment in their expression and have greater possibility of genetic improvement through selection methods (Patel *et al*., 2012). Whereas, panicle length (34.80%), days to 50% flowering (38.65%), number of filled grains per panicle (58.34) and plant height (59.32%) had moderate heritability.

The heritability estimates along with genetic advance can be useful for predicting the effect of selection in breeding programme. In the present study, genetic advance as percent of mean was highest for single plant yield (57.58%), number of productive tillers (38.05%), LB ratio and leaf blade width (32.89%), 1000 grain weight (26.14%) and number of filled grains per panicle (22.14%) and lowest for days to 50% flowering (3.64%). The traits *viz*., number of productive tillers, leaf blade width, 1000 grain weight, LB ratio and single plant yield has high heritability along with genetic advance as percent of mean indicate that these characters attributable to addictive gene effects which are fixable revealing that improvement in these characters would be possible through direct selection.The D^2 analysis of the Qualitative and quantitative characters grouped the mutant lines into seven clusters (Fig.1). Cluster IV comprised of maximum number of genotypes (27 lines) followed by cluster II (6 lines) and cluster V (5 lines). The cluster III comprised four genotypes and clusters both VI and VII comprised of two genotypes. Cluster I comprised of only one genotype. The divergence between the mutant lines was less due to these mutant lines are derived from only two parents. However some level of divergence was observed between these lines. The intra cluster distance was maximum in cluster I (4.874) and minimum in cluster VII (2.107) (Table 7). Hence the genotypes within the cluster I was more divergent from each other than those in cluster VII. The highest inter-cluster distance (12.164) was recorded between clusters I and cluster VI and followed by cluster I and Cluster III. The minimum inter-cluster distance (6.979) was observed between cluster II and III. The values of inter-cluster and intra-cluster distances are independent of the number of mutant lines grouped into a particular cluster. The lines belonging to distantly located clusters may be used for further improvement of desired traits (Chakraparthy *et al*., 2012).

It is concluded from the present investigation that five mutant lines *viz*., M6, M66, M79, M85 and M88 of ADT (R) 45 were identified as desirable lines based on non-lodging habit and increase in 1000 grain weight and six mutant lines *viz*., M69, M71, M78, M79, M85 and M88 of ADT 37 with medium slender grain type were selected. These lines will be evaluated in the yield trials and the promising mutant lines will be nominated for Multi Location Trial (MLT). Two novel mutant lines M 37 and M 39 which were distinct from the parental variety ADT (R) 45 for culm attitude and flag leaf attitude will be registered under PPV&FR Act for obtaining plant breeder's rights.

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Table 1. List of mutant lines

Mutants of ADT (R) 45		
S.No.	**Mutant lines**	**Particulars of irradiation**
1.	M1	100 Gray of Gamma radiation
2.	M2	200 Gray of Electron beam radiation
3.	M3	200 Gray of Electron beam radiation
4.	M5	300 Gray of Electron beam radiation
5.	M6	300 Gray of Electron beam radiation
6.	M7	200 Gray of Electron beam radiation
7.	M11	400 Gray of Gamma radiation
8.	M17	200 Gray of Electron beam radiation
9.	M18	300 Gray of Electron beam radiation
10.	M19	500 Gray of Electron beam radiation
11.	M20	200 Gray of Electron beam radiation
12.	M21	600 Gray of Electron beam radiation
13.	M24	400 Gray of Electron beam radiation
14.	M26	300 Gray of Electron beam radiation
15.	M27	500 Gray of Electron beam radiation
16.	M28	300 Gray of Gamma radiation
17.	M30	400 Gray of Electron beam radiation
18.	M33	200 Gray of Electron beam radiation
19.	M35	200 Gray of Electron beam radiation
20.	M37	400 Gray of Electron beam radiation
21.	M39	300 Gray of Gamma radiation
22.	M43	500 Gray of Electron beam radiation
23.	M44	400 Gray of Electron beam radiation
24.	M46	300 Gray of Electron beam radiation
25.	M49	500 Gray of Gamma radiation
26.	M50	400 Gray of Electron beam radiation
27.	M52	200 Gray of Gamma radiation
28.	M55	300 Gray of Electron beam radiation
29.	M57	400 Gray of Electron beam radiation
30.	M58	200 Gray of Electron beam radiation
31.	M60	300 Gray of Gamma radiation
32.	M63	100 Gray of Gamma radiation
33.	M64	600 Gray of Electron beam radiation
34.	M65	600 Gray of Electron beam radiation
35.	M66	500 Gray of Electron beam radiation
36.	M67	300 Gray of Gamma radiation
Mutants of ADT 37		
S.No.	**Mutant lines**	**Particulars of irradiation**
37.	M68	400 Gray of Electron beam radiation
38.	M69	400 Gray of Electron beam radiation
39.	M71	200 Gray of Electron beam radiation
40.	M74	400 Gray of Electron beam radiation
41.	M78	200 Gray of Electron beam radiation
42.	M79	200 Gray of Electron beam radiation
43.	M85	100 Gray of Gamma radiation
44.	M88	300 Gray of Electron beam radiation
45.	M92	500 Gray of Electron beam radiation

Table 2. Characterization of rice mutant lines based on morphological DUS descriptors

Lines	Culm attitude	Shape of ligule	Colour of ligule	Flag Leaf attitude	Awns	Dis. Of awns	Panicle Secondary branching	Panicle exertion	Sterile Lemma colour	Stigma colour	Panicle attitude	Grain shape
M1	SE	Split	Colourless	SE	P	UH	Present	WE	Straw	White	E to SE	LS
M2	SE	Split	Colourless	SE	A	A	Present	WE	Straw	White	E to SE	MS
M3	SE	Split	Colourless	SE	P	UH	Present	ME	Straw	White	E to SE	LS
M5	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M6	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M7	E	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M11	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M17	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M18	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M19	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	SB
M20	SE	Split	Colourless	SE	A	A	Present	WE	Straw	White	E to SE	SB
M21	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M24	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M26	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M27	SE	Split	Colourless	E	A	A	Present	ME	Straw	White	E to SE	MS
M28	SE	Split	Colourless	SE	P	Tips only	Present	ME	Straw	White	E to SE	MS
M30	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M33	E	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	SB
M35	E	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M37	E	Split	Colourless	E	A	A	Present	ME	Straw	White	E to SE	MS
M39	E	Split	Colourless	E	A	A	Present	ME	Straw	White	E to SE	LS
M43	E	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M44	E	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M46	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M49	SE	Split	Colourless	SE	A	A	Present	WE	Straw	White	E to SE	LS
M50	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M52	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M55	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M57	SE	Split	Colourless	SE	A	A	Present	WE	Straw	White	E to SE	LS
M58	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M60	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M63	SE	Split	Colourless	E	A	A	Present	WE	Straw	White	E to SE	MS
M64	SE	Split	Colourless	SE	A	A	Present	WE	Straw	White	E to SE	MS
M65	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M66	SE	Split	Colourless	SE	P	UH	Present	ME	Straw	White	E to SE	MS
M67	SE	Split	Colourless	SE	P	UH	Present	ME	Straw	White	E to SE	SB
ADT (R)45	SE	SPLIT	COLOURLESS	SE	A	A	PRESENT	WE	STRAW	WHITE	E to SE	MS
M68	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
M69	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M71	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M74	SE	Split	Colourless	SE	P	UH	Present	ME	Straw	White	E to SE	LS
M78	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M79	SE	Split	Colourless	SE	A	A	Present	WE	Straw	White	E to SE	MS
M85	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M88	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	MS
M99	SE	Split	Colourless	SE	A	A	Present	ME	Straw	White	E to SE	LS
ADT37	SE	SPLIT	COLOURLESS	SE	A	A	PRESENT	ME	STRAW	WHITE	E to SE	SB

SE- Semi erect, A- Absent, P- Present, UH- Upper half only, WE- Well exerted, ME- Mostly exerted, E to SE- Erect to semi erect, MS- Medium slender, LS- Long slender, SB- Short bold

Table 3. Frequency distribution of Qualitative characters

S. No	Characteristics	States	Score	No. of. genotypes				Frequency Distribution (%)
				ADT (R) 45 mutant lines	ADT (R) 45	ADT 37 mutant lines	ADT 37	
1.	Culm attitude	Erect	1	7	0	0	0	14.89
		Semi erect	3	29	1	9	1	85.11
		Open	5	0	0	0	0	0
		Spreading	7	0	0	0	0	0
2.	Shape of the ligule	Truncate	1	0	0	0	0	0
		Acute	2	0	0	0	0	0
		Split	3	36	1	9	1	100
3.	Colour of the ligule	White	1	36	1	1	9	100
		Light purple	2	0	0	0	0	0
		Purple	3	0	0	0	0	0
4.	Flag leaf attitude	Erect	1	4	0	0	0	8.51
		Semi- erect	3	32	1	9	1	91.49
		Horizontal	5	0	0	0	0	0
		Deflexed	7	0	0	0	0	0
5.	Panicle exertion	Partly exerted	0	0	0	0	0	0
		Mostly exerted	5	29	0	8	1	80.85
		Well exerted	7	7	1	1	0	19.15
6.	Panicle attitude	Erect	1	0	0	0	0	0
		Erect to semi erect	3	36	1	9	1	100
		Semi- erect	5	0	0	0	0	0
		Semi-erect to Spreading	7	0	0	0	0	0
		Spreading	9	0	0	0	0	0
7	Panicle length of main axis	Very short (<16 cm)	1	0	0	0	0	0
		Short (16-20 cm)	3	9	0	0	1	21.28
		Medium (21-25 cm)	5	27	1	8	1	78.72
		Long (26-30 cm)	7	0	0	0	0	0
		Very long (>30 cm)	9	0	0	0	0	0
8.	Panicle secondary branching	Absent	1	0	0	0	0	0
		Present	9	36	1	9	1	100
9.	Sterile lemma colour	Straw	1	36	1	9	1	100
		Gold	2	0	0	0	0	0
		Red	3	0	0	0	0	0
		Purple	4	0	0	0	0	0
10.	Presence of Awns	Absent	1	32	1	8	1	87.23
		Present	9	5	0	1	0	12.77
11.	Distribution of awns	Tips only	1	1	0	0	0	6.38
		Upper half only	3	4	0	1	0	10.64
		Whole length	5	0	0	0	0	0
12.	Shape of the grain	Short slender	1	0	0	0	0	0
		Short bold	2	4	0	0	1	10.64
		Medium slender	3	16	1	7	0	51.06
		Long slender	4	15	0	3	0	38.30
		Long bold	5	0	0	0	0	0
		Basmati type	5	0	0	0	0	0
		Extra-long slender	6	0	0	0	0	0

Table 4. Mean performance of quantitative characters of mutant lines and parents

LINES	Leaf	Leaf Blade Width (cm)	Days to 50% flowering	Plant Height ** (cm)	No. of. Productive tillers	Panicle length (cm)	No. of. Filled grains per panicle	Single Plant Yield (g)	1000 Grain Weight ** (g)	Kernel Length (mm)	Kernel Breadth(mm)	LB ratio ***
M1	31.4	1.8	84.0	92.7*	17.0	20.9	122.0	36.1	16	5.9	1.9	3.1
M2	30.3	1.3	83.0	102.6*	14.0	22.2	162.4	46.7	17	6.1	2.1	2.9
M3	31.6	1.2	84.0	93.0*	17.0	21.0	130.0	24.4	17	6.2	1.9	3.3
M5	30.4	1.6	85.0	96.1*	16.0	22.8	130.0	25.0	17	6.0	1.9	3.2
M6	30.6	1.4	84.0	94.7*	17.0	23.7	118.0	37.6	23*	5.9	2.0	3.0
M7	33.2	1.8	84.0	94.7*	18.0	23.8	118.0	31.6	21*	5.9	2.3	2.6
M11	31.4	2.0	84.0	98.3*	18.0	22.7	114.0	25.6	17	5.9	1.7	3.5
M17	31.8	1.2	83.0	92.6*	19.0	21.7	125.0	33.0	14	5.9	2.0	3.0
M18	30.8	1.4	86.0	101.4*	20.0	19.5	116.0	30.9	16	5.9	1.8	3.3
M19	32.3	1.4	85.0	104.2*	16.0	21.2	126.0	24.1	16	5.5	2.3	2.4
M20	31.2	1.6	85.0	95.8*	16.0	22.4	134.0	34.0	16	5.2	2.1	2.5
M21	30.6	1.9	84.0	106.2	13.0	19.5	154.0	28.3	15	5.5	2.0	2.6
M24	32.0	1.2	84.0	106.5	17.0	21.2	106.0	17.5	17	5.6	1.9	2.9
M26	31.3	1.4	84.0	93.8*	18.0	20.8	137.0	22.3	18*	6.2	1.9	3.3
M27	31.4	1.4	86.0	94.8*	14.0	19.5	146.0	17.6	19*	6.0	2.2	2.7
M28	30.8	1.6	85.0	99.0*	19.0	19.0	156.0	16.2	19*	5.8	2.0	2.9
M30	30.4	1.3	84.0	96.3*	15.0	19.8	120.0	22.4	18*	6.3	1.8	3.5
M33	32.1	1.8	84.0	97.5*	18.0	20.3	137.0	20.4	16	5.8	2.0	2.1
M35	31.4	1.7	86.0	98.2*	19.0	22.4	132.0	25.8	19*	5.9	2.1	2.8
M37	31.0	1.4	85.0	90.4*	14.0	21.5	143.0	14.5	23*	6.3	2.1	3.0
M39	31.6	1.5	84.0	97.0*	17.0	20.0	116.0	21.4	17	6.0	1.9	3.2
M43	30.2	1.3	84.0	116.0	16.0	20.0	117.0	27.6	17	6.2	1.7	3.4
M44	32.1	1.3	88.0	94.8*	15.0	20.5	142.0	21.9	14	5.7	2.0	2.9
M46	31.6	1.7	85.0	95.0*	14.0	20.3	157.0	22.4	18*	6.3	1.8	3.5
M49	30.6	1.7	85.0	92.4*	11.0	22.2	143.0	24.0	17	6.0	1.8	3.3
M50	34.0	1.6	84.0	96.4*	16.0	21.4	147.0	22.4	17	5.8	1.9	3.1
M52	33.2	1.7	86.0	89.0*	9.0	20.7	128.0	12.7	21*	5.6	1.8	3.1
M55	33.0	1.4	84.0	90.0*	15.0	20.7	168.0	25.9	17	6.0	2.0	3.0
M57	31.6	1.6	84.0	89.0*	16.0	21.8	152.0	26.3	18*	5.3	1.7	3.1
M58	30.7	2.1	85.0	77.5*	8.0	19.4	148.0	18.3	16	6.2	2.1	3.0
M60	30.4	1.5	86.0	82.3*	9.0	20.4	148.0	16.4	17	6.1	1.8	3.4
M63	30.8	1.4	84.0	84.7*	15.0	22.1	108.6	20.3	16	5.9	2.1	2.8
M64	31.6	1.8	88.0	85.5*	10.0	21.1	144.0	25.9	19*	5.8	2.2	2.6
M65	31.0	1.4	85.0	77.0*	6.0	18.4	152.0	15.1	18*	5.8	2.2	2.6
M66	31.1	1.2	84.0	86.5*	10.0	20.8	206.0	30.5	23*	5.8	2.4	2.5
M67	31.4	1.9	87.0	95.5*	11.0	24.8	189.0	31.2	21*	5.7	2.4	2.4
ADT(R)45	31.2	1.7	84.0	112.3	13.0	21.5	188	29.7	17	6.3	2.1	3.0
M68	31.4	1.3	87.0	97.4	14.0	22.7	129.0	21.1	17	6.1	1.9	3.2
M69	30.8	1.8	89.0	101.2	13.0	18.7	186.0	29.2	19	5.9	2.0	3.0*
M71	30.7	1.6	89.0	99.7	13.0	20.8	170.0	22.2	16	5.7	2.1	2.7*
M74	31.4	2.2	87.0	96.2	11.0	21.8	121.0	22.0	21	6.2	1.9	3.3
M78	31.3	1.6	85.0	101.8	12.0	21.9	144.0	22.5	17	6.4	2.2	2.9*
M79	30.6	1.8	85.0	98.4	14.0	20.6	174.0	28.5	18	6.0	2.1	2.9*
M85	30.1	1.3	88.0	88.9	15.0	21.4	168.0	29.5	19	6.6	2.2	3.0*
M88	32.4	1.5	84.0	87.4	14.0	21.2	112.0	18.4	18	6.2	2.2	3.0*
M92	30.9	1.6	85.0	86.8	18.0	21.7	106.0	21.7	19	6.4	2.0	3.2
ADT37	32.6	1.8	84.0	106.4	14.0	20.8	184.0	34.6	23	5.1	2.5	2.0
Mean	31.42	1.57	85.08	95.2	14.52	21.16	142.06	25	17.9	5.93	2.00	2.95
S. Ed	0.344	0.045	0.989	3.754	2.072	1.424	14.271	2.652	0.005	0.080	0.012	0.047
CD	0.684	0.090	1.964	7.456	4.116	2.829	28.347	5.268	0.010	0.159	0.023	0.093

***significance at 5% level**

****** Significance is given for the mutant lines of ADT (R) 45 in comparison with parental check for plant height and 1000 grain weight

*** - Significance is given for the mutant lines of ADT 37 in comparison with parental check for LB ratio

Table 5. Analysis of variance for different quantitative traits

S. No	Character	Genotype Sum of squares (d.f.=46)
1.	Leaf blade length	2.2463
2.	Leaf blade width	0.1919
3.	Days to 50% flowering	4.2369*
4.	Plant height	113.5752**
5.	Number of productive tillers	39.9923**
6.	Panicle length	7.9128**
7.	Number of filled grains per panicle	1589.1160**
8.	1000 seed weight	0.1616
9.	Single plant yield	105.3685**
10.	Kernel length	0.3266
11.	Kernel breadth	0.1091
12.	LB ratio	0.3291

Table 6. Estimates of variability, heritability and Genetic advance as percentage of mean

S.No	Characters	GCV (%)	PCV (%)	Heritability (%)	GA (%) of mean
1.	Leaf blade length	2.71	3.04	79.52	4.98
2.	Leaf blade width	16.35	16.75	95.31	32.89
3.	Days to 50% flowering	1.13	1.81	38.65	1.44
4.	Plant height	5.86	7.61	59.32	9.29
5.	No. of. productive tillers	23.19	29.11	63.45	38.05
6.	Panicle length	6.09	10.33	34.80	7.41
7.	No. of. filled grains per panicle	16.07	18.42	58.34	22.14
8.	1000 grain weight	12.98	12.99	99.93	26.14
9.	Single plant yield	21.07	24.34	74.97	57.58
10.	Kernel length	5.50	5.75	91.67	10.85
11.	Kernel breadth	9.44	9.46	99.43	19.38
12.	LB ratio	11.16	16.75	95.31	32.89

Table 7. Intra and inter-cluster distances among the mutant lines

Cluster no	1	2	3	4	5	6	7
1	**4.874**	6.748	**12.164**	5.978	11.784	6.476	5.178
2		4.165	**6.979**	8.634	9.635	9.764	7.845
3			3.231	9.675	11.897	8.528	9.898
4				3.67	6.253	9.456	6.143
5					2.879	7.543	7.634
6						3.713	10.724
7							2.107

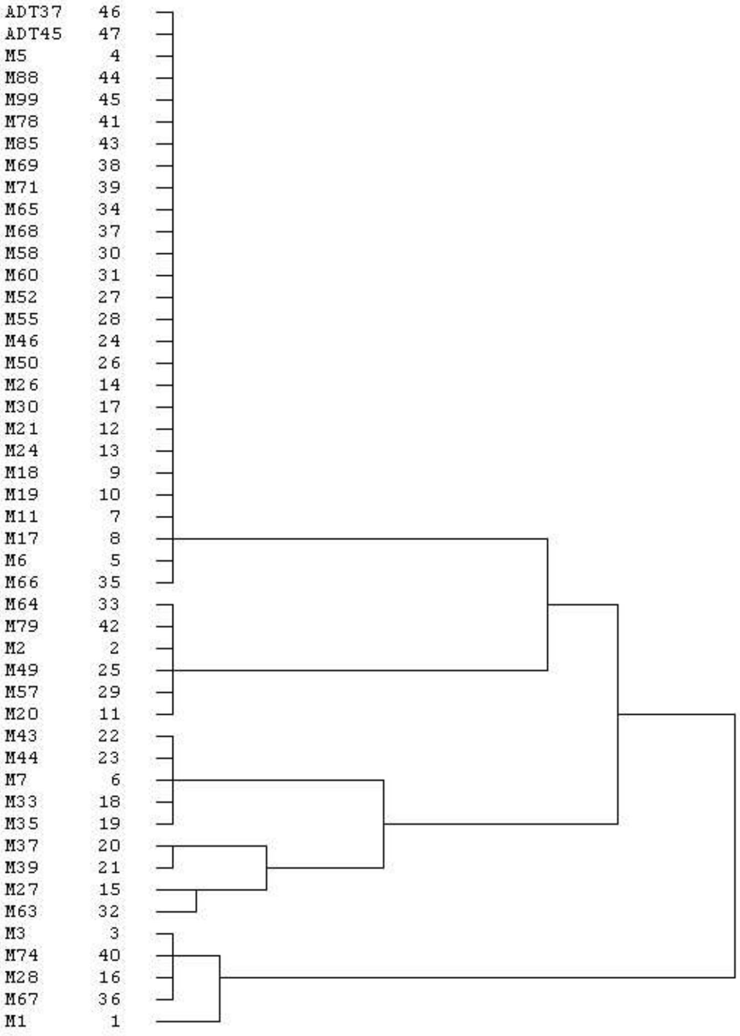

Fig 1. Dendogram showing genetic relationship among the mutant lines

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