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## Genetic Variability and Association Studies in Salt Tolerant Rice Mutant

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### ABSTRACT

Among the various factors limiting rice yield, salinity is one of the oldest and most serious environmental problems in the world. The available rice germplasm has limited variability for salt tolerance. Hence, the study was to develop salt tolerant rice varieties by inducing variability through mutation and selecting high yielding salt tolerant mutants. Variability and correlation studies were conducted to isolate salt tolerant mutants from two rice varieties ADT 43 and ASD 16. Gamma irradiated (10, 20, 25, 30, 40 and 50 kR) salt tolerant mutants were identified in M<sub>2</sub> generation. M<sub>3</sub> and M<sub>4</sub> generations of the mutant population were investigated for correlation among yield and its components which can be utilized for selection. Altered conditions were observed in the mutant population when compared to the unaltered population depending on the dose, genotype and the character pairs. Morphologically stable salt tolerant mutants till M<sub>5</sub> were selected based on the characters identified using correlation studies and for increased yield. Seed yield of mutant lines showed an increase upto 446.94 (20 kR of ADT 43) which was higher than the parental varieties (255.56 and 384.13 for ADT 43 and ASD 16). The number of tillers, panicle length and plant height were also much higher in some mutants than in parent varieties. Results on yield and contributing characters possesses sufficiently high values of heritability and genetic advance which can be utilized for further improvement in rice and in evolving a high yielding saline tolerant variety.

**Key words:** Genetic advance, heritability, mutation, *Oryza sativa*, salinity, genetic variability

### INTRODUCTION

It is notable that the grain yield, especially of rice has not been harvested in commensuration to its existing genetic potential in almost all rice-growing ecosystems. One of the major reasons behind this failure is the sensitivity of this crop to abiotic stresses particularly salinity (Grover *et al.*, 2000). Salt stress is one of the major abiotic stresses, which adversely affect the crop productivity (Yasseen *et al.*, 2010; Joseph and Jini, 2010). It causes reduction of crop yield and alterations in plant metabolism, including a reduced water potential, ion imbalances and toxicity and sometimes severe salt stress may even threaten survival (Joseph and Jini, 2011). So the need of the hour is to develop plants with resistance to abiotic stresses. In a study conducted by Naifer *et al.* (2011), it is inferred that losses incurred by farmers due to salinity were estimated at \$ 1,604 ha<sup>-1</sup> (28%) if salinity increases from low salinity to medium salinity level and \$ 4,352 ha<sup>-1</sup>

(76%) if it jumps from low salinity to high salinity level. So excess of salt in the soil limits the yield potential. Rice is the most economically important cereal crop in many parts of the world and considered as a salt sensitive species (Htwe *et al.*, 2011). Even a low concentration of 50 mM is not tolerable (Flowers and Yeo, 1981). In order to produce new rice genotypes with better adaptation to salinity, mutation techniques can be used (Mba *et al.*, 2007). Mason *et al.* (2010) reported that the gene Arabidopsis high-affinity K<sup>+</sup> transporter 1;1 (AtHKT1;1) responsible for removing sodium ions from the root xylem was repressed by cytokinin treatment, but showed significantly elevated expression in the cytokinin response double mutant *arr1-3 arr12-1*. They also find out that cytokinin, acting through the transcription factors ARR1 and ARR12, regulates sodium accumulation in the shoots by controlling the expression of AtHKT1;1 in the roots.

Plants respond to stress via physiological, cellular and molecular process to survive. This is expressed in the form of change in expression of phenotypic traits. The characters affected by salinity vary with crop. In rice, plant height, total number of tillers, panicle length, grain weight per panicle, 1000-seed weight and quality and quantity of grains decreased progressively with increase in salinity levels (Abdullah *et al.*, 2001). The differences between salt tolerance lines and the sensitive lines were much larger for all traits except for chlorophyll content (Thomson *et al.*, 2010). Negative characters in traditional varieties and complex traits involved in salinity tolerance have presented challenges for conventional breeding (Yamaguchi and Blumwald, 2005). Breeding saline tolerant lines necessitates the understanding of salinity and the characters affected. Important components of grain yield such as the number of productive tillers and panicle length are affected by salinity and grain yield gets reduced. Other morphological traits such as plant height also get affected at high salt concentrations (Navarro, 2002). The association of characters is reported to change with mutation, hence the knowledge of nature and extent of correlation between yield and its component traits in salt tolerant lines is essential. Based on the characters identified, the selection for high yielding salt tolerant mutants can be identified in presence of a variable population. Therefore, the variability present for selecting saline tolerant lines is a prerequisite. The objective of the study being development and establishment of efficient methodologies for the induction of mutants, screening and development of rice varieties tolerant to salinity stress the mutation was used to induce variability for saline tolerance in two high yielding varieties. The correlation and variability was worked out to identify high yielding salt tolerant mutants.

## MATERIALS AND METHODS

A field experiment was conducted at the Agricultural College and Research Institute, Killikulam, Tamil Nadu during the year 2007 to 2010. Two varieties of rice (*Oryza sativa*) namely, ASD 16 and ADT 43 were used as experimental materials. Dry seeds were irradiated with 10, 20, 25, 30, 40 and 50 kR dose of gamma rays from <sup>60</sup>Co source at Tamil Nadu Agricultural University, Coimbatore. In the present study, from M<sub>2</sub> progenies, 10 salt tolerant single plants from each treatment (Gamma rays 10, 20, 25, 30, 40 and 50 kR) were selected by artificially inducing salt stress (EC 12 ds m<sup>-1</sup>) under field conditions and M<sub>3</sub> generation were raised subsequently. In M<sub>3</sub>, 10 single plants were selected. The seeds of the individual plants were sown in progeny rows in Randomized Block Design with three replications. Observations were made on 15 randomly selected plants at the rate of five plants per replications. The single plants with increased yield were selected for M<sub>4</sub> generation. Selection on individual plant was practised in M<sub>4</sub> generation based on increased plot yield. The seeds of selected plants in M<sub>4</sub> were forwarded to M<sub>5</sub> generation. Each mutant line and control was grown in uniform size plots.

**Statistical analysis:** The estimates of the intercomponent correlations were calculated in both  $M_3$  and  $M_4$  generations as per the standard method for correlation analysis suggested by Goulden (1952). Using data on  $M_3$  generation, analysis of variance was done following the method suggested by Singh and Chaudhary, 1985. Genotypic variance was determined by the formula suggested by Burton (1952). Heritability in broad sense was computed by the formula suggested by Johnson *et al.* (1955) and the genetic advance according to the formula given by Allard (1960).

## RESULTS AND DISCUSSION

**Correlation studies:** Significance was observed in association between panicle length and yield in  $M_3$  population at 30 and 40 kR (0.9999 and 0.8705) of ASD 16 and at 40 and 50 kR of ADT 43 (-0.8519 and -0.9055) as against non significance in all other doses and control population. Association of yield with productive tiller was significant in 50 kR of ADT 43 (0.9690) and control (0.9308 and 0.9707) whereas it was non significant in all the other treatments. In ASD 16 of  $M_3$  population, significance was noted at 10 (0.9604), 25 (0.8882) and 40 kR (0.8862) alone as in control with reversal in the other doses. Association was significant between plant height and yield at 10 (0.9034), 25 (0.9799) and 40 kR (0.9598) in ASD 16 and at 25 (0.9912) and 50 kR (0.9707) in ADT 43 as in control (0.9992 and 0.9986) with non significance in the other population (Table 1). Kole *et al.* (2008) reported that grain yield was found to be positively and significantly correlated with plant height and panicle number per plant in induced mutants of aromatic basmati rice and also suggested selection for medium plant height indicating reversal in association in some mutants.

Association reversal was noted between boot leaf length and yield at 10 (0.9966) and 40 kR (0.9782) of ASD 16 and at 25 (0.9912) and 50 kR (0.9707) of ADT 43 in  $M_3$  population. Significance between chlorophyll content a (chl<sub>a</sub>) and yield was found in 25kR (0.9842) and 40 kR (0.9791) of ASD 16 and 25 kR (0.9461) and 50 kR (1.000) of ADT 43 as against non significance in control population. Similarly, Chl b also show significance with yield in 10 kR (0.9941), 40 kR (0.8607) and 50 kR (-0.8565) of ASD 16 and 50 kR (-0.8700) of ADT 43 (Table 1). Chlorophyll content was found to be increased with an increase in radiation dose under saline conditions (Shereen *et al.*, 2009). This supports our study where we have observed an increase in chlorophyll contents with an increase in yield in some mutants.

The non significant association of 100 seed weight and seed yield in control population of ASD 16 (0.0345) and ADT 43 (0.7302) was altered in  $M_4$  generation at 20 kR (0.9827 and -0.9464) and 25 kR (0.9951 and -0.9748) for both the genotypes respectively. Besides, ADT 43 also shows a significant association at 30 kR (-0.9915) and 40 kR (0.9985) for the above parameters. The association of yield with number of productive tillers was non significant in the irradiated population at all the doses except 40 kR of ASD 16 (0.8195) and 20 kR of ADT 43 (0.8990) in  $M_4$  population, whereas it was significant in the control population (0.9308 and 0.9707). Negative significance was found between plant height and yield at 30 kR (-0.9221) and 50 kR (-0.9223) in  $M_4$  of ASD 16 as in control while significance was positive at 25 kR (0.8941) of ADT 43. In irradiated population the association was non significant at all the other doses. Reversion in association between days to 50% flowering and seed yield was noted in  $M_4$  population at 10, 20 and 25 kR of ASD 16 and at 20, 30, 40 and 50 kR of ADT 43 as compared to control (0.8856 and -0.9860) (Table 2).

The nature of alternation in the association varied with the mutagenic doses, genotypes and the character pairs (Rafi, 1987). These results indicate that the situation can be exploited by

Table 1: Association between yield and yield components in ASD 16 and ADT 43 in the M<sub>3</sub> generation

Characters	Treatment	Productive tillers		Plant height		boot leaf length		Yield		chl a		chl b	
		ASD 16	ADT 43	ASD 16	ADT 43	ASD16	ADT 43	ASD16	ADT43	ASD16	ADT43	ASD16	ADT43
Panicle length	control	0.8660*	-0.5000	0.9820**	0.3273	0.9177**	0.7857	-0.3654	-0.2774	0.9923**	-0.5155	0.9298**	0.9574**
	10kR	-0.6483	-0.3925	0.9902**	0.9774**	0.7867	0.7998	-0.8348	-0.3054	0.9920**	0.9857**	0.7704	0.6083
	20kR	-0.2803	-0.5668	0.9843**	-0.9931**	0.9177**	0.3500	0.0000	0.0000	0.9603**	0.9841**	0.8317	0.9404**
	25kR	0.5283	-0.5117	0.2761	-0.6278	1.0000**	-0.6658	0.0790	-0.5614	-0.0985	-0.7991	0.9749**	-0.5588
	30kR	-0.8171*	-0.6944	-0.6186	-0.1865	0.6186	0.9006*	0.9999**	-0.5290	0.5005	-0.6241	0.0759	0.8897*
Productive tillers	control	-0.9995**	0.1214	0.9737**	-0.5389	0.9538**	0.3966	0.8705*	-0.8519*	0.9524**	-0.4005	0.9998**	0.2964
	10kR	0.9820**	0.9823**	0.8660*	0.9526**	-0.8322*	0.9809**	0.2774	-0.9055*	0.9558**	0.9051*	-0.7335	0.5785
	20kR	1	1	0.9449**	-0.9820**	-0.5960	0.1429	0.9308**	0.9707**	0.7973	-0.4844	0.6211	0.7288
	25kR	1	1	0.7482	-0.1890	0.9800**	-0.8660*	0.9604**	-0.7559	0.5468	-0.2320	0.9849**	0.9688**
	30kR	1	1	0.1063	0.4662	0.1242	0.5734	0.0000	0.0000	0.0015	-0.7042	0.2399	-0.8132*
Plant height	control	1	1	0.9619**	0.9900**	0.5229	-0.3004	0.8882*	-0.4237	0.7929	-0.1076	-0.7040	0.9984**
	10kR	1	1	0.0524	0.8365*	-0.0524	0.9381**	0.8096	-0.2433	-0.9081*	0.9956**	0.5129	0.9463**
	20kR	1	1	0.9806**	0.7707	0.9631**	0.9594**	-0.8862*	0.4163	0.9618**	0.9582**	0.9986**	0.9840**
	25kR	1	1	0.7559	-0.8786*	-0.7125	1.0000**	0.0908	0.9690**	0.8830*	0.9688**	-0.5918	-0.7212
	30kR	1	1	1	1	0.8260*	-0.3273	0.9992**	0.9986**	-0.9510**	0.6410	-0.8434*	-0.5863
Boot leaf length	control	1	1	1	1	-0.8651*	0.6547	0.9034*	0.3273	0.9646**	0.9990**	-0.8518*	0.4266
	10kR	1	1	1	1	0.9734**	-0.4574	0.0000	0.0000	0.9945**	0.9564**	-0.9167*	-0.8940*
	20kR	1	1	1	1	0.2701	-0.11628	0.9799**	0.9912**	0.9292**	0.0337	-0.4832	0.9963**
	25kR	1	1	1	1	1.0000**	-0.5949	0.6286	-0.1076	0.3706	0.8840*	-0.8304*	-0.6144
	30kR	1	1	1	1	0.9972**	0.5596	0.9598**	0.1429	0.9968**	-0.5561	0.9690**	0.6448
Yield	control	1	1	1	1	0.9979**	-0.8752*	0.7206	0.9707**	0.9748**	0.7328	0.9751**	0.3029
	10kR	1	1	1	1	1	1	-0.0345	0.3764	-0.9599**	0.9351**	0.9995**	-0.5736
	20kR	1	1	1	1	1	1	0.9966**	0.3273	-0.7024	0.6872	0.9997**	0.9630**
	25kR	1	1	1	1	1	1	0.0000	0.0000	0.9921**	0.1778	0.9838**	0.0105
	30kR	1	1	1	1	1	1	0.0727	0.9912**	-0.1048	0.9806**	0.9735**	-0.2467
Yield	control	1	1	1	1	1	1	-0.6286	-0.1076	-0.3706	-0.9016*	0.8304*	0.9997**
	10kR	1	1	1	1	1	1	0.9782**	0.1429	1.0000**	1.0000**	0.9478**	0.9949**
	20kR	1	1	1	1	1	1	-0.7635	0.9707**	0.9585**	0.9705**	0.9873**	-0.7261
	25kR	1	1	1	1	1	1	1	1	-0.2471	-0.6803	0.0029	0.5430
	30kR	1	1	1	1	1	1	1	1	0.7585	-0.4615	0.9941**	0.5700

Table 1: Continued

Characters	Treatment	Productive tillers			Plant height			boot leaf length			Yield			chl a			chl b		
		ASD 16	ADT 43	ADT 43	ASD 16	ADT 16	ADT 43	ASD 16	ADT 43	ADT 43	ASD 16	ADT 43	ADT 43	ASD 16	ADT 43	ADT 43	ASD 16	ADT 43	ADT 43
Chlorophyll a	20kR	1	1	1	1	1	1	1	1	1	1	1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
	25kR	1	1	1	1	1	1	1	1	1	1	1	0.9842**	0.9461**	0.9461**	-0.2990	-0.2990	-0.3726	-0.3726
	30kR	1	1	1	1	1	1	1	1	1	1	1	-0.4894	-0.3329	-0.3329	-0.0887	-0.0887	-0.0883	-0.0883
	40 kR	1	1	1	1	1	1	1	1	1	1	1	0.9791**	-0.1386	-0.1386	0.8607*	0.8607*	0.2476	0.2476
	50 kR	1	1	1	1	1	1	1	1	1	1	1	0.5476	1.0000**	1.0000**	-0.8565*	-0.8565*	-0.8700*	-0.8700*
Chlorophyll b	control	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.9683**	0.2460	0.2460
	10 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-0.6836	0.4660	0.4660
	20 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.9535**	0.9850**	0.9850**
	25 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-0.1255	-0.0521	-0.0521
	30 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-0.8252*	-0.9120*	-0.9120*
Chlorophyll b	40 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.9463**	0.9938**	0.9938**
	50 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-0.9009*	0.8704*	0.8704*
	control	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	10 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	20 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
25 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
30 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
40 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
50 kR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	

\*\* Significant at 1% level. \* Significant at 5% level

Table 2: Association between yield and yield components in ASD 16 and ADT 43 in the M<sub>4</sub> generation

Parameter	Treatment	DTF			Plant height			Productive tillers			100 seed weight			Yield		
		ASD16	ADT43	ADT 43	ASD16	ADT43	ADT 43	ASD16	ADT43	ADT 43	ASD16	ADT43	ADT 43	ASD16	ADT43	
DTF	Control	1	1	0.9934**	0.6547	-0.9972**	-0.4336	-0.6061	0.8856*	-0.9860**						
	10KR	1	1	-0.7267	-0.0604	-0.7052	-0.9989**	0.5494	-0.7206	-0.9368**						
	20KR	1	1	0.9042*	0.1749	0.1147	-0.8364*	0.0093	-0.7206	-0.3319						
	25KR	1	1	0.5000	-0.8985*	0.9333**	-0.7857	-0.9367**	-0.7206	0.8350*						
	30KR	1	1	-0.5000	0.7455	-0.5960	0.0949	0.7477	-0.9933**	-0.6547						
Plant height	40KR	1	1	-0.5000	0.6186	-1.0000	0.9078*	-0.7053	0.9590**	0.6649						
	50 KR	1	1	0.8660**	-0.0582	-0.6286	-0.3190	1.0000	-0.9987**	-0.0165						
	Control	1	1	1	-0.9449**	-0.9820**	-0.0751	-0.6934	-0.992**	-0.9986**						
	10KR	1	1	1	0.7033	0.9995**	-0.6316	-0.9732**	0.0358	0.4404						
	20KR	1	1	1	0.9767**	0.5280	-0.5140	-0.4187	-0.6638	0.1028						
Tillers	25KR	1	1	1	0.9945**	0.1555	0.3379	-0.7716	0.2431	0.8941*						
	30KR	1	1	1	0.9011*	0.9934**	-0.1850	0.2013	-0.9221**	-0.3273						
	40KR	1	1	1	-0.4263	0.5000	0.7809	-0.2612	0.1753	0.3144						
	50 KR	1	1	1	-0.4840	-0.1555	0.1220	0.8670*	-0.9223**	-0.5142						
	Control	1	1	1	1	1	0.3974	0.5447	0.9308**	0.9707**						
100 Seed wt	10KR	1	1	1	1	1	0.1070	-0.9798**	0.7357	0.4125						
	20KR	1	1	1	1	1	-0.6860	-0.9923**	-0.8087	0.8990*						
	25KR	1	1	1	1	1	0.4344	-0.7484	0.3431	0.5815						
	30KR	1	1	1	1	1	-0.5927	0.0876	-0.6632	-0.2168						
	40KR	1	1	1	1	1	0.2321	0.7053	0.8159*	-0.6649						
Yield	50 KR	1	1	1	1	1	-0.9276**	-0.6272	0.1082	-0.7672						
	Control	1	1	1	1	1	1	1	0.0345	0.7302						
	10KR	1	1	1	1	1	1	1	0.7522	-0.2222						
	20KR	1	1	1	1	1	1	1	0.9827**	-0.9464**						
	25KR	1	1	1	1	1	1	1	0.9951**	-0.9748**						
Yield	30KR	1	1	1	1	1	1	1	-0.2097	-0.9915**						
	40KR	1	1	1	1	1	1	1	0.7518	-0.9985**						
	50 KR	1	1	1	1	1	1	1	0.2710	-0.0184						

\*\* Significant at 1% level. \* Significant at 5% level

selection for positively associated traits for improving yield in rice. Based on the above, selection was practiced for decrease in plant height as negative association was noticed. Similarly the other characters were also selected.

**Variability studies:** The application of mutation breeding in identifying abiotic stress resistant mutants has been successful in some crop plants including rice (Ahloowalia *et al.*, 2004; Lee *et al.*, 2003a). In the present study, salt tolerant mutants isolated from 20, 30, 40 and 50 kR treatment showed significant increase in yield as compared to the other treatments and parental varieties (255.56 and 384.13 for ADT 43 and ASD 16) (Table 3). In this 20 kR of ADT 43 (446.94) showed highly significant yield increase than other mutants. Plant height was found to be significantly higher in all the treatments when compared with the control varieties (82.73 for ASD 16 and 72.94 for ADT 43) Among all the treatments the maximum value was recorded by 10 kR in both ASD 16 (97.81) and ADT 43 (88.47) (Table 4). All the treatments showed significant increase in number of tillers as compared to control varieties. The control mean of ADT 43 was 10.72; the maximum mean was recorded by 10 kR of ADT 43 (15.83) and minimum by 25 kR (14.50). The mean of the control variety ASD 16 was 5.87 while the mutants of ASD 16 recorded mean of range 13.00 for 40 kR to 10.94 for 30 kR (Table 5) Similar study was conducted by Uddin *et al.* (2007) where the number of tillers and grain yield were found to be substantially increased in the mutated plants than the parent variety 'Drew' under salt stress condition. Plant height, panicle length and No. of tillers were found to be substantially increased in the M<sub>3</sub> lines tested under saline conditions than the control plants (Lee *et al.*, 2003b).

Since yield is a quantitatively inherited character and is subject to different degree of non heritable variability and more particularly its genetic components are the most important factor in any breeding material. This has a close bearing on the response to selection. The results obtained in our study on yield and its associated parameters (Table 3, 5) are highly heritable which can be effectively used in developing salt tolerant rice. In the present study, heritability estimates were high for all the three traits under study. High heritability indicates that the induced

Table 3: Estimates of mean values (x) and genetic parameters for yield of the mutants (M<sub>5</sub> generation)

Source	Treatment	Mean±SE	Shift in x	Genotypic variation (δ <sup>2</sup> g)	Heritability (h <sup>2</sup> )	Genetic advance (Gs)
ADT 43	10 kR	295.83±17.87	40.27**	31.14	86.50	64.15
	20 kR	446.94±19.10	191.39**	19.01	83.81	39.16
	25 kR	307.50±14.21	51.94**	17.15	73.93	9.68
	30 kR	365.21±22.16	109.65**	17.15	73.93	9.68
	40 kR	356.39±31.95	100.83**	28.20	68.63	16.30
	50 kR	358.89±27.82	103.33**	50.44	83.86	28.95
	Control	255.56±28.58	0.00	1.24	25.96	2.55
	CD (1%)			11.97		
ASD 16	10 kR	301.94±26.60	-66.73**	55.47	84.02	37.85
	20 kR	382.22±9.30	13.55	8.89	89.72	4.79
	25 kR	374.17±29.43	5.50	39.01	78.92	21.48
	30 kR	385.17±7.54	16.50	3.16	82.62	1.69
	40 kR	388.75±6.32	20.08	2.64	85.09	1.40
	50 kR	392.33±9.77	23.66**	5.43	83.22	2.85
	Control	384.13±27.82	0.00	0.67	33.48	0.38
	CD (1%)			20.29		

\*\* Significant at 1% level



Table 4: Estimates of mean values ( $\bar{x}$ ) and genetic parameters for plant height of the  $M_5$  mutants

Source	Treatment	Mean $\pm$ SE	Shift in $\bar{x}$	Genotypic variation ( $\delta^2g$ )	Heritability ( $h^2$ )	Genetic advance (Gs)
ADT 43	10 kR	88.47 $\pm$ 3.64	15.52**	181.48	75.25	4.23
	20 kR	87.47 $\pm$ 2.38	14.52**	72.15	73.81	1.94
	25 kR	83.90 $\pm$ 0.79	10.96**	18.58	86.76	0.54
	30 kR	83.08 $\pm$ 1.75	10.13**	64.56	82.45	1.93
	40 kR	82.44 $\pm$ 1.52	9.49**	77.77	88.15	2.36
	50 kR	86.74 $\pm$ 2.73	13.79**	57.38	63.13	1.36
	Control	72.94 $\pm$ 0.69	0.00	1.49	41.18	0.04
	CD (1%)		1.22			
ASD 16	10 kR	97.81 $\pm$ 1.66	15.08**	90.22	87.92	1.94
	20 kR	91.53 $\pm$ 1.18	7.84**	20.83	76.91	0.51
	25 kR	86.94 $\pm$ 1.11	4.21**	23.39	80.78	0.64
	30 kR	87.82 $\pm$ 0.86	5.09**	17.79	84.20	0.48
	40 kR	88.75 $\pm$ 0.92	6.02**	19.30	83.49	0.50
	50 kR	91.40 $\pm$ 0.64	8.67**	9.56	83.96	0.24
	Control	82.73 $\pm$ 0.90	0.00	3.44	48.31	0.10
	CD (1%)		0.90			

\*\*Significant at 1% level

Table 5: Estimates of mean values ( $\bar{x}$ ) and genetic parameters for number of tillers of the  $M_5$  mutants

Source	Treatment	Mean $\pm$ SE	Shift in $\bar{x}$	Genotypic variation ( $\delta^2g$ )	Heritability ( $h^2$ )	Genetic advance (Gs)
ADT 43	10 kR	15.83 $\pm$ 1.07	5.11**	38.93	88.28	5.07
	20 kR	14.88 $\pm$ 0.67	4.16**	5.36	72.82	4.99
	25 kR	14.50 $\pm$ 0.51	3.78**	6.93	85.60	6.79
	30 kR	14.87 $\pm$ 0.87	4.15**	20.03	85.36	18.64
	40 kR	15.11 $\pm$ 0.10	4.39**	32.20	87.82	29.05
	50 kR	15.67 $\pm$ 1.58	4.94**	21.03	65.19	2.76
	Control	10.72 $\pm$ 0.75	0.00	4.73	65.24	0.91
	CD (1%)		0.69			
ASD 16	10 kR	11.83 $\pm$ 0.84	5.96**	13.83	81.21	20.35
	20 kR	12.78 $\pm$ 0.55	6.91**	7.33	84.18	9.25
	25 kR	11.67 $\pm$ 0.81	5.80**	8.29	73.98	12.54
	30 kR	10.94 $\pm$ 0.64	5.07**	5.67	75.33	9.75
	40 kR	13.00 $\pm$ 0.59	7.13**	4.15	72.38	5.06
	50 kR	12.27 $\pm$ 0.59	6.40**	9.04	85.39	12.38
	Control	5.87 $\pm$ 0.41	0.00	0.64	45.28	3.83
	CD (1%)		0.70			

\*\*Significant at 1% level

variability in mutant lines was fixed by selection. Johnson *et al.* (1955) suggested that heritability estimates coupled with genetic advance are more helpful than the heritability values alone. This is because heritability estimates are subject to genotype environment interactions. Furthermore, genetic advance gives the extent of stability and genetic progress for a particular trait under a suitable selection system. Results on yield and contributing characters possesses sufficiently high values of heritability and genetic advance which can be utilised for further improvement in rice and in evolving a high yielding saline tolerant variety. Lee *et al.* (2003b), Uddin *et al.* (2007) and Shereen *et al.* (2009) reported that induced mutation could be successfully used for enhancing salt tolerance in rice.

## CONCLUSION

Gamma ray treatment resulted in generation of high genetic variability in both the varieties used for this study. The mutants differs significantly for all yield related parameters assessed, thereby providing a wide genetic base for selection. The mutagenic treatment also results in alternation of character association, hence correlation was worked out and selection was based on the characters identified. Estimated variations of segregating generations increased depending on the character investigated and the mutagenic dose used. The high heritability estimates in response to selection shows that the treatment has generated inheritable variability. As expected genetic advance is high in  $M_5$  generation saline tolerable plants with higher yield can be obtained.

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