

# GENETIC VARIABILITY STUDIES ON RICE (*Oryza sativa* L.) MUTANTS FOR YIELD AND YIELD COMPONENTS IN NORMAL AND SALINE STRESS SOIL

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## INTRODUCTION

Rice (*oryza sativa* L.) is the major staple food for more than half of the global population and considered as the "global grain". In India, rice is grown on 44.40 million hectares, with an annual production of about 106.23 million tons and productivity of about 2395 kg ha<sup>-1</sup> (FAO, 2013). Generally, salinity tolerance is a polygenic trait. Development of salt tolerant varieties has been considered as one of the strategies to increase rice production in saline area. The response of rice to salinity varies with growth stages. Several studies indicated that rice is tolerant during germination and becomes very sensitive during early seedling stage (2-3 leaf stage), gains tolerance during vegetative growth stage becomes sensitive during pollination and fertilization and then become increasingly more tolerant at maturity (Bhowmik *et al.*, 2009).

There are rice varieties which yield high under normal condition; they fail to perform in salt affected soil. So genetic diversity screening for a trait of interest is an essential part of the commencement of breeding program. Babu *et al.* (2006) reported that genetic improvement mainly depends on the amount of variability present in the population. Hence, estimation of genetic diversity for salt tolerance parameters among the genotypes is important for planning the future breeding programme.

Salinity stress in the Tunga Bhadra Project (TBP) area of northern part of Karnataka, India is constantly increased at alarming rate, out of 3.5 lakh hectare of paddy growing area in TBP; 80,000 hectare had already converted in to saline stress soil. Every year salinity adds approximately 1000 hectare of total paddy area. Soil Salinity leads to drastic reduction in the paddy yields. The popular variety of TBP area BPT-5204 is long duration variety, matures around 140-150 days, this variety is excellent in grain quality and suitable for growing only in Kharif season in TBP area under normal soils but yields very less in saline stress soil.

In the present study, an attempt has been made to evaluate variability created by induced mutation. And keeping all these points in view, the present investigation was carried out with the objectives as assessing genetic variability in M4 mutant lines for yield and yield components and assessing genetic diversity in M4 mutant lines for yield and yield components.

## MATERIALS AND METHODS

The present field experiment was carried out at the Agricultural Research Station (ARS), Gangavathi during *kharif* 2013. The material for the present study consists of two popular rice varieties *viz.*, BPT-5204 and RP-BIO-226, the seeds of both the varieties were exposed to 30 Kr and 40 Kr gamma rays treatments from Cobolt

## ABSTRACT

The trials were set up in augmented design. Highly significant differences were observed for all the characters studied. Genetic variability parameters showed that phenotypic coefficient of variation (PCV) was higher than the respective genotypic coefficient of variation (GCV) and heritability is high for most of the characters. The characters studied in the present investigation expressed low to high heritability estimates ranging from 37.00 to 99.00 percent for normal soil and 52.00 to 99.00 percent for saline soil. High genetic advance as percent of mean along with high estimate of heritability and GCV are also observed for most of the characters. In normal soil, genetic advance was highest (190.58) for number of filled grains per panicle followed by number of grains per panicle (180.8) and lowest (4.47) for panicle length among yield characters. In case of saline soil, number of grains per panicle recorded highest (171.74) genetic advance followed by number filled grains per panicle (166.77) and the lowest (4.76) for percent chaffiness. Biological yield, number of grains per panicle and number of filled grains per panicle are important in selection programmes aiming to rice yield improvement and the breeder may consider these characters as the main selection criteria.

## KEY WORDS

Rice, Mutants, Genetic advance, Heritability, GCV, PCV, Variability

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60 source at Bhabha Atomic Research Centre (BARC) Trombay. The salinity stress

tolerant 400 M<sub>4</sub> mutants were selected from M<sub>3</sub> mutant populations grown under saline stress area during *khari* 2012 at ARS, Gangavathi (Baba Fakruddin, 2013). These 400 M<sub>4</sub> mutants were sown in normal and saline stress soil in an Augmented design (Federer, 1977), mutants in three meter row length with spacing of 20 cm between the rows and 10cm between the plants. Each block contained 50 mutants with 2 parental checks (BPT-5204, RP-Bio 226) replicated twice after every 50 entries. The observations were recorded for 12 quantitative characters plant height, number of tillers per plant, day to 50% flowering, panicle length, number of grains per panicle, biological yield, grain yield per plant, harvest index, 1000 grain weight, filled grains per panicle and per cent of chaffyness. Genotypic Variance and phenotypic variance were estimated using the formula (Burton and De Vane, 1953).

The statistical analysis of the data on individual character was carried out on the mean values of each mutants using INDOSTAT package.

**Analysis of variance (ANOVA)**

The data recorded on five randomly selected plants in each mutant line. The mean values were subjected to statistical analysis as per Federer (1977) was recorded in order to assess the variability among the mutants.

Parameters estimated were the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h<sub>2</sub>) and expected genetic advance (GA). All were estimated in the standard manner, expect genetic advance. The estimate of the genetic advance (GA, expressed as a percentage of the mean value).With assumed 1 per cent selection intensity was computed by the formula of Johnson *et al.* (1955):

$$GA = k \cdot \sigma_p \cdot h_2$$

Where,

h<sub>2</sub> = Broad-sense heritability

σ<sub>p</sub> = Phenotypic standard deviation of the mean performance of the treated population

k = 2.64, constant for 1 per cent selection intensity (i.e. the highest performing 1% are selected)

**RESULTS AND DISCUSSION**

**Analysis of variation**

In normal soil the analysis of variance showed highly significant differences among the rice mutants for all the parameters except number of productive tillers per plant, number of grain per panicle, number of filled grains per panicle, percent chaffyness and test weight and in saline soil condition analysis of variance showed highly significant differences among the rice mutants for few characters *viz.* Plant height, panicle length, biological yield and test weight in M<sub>4</sub> generation were given in Table 1 & 2.

**Genetic Variability**

Environment has great influence on many quantitative and qualitative characters of plants. This influence showed heritable and non-heritable variation, which can be estimated by the

**Table 1: Analysis of variance for yield, yield attributing traits of rice for normal soil**

SV	DF	DF	TNT	NPT	PH	PL	BY	GYP	HI	NGP	NFG	%CF	TW
Block	7	12.99	7.80	8.83	14.00	2.26	801.45*	97.44*	12.81	14549.92	15105.71*	75.69	17.18
Entries	403	42.982**	7.897*	6.803	122.72**	6.778*	4316.157**	58.69*	32.378*	7540.011	8381.322	55.469	14.22
Checks	3	106.53**	6.428	4.485	17.20	4.524	100.00	85.36*	57.694*	16064.78	14894.39	25.038	16.876
Varieties	399	42.58**	7.92*	6.835	118.05**	6.695*	4355.334**	58.34	32.186*	7492.292	8351.973	55.777	14.191
Ch v/s Var	1	12.089	1.27	1.124	2302.08**	46.64**	1333.176*	119.24*	32.8	1005.784	52.64	24.225	17.76
Error	21	15.031	3.726	4.509	14.146	3.25	266.624	25.02	15.115	6285.068	6050.743	33.748	20.522

**Table 2: Analysis of variance for yield, yield attributing traits of rice for saline soil**

SV	DF	DF	TNT	NPT	PH	PL	BY	GYP	HI	NGP	NFG	%CF	TW
Block	7	40.67	6.83	8.35	36.54	16.02**	59.24	23.53	38.73	22913.17	1860.9	31.22	11.66
Entries	403	38.28	8.04	7.49	126.09**	11.96**	403.97**	68.82	56.65	6277.64	5930.21	21.22	54.53**
Checks	3	76.86	0.34	1.12	612.17**	2.76	54.78	25.32	9.86	3740.46	2885.78	37.27	1.89
Varieties	399	37.056	8.11	7.56	115.40*	12.04**	407.29**	69.27	57.04	6292.95	5950.96	21.11	54.51**
Ch v/s Var	1	405.90**	2.81	0	2931.93**	7.72	127.50	21.89	44.04	7777.68	6782.5	19.29	217.69**
Error	21	33.244	10.95	8.22	54.08	4.19	110.45	76.49	34.13	13014.46	12103.27	32.58	12.37

DF = Days to 50% flowering; TNT = total number of tillers per plant; NPT = Number of productive tillers per plant; PH = Plant height; PL = Panicle length; BY = biological yield; GYP = grain yield per plant; HI = Harvest index NGP = number of grains per panicle; NFG = Number filled grains per panicle; %CF = percent chaffyness; TW = Test weight.

**Table 3: Estimation of range, mean and different genetic parameters for yield, yield attributing characters of Mutant Rice ( $M_4$  generation/ *Kharif*, 2013) for normal soil**

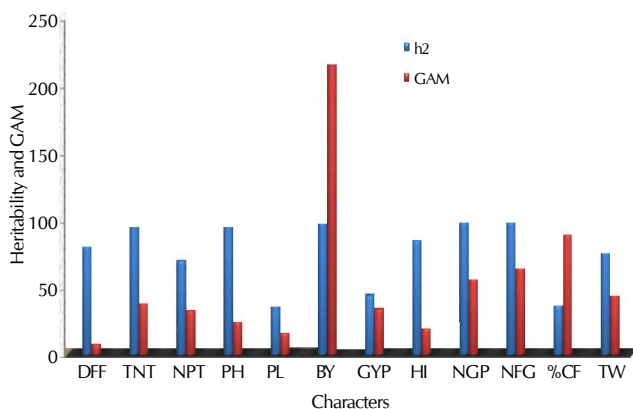
Character	Range		Mean	Co-efficient of variability		$h^2$	Expected Genetic advance@ 5%	Genetic advance mean
	Min	Max		PCV	GCV			
DFF	80	123	101.67	4.74	4.27	81	8.07	-93.73
TNT	8.2	25.5	14.92	18.62	18.59	99	5.71	+38.22
NPT	7.6	22.8	13.61	22.54	18.95	70	4.47	+32.83
PH	62.8	117.8	86.92	12.43	12.31	98	21.67	-25.13
PL	13.6	25.6	19.64	21.07	12.99	38	3.22	+16.51
BY	41.60	89.26	70.61	106.27	106.25	99	133.78	+218.85
GYP	12.20	55.00	29.04	37.57	24.93	44	9.77	+34.08
HI	14.23	67.87	40.23	11.18	10.35	85	10.17	+19.74
NGP	105	610.2	321.51	27.62	27.61	99	180.80	+56.86
NFG	97.6	370	295.85	31.61	31.59	99	190.58	+65.04
%CF	1.72	61.4	10.66	115.19	70.62	37	9.42	-89.19
TW	8.24	31.10	15.45	28.59	25.09	77	7.08	+45.38

DFF = Days to 50% flowering; TNT = total number of tillers per plant; NPT = Number of productive tillers per plant; PH = Plant height; PL = Panicle length; BY = biological yield. GYP = grain yield per plant; HI = Harvest index; NGP = number of grains per panicle; NFG = Number filled grains per panicle; % CF = percent chaffyness; TW = Test weight

**Table 4: Estimate of range, mean and different genetic parameters for yield, yield attributing characters of Mutant Rice ( $M_4$  generation /*Kharif*, 2013) for saline soil**

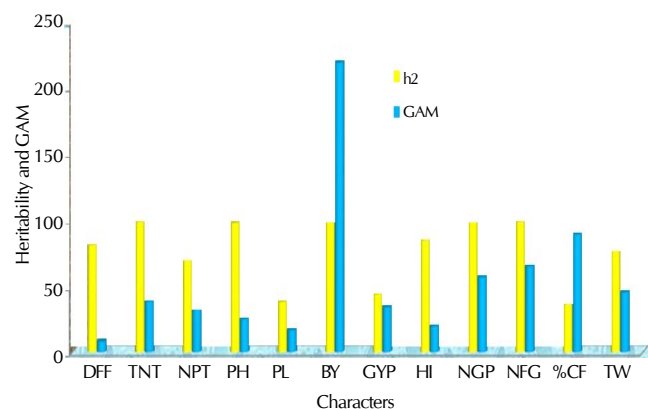
Character	Range		Mean	Co-efficient of variability		$h^2$	Expected Genetic advance @ 5%	Genetic advance mean
	Min	Max		PCV	GCV			
DFF	87	131	118	4.57	4.59	99	9.82	109.59
TNT	9	23.4	15.03	19.03	19.00	99	5.83	+39.07
NPT	7	21.4	12.56	25.85	22.05	72	4.8	+38.76
PH	63.2	113.2	87.23	12.79	12.66	98	22.41	-28.84
PL	13.6	26.4	20.41	23.38	16.98	52	5.21	+25.40
BY	34.62	88.56	70.61	34.28	34.17	99	41.27	+70.17
GYP	9.20	49.20	30.15	31.26	27.56	76	15.17	+50.05
HI	26.57	58.23	41.21	15.07	14.17	88	14.43	+27.43
NGP	115.4	758	296.64	28.39	28.38	99	171.74	+58.43
NFG	100.6	575.8	279.06	29.24	29.23	99	166.77	+60.17
%CF	0.63	32.71	2.87	59.14	48.14	66	4.76	-80.75
TW	7.98	30.75	16.28	42.81	41.12	95	14.46	+84.58

DFF = Days to 50% flowering; TNT = total number of tillers per plant; NPT = Number of productive tillers per plant; PH = Plant height; PL = Panicle length; BY = biological yield. GYP = grain yield per plant; HI = Harvest index; NGP = number of grains per panicle; NFG = Number filled grains per panicle; % CF = percent chaffyness; TW = Test weight



DFF = Days to 50% flowing; TMT = total number of tillers per plant; NPT = Number of productive tillers per plant; PH = Plant height; PL = Panicle length; BY = biological yield; GYP = grain yield per plant; HI = Harvest Index; NGP = number of grains per plants; NFG = Number filled grains per panicle; %CF = percent chaffyness; TW = Test Weight.

**Figure 1: Heritability ( $h^2$ ,%) and Genetic advance percent mean (GAM) for 12 yield and attributing character of normal soil in mutant rice**



DFF = Days to 50% flowering; TNT = total number of tillers per plant; NPT = Number of productive tillers per plant; PH = Plant height; PL = Panicle length; BY = biological yield; GYP = grain yield per plant; HI = Harvest index; NGP = number of grains per plant; NFG = Number filled grains per panicle; % CF = Percent Chaffyness; TW = Test Weight.

**Figure 2: Heritability ( $h^2$ ,%) and Genetic advance percent mean (GAM) for 12 yield and attributing characters of saline soil in mutant rice**

parameters like genotypic coefficient of variation (GCV), heritability and genetic gain. Mean standard error, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance as per cent of mean were given in Table 3 & 4. It revealed that phenotypic coefficient of variation (PCV) was higher than respective genotypic coefficient of variation (GCV) for all characters, but a relatively marginal difference was observed between PCV and GCV for days to 50 per cent flowering, total number of tillers per plant, plant height, biological yield, number of grains per panicle and number filled grains per panicle revealed that variability was due to genotypic differences.

GCV and PCV were moderate both in normal and saline soil condition for total number of tillers per plant (18.59, 18.62 per cent and 19.00 and 19.03 per cent), plant height (12.31, 12.43 and 12.66, 12.79 per cent) and harvest index (10.35, 11.18 and 14.17, 15.07 per cent) which is in conformity with findings of Mamta *et al.* (2007), Jaiswal *et al.* (2007), Sharma and Sharma (2007) and Pillai *et al.* (2011). GCV and PCV were low in both normal and saline soil condition with respect to days to 50 % flowering (4.27, 4.74 and 4.59, 4.57 per cent) as also revealed by the findings of Vaithiyalingan and Nadarajan (2006), Gangashetty *et al.* (2012) and Pandey *et al.* (2012) respectively. GCV and PCV were high in normal as well as in saline condition for biological yield (106.25%, 106.27% and 34.17%, 34.28%), grain yield per panicle (24.93%, 37.57% and 27.56%, 31.26%), number of filled grains per panicle (31.59%, 31.61% and 29.23%, 29.24%) and percentage of chaffyness (70.62%, 115.19% and 48.14%, 59.14%) as conformed by Pandey *et al.* (2012), Karim *et al.* (2007), Babu *et al.* (2012) and Azad *et al.* (2014) respectively. PCV and GCV were found to be differing very narrowly indicating lesser influence of environment over these characters.

### Genetic advance

The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.* 1955). In normal soil, genetic advance was highest (190.58) for number of filled grains per panicle followed by number of grains per panicle (180.8) and lowest (4.47) for panicle length among yield characters. In case of saline soil, number of grains per panicle recorded highest (171.74) genetic advance followed by number filled grains per panicle (166.77) and the lowest (4.76) for percent chaffyness. For normal soil, genetic advance as per cent of mean was highest (218.85) in case of biological yield, while lowest (-93.73) recorded by days to 50% flowering, whereas, in saline soil, days to 50% flowering recorded the highest (109.59) genetic advance as per cent mean, while the lowest (80.75) was recorded by percent chaffyness. The information on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study. In general, the characters that show high heritability with high genetic advance are controlled by additive gene action (Panse and Sukhatme, 1957) and can be improved through simple or

progeny selection methods. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance.

### Heritability

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%). The characters studied in the present investigation expressed low to high heritability estimates ranging from 37.00 to 99.00 percent for normal soil and 52.00 to 99.00 percent for saline soil. Among the characters studied, highest heritability (99%) was recorded by total number of tillers per plant, biological yield, number of grains per panicle and number filled grains per panicle under normal soil, whereas, in saline soil highest heritability (99%) was recorded by days to 50% flowering, total number of tillers per plant, biological yield, number of grains per panicle and number filled grains per panicle. High heritability values indicate that the characters under study are less influenced by environment in their expression. The plant breeder, therefore, may make his selection safely on the basis of phenotypic expression of these characters in the individual plant by adopting simple selection methods. High heritability indicates the scope of genetic improvement of these characters through selection. Heritability estimates were high for all the characters studied in both saline and normal condition, except for panicle length and number of grains per panicle. So this higher heritability suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programme as the genetic variance is mostly is due to additive gene expression and the results are conformed to Siddiqui and Sanjeeva (2010), Selvaraj *et al.* (2011), Singh *et al.* (2011), Chandan Kumar *et al.* (2015), Pandey *et al.* (2012), Babu *et al.* (2012) Sarawgi *et al.* (2015) and Satish *et al.* (2009).

High heritability coupled with high genetic advance as per cent of mean was observed in normal and also in saline soil condition for the characters plant height, biological yield, number of grains per panicle and number of filled grains per panicle. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance, hence are amenable for simple selection (Alok *et al.*, 2013). The high genetic advance over per cent mean coupled with moderate to high heritability suggested the importance of additive gene action for these traits. The moderately high heritability and low genetic advance for remaining characters indicating the presence of non additive gene action and role of environment in expression of these traits.

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