

**GENETIC AND MOLECULAR ASSESSMENT OF SALINE
TOLERANT RICE MUTANTS FOR YIELD AND QUALITY
ATTRIBUTES**

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ATTRIBUTES**

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CERTIFICATE

This is to certify that the thesis entitled “**GENETIC AND MOLECULAR ASSESSMENT OF SALINE TOLERANT RICE MUTANTS FOR YIELD AND QUALITY ATTRIBUTES**” submitted by **Mr. PRASHANTH B. KATAGERI**, in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, College of Agriculture, Raichur, University of Agricultural Sciences, Raichur, is a record of research work done by him during the period of his study in this University under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

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AFFECTIONATELY DEDICATED

TO

***MY BELOVED PARENTS,
BASAPPA KATAGERI,
LALITA KATAGERI***

MY BROTHER SHANTESH

***MY SISTER TEJASHWINI SHETTAR AND
MY BROTHER IN LAW AMIT SHETTAR***

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(PRASHANTH B. KATAGERI)

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LIST OF ABBREVIATIONS

%	: Percentage
/	: Per
°C	: Degree Celsius
ANOVA	: Analysis of Variance
CD	: Critical Difference
cm	: Centimeter
CV	: Coefficient of Variation
df	: Degrees of freedom
ErMS	: Error mean sum of squares
ErSS	: Error sum squares
<i>et al.</i>	: And others
Fig.	: Figure
GA	: Genetic Advance
GAM	: Genetic advance as percent of mean
GCV	: Genotypic Coefficient of Variation
PCV	: Phenotypic Coefficient of Variation
h^2	: Heritability
ha	: Hectare
kg	: Kilo grams
μ L	: Micro liter
mL	: Milli liter
sq m	: Square meter

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INTRODUCTION

I. INTRODUCTION

Rice ($2n=24$) is popular as “global grain” as almost 515 mt of it is grown each year in an area of about 161.40 mha with productivity of 3.14 t/ha (Anon, 2015). Rice is the staple food for more than half of the global population. It is widely grown in South-east Asia and is a plant of Asian origin. Rice is the most important crop providing food to over 75 % of Asian population and more than three billion of world population, which represents 50 to 80 % of their daily calorie intake.

In India, rice is grown in an area of 43 m ha with the production and productivity levels of 106.54 mt and 2424 kg/ha, respectively (Anon, 2015). “Rice is life” was the famous theme of International Year of Rice, 2004 denoting its overwhelming importance as an item of food, commerce and the close connection between rice-based systems and many cultures and people worldwide, in particular the poor and developing nations. Devoting an International Year to a single crop is unprecedented in the world history. Today rice is grown and harvested on every continent except Antarctica.

It belongs to the family *Poaceae*, sub-family *Bamboosoideae*, tribe *Oryzeae*. It has its origin in Jeypore tract of Odisha. There are 24 known species of the genus *Oryza*, of which only two i.e., *Oryza sativa* and *Oryza glaberrima* are cultivated and the rest are wild spp. *O. sativa*, the Asian rice is grown worldwide, while *O. glaberrima* Steud. is grown on limited acreage in a few African countries.

Rice being grown under a wide range of latitudes so, became the anchor's of food security in the world (Anon, 2008). Rice being a tropical plant flourishes comfortably in hot and humid climate, mainly grown in rainfed areas that receive heavy rainfall. It demands a temperature of around 25°C and a rainfall of more than 100 cm per annum. Also grown in the irrigated areas that receive comparatively less rainfall. The importance and demand for rice is expected to increase in the coming decades. According to Food and Agriculture Organisation (FAO), the global rice requirement in 2025 will be to the tune of 800 mt which is about 21% more than that of the year 2000.

The leading producers of rice in the world with more than 10 m ha area in South and South-east Asian countries like Bangladesh, China, India, Indonesia and Thailand that make up a little over two-thirds of the total area under rice. The major rice growing states in India are Andhra Pradesh, Telangana, Bihar, Karnataka, Madhya Pradesh,

Punjab, Uttar Pradesh and West Bengal. In Karnataka, rice is being cultivated in an area of 1.39 m ha with an annual production of 3.17 mt and productivity of 2.89 t/ha. The northern dry zone of Karnataka consists irrigated area of 0.21 m ha with the production of 3.8 lakh tonnes and the productivity is 2.53 t/ha (Rajanna, 2014).

India, having the largest area under rice is facing a stiff competition in the world market. A large number of factors such as drought, lodging, weeds, soil salinity, poor soil fertility, insect-pests, diseases, rodents *etc.*, are responsible for the reduced quality and quantity of the crop, among these salt-sensitivity being the major one. Millions of hectares in the humid regions of South and South-east Asia are technically suited for rice production but are left uncultivated or grown with low yields because of saline and problematic soils. It is notable that the grain yield of rice has not been harvested in commensuration to its existing genetic potential in almost all rice growing ecosystems. Salinity is one of the major abiotic stress and became obstacle in increasing production in rice growing areas worldwide is an ever-present threat to crop yield (Grover *et al.*, 2000; Bhowmik *et al.*, 2009; Yasseen *et al.*, 2010; Joseph and Jini, 2010). It causes reduction of crop yield through alteration in plant metabolism, reduced water potential, ion imbalances, toxicity and sometimes severe salt stress may even threaten survival (Joseph & Jini, 2011). Recent studies indicated that injury is due to the excessive sodium (Na) uptake, and chloride (Cl), being essentially a neutral anion, is tolerated over a wide range of concentrations (Clarkson & Hanson 1980). The disruptive effect of Na and its interference with the role of cytoplasmic potassium (K) preempted Cl toxicity. Moreover, Na-K imbalance adversely affects grain yield (Devitt *et al.*, 1981). The typical mechanism of salinity tolerance in rice is the exclusion or reduction of Na uptake and increased absorption of K to maintain a good Na-K balance in the shoot.

Salt tolerance is a complex quantitative genetic trait controlled by many genes. Development of salt tolerant varieties is an important strategy to combat the decrease in rice production in saline area. Rice exhibits variable response to salinity at different growth stages. Several studies indicated that rice is tolerant during germination, becomes very sensitive during early seedling stage (2-3 leaf stage), gains tolerance during vegetative growth stage, becomes sensitive during pollination and fertilization, and increasingly more tolerant at maturity (Pearson *et al.*, 1966; International Rice Research Institute, 1967). However, some studies reported that at flowering, rice is not sensitive to

salinity (Kaddah *et al.*, 1975). Hence, to know the response of the rice plant to salinity as a whole, it is imperative that the effects be observed in all the various stages of its development, that is at early seedling, vegetative and reproductive stages. The challenge is to develop high-yielding, salinity-tolerant cultivars for the various salt affected areas of Asia. Screening rice germplasm to locate salt tolerant genes for use in improving the currently grown varieties is of continuous importance to the breeder. One major approach in plant breeding is to identify the variability among the lines for yield and yield attributing traits and also salt tolerance. There are rice varieties which yield high under normal condition; they fail to perform in salt affected soil. Babu *et al.* (2006) reported that genetic improvement mainly depends on the amount of variability present in the population. Hence, evaluation of lines for yield and salt tolerance parameters is important for planning the future breeding programme.

Screening is an essential part of the breeding programs and several screening and selection schemes have been proposed for salt tolerance improvement in wheat and other crops (Dewey, 1962; Kingsbury & Epstein, 1984 and Gorham, 1997). Also, selection for improved salt tolerance on the basis of seedling stage has been used in various crop species, for example in rice (Shannon *et al.*, 1998), maize (Rao and McNeilly, 1999) and wheat (Qureshi *et al.*, 1990). Additionally, selection for salinity tolerance based on seedling response has suggested that the variation at this stage is genetically controlled (Maiti *et al.*, 1996). For enhancing salt tolerance in crop plants, it is very important to find sufficient variation and to devise such screening techniques which are reliable to identify tolerant genotypes. Variation for salt tolerance has been reported in many crop species, both between and within plant species of rice (Alam *et al.*, 2004), cotton (Noor *et al.*, 2001) and other crop plants. As salinity tolerance is a complex quantitative genetic character controlled by many genes, using conventional breeding methods, plant selection for salt tolerance is not easy because of the large effect of environment and low heritability of salt tolerance. Because of the complexity of the trait, it has been difficult to develop an accurate, rapid and reliable screening technique (Islam *et al.*, 2011).

Advancement in rice breeding for salt tolerance has accelerated with the identification of major loci conferring salt tolerance especially at the seedling stage. Microsatellite markers have been used to map QTLs associated with salt tolerance (Lang *et al.*, 2009; Mohammadi-Nejad *et al.*, 2012; Hossain *et al.*, 2015). A major QTL for salt

tolerance at the seedling stage, Saltol was identified using F8 recombinant inbred lines (RILs) of Pokkali/ IR29 (Gregorio *et al.*, 1997). This QTL governs the Na⁺/K⁺ uptake and accounts for 64.3% to 80.2% of the phenotypic variation in salt tolerance at the seedling stage (Mohammadi-Nejad *et al.*, 2008). A newly developed RIL FL478 with Saltol derived from IR29 and Pokkali was used as a novel source of salt tolerance at the seedling stage (Harkamal *et al.*, 2005). Among the several classes of available DNA markers, microsatellite or simple sequence repeat (SSR) markers are considered the most suitable due to their multi allelic nature, high reproducibility, co-dominant inheritance, abundance and extensive genome coverage. A large number of SSR markers have been developed and mapped in rice (Temnykh *et al.*, 2000, McCouch *et al.*, 2002), which vary in the degree of polymorphism depending on their position in the coding or non-coding segments, nature of their repeat motifs and the genome wide abundance. Therefore, an ideal set of SSR markers providing genome wide coverage will facilitate an unbiased assay of genetic diversity which in turn will provide a robust, unambiguous molecular description of rice cultivars.

In northern parts of Karnataka, under Tungabhadra Project (TBP) command area paddy is been grown in an area of 3.5 lakh hectares. Day by day soil salinity in the Tungabhadra Project area is increasing. Every year salinity adds approximately 1000 ha to the salinity affected area and leads to drastic reduction in the paddy yields. Already one lakh hectare area is converted into saline stress soil. The popular variety BPT-5204 locally called Sambhamahsuri is a long duration variety, matures at around 140-150 days. This variety is excellent in grain quality and is better than other varieties in quality. BPT-5204 is suitable for growing in *kharif* season in TBP area under normal soils but its yield levels very less in salt affected soils. The yield reduction in BPT-5204 is as high as 50 *per cent* in saline soil. Therefore, there is an urgent need to develop stress tolerant paddy varieties suitable for TBP area for *kharif* season along with medium slender grain, good cooking quality and early maturity as that of BPT-5204.

Keeping all these points in view, the present investigation was carried out with the following objectives.

1. Evaluation of advanced M₆ mutants lines for salinity tolerance for yield and quality traits.
2. Association of traits in salt tolerant mutant lines.
3. Genotyping of salinity tolerant mutant through SSR markers.

REVIEW OF LITERATURE

II. REVIEW OF LITERATURE

The literature relevant to experiment of this investigation is reviewed and presented under the following heading

2.1 Assessing of genetic variability, heritability and genetic advance in M₆ Mutant lines for yield and yield components

2.2 Association of traits in saline tolerant mutant lines

2.3 Screening of rice mutants for salinity tolerance

2.4 Molecular characterization of salinity tolerant mutant lines

2.1 Assessing of genetic variability, heritability and genetic advance in M₆ Mutant lines for yield and yield components:

Bhattacharya and Sowbhagya (1980) and Das *et al.* (1983) classified the rice genotypes using various grain characters (*viz.*, length, shape, 1000 grain weight or 100 grain weight and profile value).

Shivapriya (2000) reported moderate GCV and PCV for days to first flowering, plant height, days to maturity, grain breadth and L:B ratio in a study involving sixty eight local rice accessions.

Chaudary and Motiramani (2003) reported that a wide range of variation for most of the characters. Heritability in broad sense was very high for all the characters exhibited high heritability coupled with high genetic advance except harvest index. Grain yield per plant showed significant positive correlation with effective tillers per plant, spikelet density and biological yield per plant. Path analysis indicated a greater contribution of effective tillers per plant, spikelet density and biological yield per plant towards grain yield.

Elayaraja *et al.* (2003) carried out investigation in Tamil Nadu, India during 2001 to study the nature and amount of induced genetic variability in *O. sativa*. The study consisted of a cv. PY 5 treated with physical mutagen *viz.*, gamma rays at 5, 10, 15 and 20 Kr. The maximum variability was observed in plant height (20 Kr), leaf area index (15 Kr), grain yield per plant (5 Kr), dry matter production and harvest index (10 Kr) in

M₂ generation. A high heritability associated with a high genetic advance as percentage of mean was observed for plant height, leaf area index, grain yield per plant and harvest index in all the treatments of M₂ generation.

Katoch *et al.* (2005) studied that locally adapted cultivar of Basmati rice (*Oryza sativa* L.), namely, T-23 was treated with ethyl methane sulfonate (EMS at 0.8, 1.0 and 2.0 %) and gamma rays (at 25, 30 and 35 Kr) in Hisar, Haryana, India. A number of various types of morphological macro mutations were induced in M₂ generation. These mutants were evaluated in M₃ generation in RBD with two replications. Estimates of variability, heritability and genetic advance were worked out for the mutants. Wide range of variability was observed for grain yield/plant, effective tillers/plant, days to flowering, days to maturity, 100 seed weight and protein content. High heritability coupled with moderate genetic advance was observed for days to flowering, days to maturity and plant height.

Panwar (2005) observed high heritability and genetic advance for grain yield per panicle, chaffy grains per panicle, grain yield per plant, filled grains per panicle and secondary branch number per panicle, indicating the effectiveness of selection for these characters.

Hasib (2005) evaluated twelve F₁ hybrids of scented rice and their seven parents involving induced mutants and basmati for eight important panicle characters. Character association analysis revealed significant positive association of all the panicle traits, except test weight with grain yield per panicle. Path coefficient analysis revealed that panicle weight had highest positive direct effect followed by panicle length and secondary branches per panicle. Selection on higher panicle weight and higher number of secondary branches per panicle could be effective for yield improvement in scented rice.

Monalisa *et al.* (2006) studied genetic variability, correlation and path coefficient were estimated from 20 low land rice varieties. Highest GCV was recorded in flag leaf, high density grains / panicle and panicle weight. High heritability (in broad sense) accompanied by high genetic advance was observed in flag leaf, spikelets, filled grains and high density grains per panicle. Grain yield/plant was positively and significantly associated with effective tillers per plant, panicle weight, spikelets and high density grains

per panicle. High positive direct effects coupled with significantly positive associations of effective tillers per plant and high density grains per panicle with grain yield per plant.

Rita *et al.* (2006) reported high heritability coupled with high genetic advance for harvest index, total number of chaffy spikelet per panicle, grain yield per plant, total number of filled spikelets per panicle and spikelet fertility percentage indicating selection may be effective for these characters.

Karim *et al.* (2007) studied the variability and genetic parameter analysis in 41 aromatic rice genotypes. Significant variations observed the phenotypic variance was higher than the corresponding genotypic variance for the characters. These differences were in case of number of panicles per hill, number of primary branches, number of filled grains per panicle, spikelet sterility (%) and grain yield per hill indicating greater influence of environment for expression of these characters. 1000 grain weight and days to maturity showed least difference between phenotypic and genotypic variance, which indicated additive gene action for expression of the characters. Considering genetic parameters, high genotypic coefficient of variation (GCV) value was observed for 1000 grain weight followed by spikelet sterility (%), grain yield per hill and number of filled grains per panicle, whereas days to maturity showed very low GCV. High heritability with high genetic advance in percent of mean (GAPM) was observed for 1000 grain weight followed by spikelet sterility (%) and number of filled grains per panicle indicated that these characters were under additive gene control and selection for improvement might be effective. Days to maturity showed high heritability but low genetic advance (GA %), which indicated that non additive gene effects were involved for phenotypic expression of this character.

Mamta *et al.* (2007) studied thirty four genotypes for their genotypic, phenotypic and environmental coefficient of variation during wet season 1999–2000. Results indicated that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) for all the traits. PCV was highest in grain yield (33.15 %) followed by biological yield (26.67 %), effective tillers per plant (25.87 %) and spikelets per panicle. GCV was highest for grain yield per plant (26.19 %) followed by effective tillers per plant (21.46 %) and biological yield per plant (20.47 %). GCV and PCV were lowest for panicle length followed by days to 50 per cent flowering and plant height. High heritability coupled with

high genetic advance was recorded for spikelet per panicle. High heritability was observed for 50 per cent flowering, test weight and panicle length. Moderate heritability and low genetic advance was recorded for total number of tiller per plant and effective tiller per plant. Days to 50 per cent flowering, plant height, seed setting percentage, grain yield and harvest index showed moderate genetic advance. Genetic advance in per cent of mean ranged from 8.39 to 40.19.

Mustafa *et al.* (2007) evaluated fourteen rice (*Oryza sativa* L.) genotypes at the Gezira Research Station Farm (GRSF) for genetic variability and correlations between yield and yield components using phenotypic markers and polygenic trait analysis. A wider genetic variability was observed using the genotypes for most of the characters studied. The highest genotypic coefficient of variation was recorded for grain yield, percent unfilled grain per panicle, number of grains per panicle and number of filled grain per panicle. Phenotypic correlations between grain yield and number of filled grain per panicle, number of panicle per m² and 1000 grain weight were 0.52, 0.36 and 0.27, respectively. These results suggested that improvement in yield could be attained by selecting rice plants for higher number of filled grain per panicle, number of panicle per square meter, and 1000 grain weight. The path analysis revealed that number of filled grains per panicle had direct positive (0.87) contribution to the grain yield per ha and positive (0.33) indirect effect on grain yield per ha through days to 50 per cent maturity and number of grains per panicle (0.089); while number of filled grains per particle had negative (-0.30) and (-0.21) indirect effect on grain yield per ha through number of tillers per plant and number of panicles per m, respectively. The relative contribution of characters towards variability and results of correlation and path coefficient indicated the importance of number of grain per panicle, number of filled grain per panicle and number of panicle per m². Genotypes having these characters would offer a good possibility for the improvement of rice through conventional selection.

Yadav *et al.* (2007) studied morphological, physiochemical and cooking properties of some Indian rice cultivars (four non-basmati, namely Jaya, P-44, HKR-120, Sharbati and two basmati, namely HBC-19 and Bas-370). Length and breadth of milled raw rice varied from 5.85 to 8.25 mm and 1.65 to 2.93 mm, respectively. HBC-19 had the highest length, whereas Jaya variety had smallest kernel with a length of 5.85 mm. Different cultivars showed significant variations in their morphological, physio-chemical

and cooking properties. Basmati cultivars showed a higher elongation ratio, a higher water uptake ratio and a lower solid loss in gruel.

Jaiswal *et al.* (2007) studied variability, correlation and path analysis for yield and quality traits in twenty five indigenous aromatic rice genotypes were estimated and reported high heritability (broad sense) coupled with high genetic advance for yield per plant, number of panicle bearing tillers and number of grains per panicle. Number of panicle bearing tillers and days to 50 per cent flowering exhibited highest positive direct effect along with positive association with yield per plant. Kernel length after cooking showed highest positive direct effect on kernel length.

Bisne and Sarawgi (2008) evaluated thirty two aromatic rice germplasm accessions for eight quality characters and noticed grain L/B ratio ranges from 2.08 to 4.85 mm, kernel L/B ratio from 1.82 mm to 3.25 mm, hulling per cent ranges between 79.33 to 82.31 per cent. Milling per cent ranges from 70.39 to 80.54 and alkali spreading value ranges from 4 to 6.33 cm. They identified some specific varieties for quality and agronomical characteristics.

Siddiqui and Sanjeeva (2010) observed the mutagenic effect of gamma rays, Ethyl Methane Sulphonate (EMS) and Sodium Azide (SA) used either singly or in combination for induced genetic variability for yield and yield traits in M_2 and M_3 generation in the two cultivars of Basmati rice. The observation mean range and coefficient of variation (CV) suggest that the mutagen treatment had wider values than the control. The mean performance showed improvement in most of the mutagenic treatments in M_3 as compared to the corresponding treatments in M_2 generation. The magnitude of CV in the treated populations as generally higher than the control for most of the traits in both the generations for both the varieties. All the three mutagens were quite effective in inducing genetic variability in Basmati rice.

Akinwale *et al.* (2011) estimated the phenotypic and genotypic coefficients of variation, broad sense heritability, genetic gain and correlations in rice (*Oryza sativa* L.). Genotypes differed significantly at ($p > 0.001$) for all the traits studied, which implies that the genotypes constitute a pool of germplasm with adequate genetic variability. Genotypic coefficients of variation were lower than the corresponding phenotypic coefficients in all the traits studied, indicating considerable influence of the environment

on the expression of the traits. High to medium broad sense heritability estimates observed for days to heading, days to maturity, plant height, grain yield and number of grains per panicle, panicle weight, number of panicles per m² and panicle length suggests high component of heritable portion of variation, which is the portion exploited by breeder and that selection for these traits can be achieved directly based on their phenotypic performance. High to medium heritability and genetic advance were recorded for the number of grains per panicle, grain yield, panicle weight and the number of panicles per plant. This suggests that these traits are primarily under genetic control and selection for them can be achieved through their phenotypic performance. Grain yield exhibited significantly positive correlation with the number of tillers per plant ($r=0.58^{**}$), panicle weight ($r=0.60^{*}$) and number of grains per panicle ($r=0.52^{*}$). Therefore, the results suggest that these traits can be used for grain yield selection.

Singh *et al.* (2011) studied eighty one rice (*Oryza sativa* L.) genotypes during *khariif* 2010 for thirteen quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. Analysis of variance revealed that the differences among eighty one genotypes were significant for all the characters except flag leaf width. Among all the traits number of spikelets per panicle exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by harvest index, grain yield per hill and number of panicles per hill. Broad sense heritability was highest for biological yield per hill, which suggested that this trait would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as per cent of mean was recorded for number of spikelets per panicle with high value of heritability.

Idris *et al.* (2011) studied genetic variability and correlation between yield, yield components in some rice genotypes. Seven characters were measured including yield, yield components. Phenotypic (PCV) % and genotypic variances (GCV) %, coefficients of variation were estimated. Phenotypic and genotypic correlation between characters was determined. There were highly significant differences ($p \leq 0.01$) between the most of the character, except for percentage of unfilled grains per panicle (%). The highest values of phenotypic and genotypic variance were recorded by yield kg per ha. Also grain yield was attained the highest values of phenotypic and genotypic coefficients of variation. Positive phenotypic and genotypic correlation coefficient was detected

between grain yield and number of filled grains per panicle, harvest index, panicle length and number of grains per panicle. This revealed that there was high genetic variability among the tested genotypes, indicating that it could be used for further improvement in rice breeding.

Hossain *et al.* (2011) studied the genetic variability, heritability and genetic advance for yield and yield components in twenty five medium duration rice genotypes. Observations were recorded for 8 traits namely, plant height, number of panicles per hill, panicle length, number of filled grains per panicle, 1000 grain weight, grain length, grain breadth and yield. High phenotypic and genotypic variances were observed for grain yield, followed by number of filled grains per panicle. Heritability ranged from 50per cent (grain yield per hill) to 90per cent (grain breadth). Genetic advance as a percentage of mean was highest for number of filled grain per panicle (70.34), followed by grain yield (68.72 q/ha). Number of filled grain per panicle, 1000-grain weight, grain length and breadth exhibited less environmental effect and high heritability coupled with moderate to high genetic advance.

Sadeghi (2011) studied to determine variability, heritability and correlations between yield and yield components in forty nine landraces of rice (*Oryza sativa L.*) for 2 years. Direct and indirect effects of yield and yield components on seed yield per plant were investigated. Broad sense heritability ranged from 69.21per cent (Plant height) to 99.53 per cent (Grain width). Grain yield was found to be positively and significantly correlated with grains per panicle, days to maturity, panicle weight, the number of productive tillers, days to flowering, plant height, panicle length, flag leaf width and flag leaf length indicating the importance of these characters for yield improvement in this population. The result of phenotypic path analysis revealed that the number of productive tillers had the highest positive direct effect followed by days to maturity, grains per panicle and 1000 grain weight.

Babu *et al.* (2012) studied the genetic parameters for yield, yield attributing, quality and nutritional characters in twenty one rice hybrids. Analysis of variance revealed significant differences for all the traits. The characters viz., number of filled grains per panicle, number of chaffy grains per panicle and iron content exhibited high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Small differences between GCV and PCV were recorded for all the characters studied

which indicated less influence of environment on these characters. The characters viz., number of filled grains per panicle and water uptake exhibited high heritability coupled with high genetic advance indicating that simple selection could be effective for improving these characters.

Bharathi *et al.* (2012) studied the two mutant generations M_2 and M_3 of rice var PY-1. High mean and wide range was observed in the treatment 15Kr + 1% EMS. High heritability coupled with high GA as percent of mean were recorded in M_2 generation compared to M_3 generation. This indicated that both additive as well as dominant gene action might be involved in controlling the above traits in the respective generation.

Bhadru *et al.* (2012) studied a total of twenty one rice genotypes (resistant to gall midge biotype 3 and BPH) for their variability and genetic divergence. The highest genotypic and phenotypic coefficient of variation, heritability and genetic advance per cent of mean corresponded to grains per panicle, seed yield, 1000 grain weight and plant height and direct selection for these traits would be useful for yield improvement in rice. The D^2 values were significant among the twenty one genotypes, which were grouped into six clusters. Most of the genotypes with same pedigree either male or female parent involved cross combination came under the same cluster and few genotypes in different cluster and genotypes of quite different pedigree may all into the same cluster. Coarse and medium slender high yielding gall midge and BPH resistant varieties genotypes could be utilized in the hybridization programme.

Fasahat *et al.* (2012) evaluated ten rice genotypes (BC_2F_7 generation) for amylose content in three environments in Peninsular Malaysia. Based on the average amylose content across the environments, the genotype G13 showed significantly ($p < 0.05$) different amylose content (23.88 %) in comparison to other genotypes. Two genotypes G13 (25.7%) and G15 (25.6%) were higher than MR219 (25.1%) in terms of amylose content in Sungai Besar environment.

Gangashetty *et al.* (2013) carried out an investigation to know the extent of genetic variability present in the local non-basmati aromatic genotypes of rice. A total of forty two genetically diverse genotypes were considered for the study. Analysis of variance was found to be significant for all the traits, indicate that there is existence of genetic variability for all the traits varying from lower to higher coefficients of variance.

The results found that the higher values of genotypic and phenotypic coefficient of variability was observed for plant height, number of tillers per plant, number of productive tillers per plant, panicle weight, grain length, test weight, iron and zinc content and grain yield per plant. The moderate genotypic and phenotypic coefficients of variance were recorded for panicle length, grain breadth and L/B ratio. The days to 50 per cent flowering had recorded lower values of genotypic and phenotypic variance. High heritability with high genetic advance was observed for all traits except days to 50 per cent flowering.

Fakruddin *et al.* (2015) studies conducted on the seeds of rice variety viz., BPT-5204 and RP Bio-226 were treated with gamma irradiation (30kR and 40kR) with the objective to assess the variability in M₃ generation. High GCV was found for flag leaf, yield per plant (16.99) and grain yield per plant (16.98). In all cases phenotypic variances were higher than the genotypic variances. Based on high heritability coefficient (h^2 b.s.) coupled with high genetic advance as per cent of mean, for panicle length (87, 21.37), panicle exertion (99, 46.20), grain yield per plant (68, 28.92%), biological yield plant⁻¹ (64, 28.05%) and test weight (61, 21.43 %) which indicated the predominance of additive gene action for the expression of these traits, hence are amenable for simple selection. Therefore, priority should be given to those traits which recorded higher estimates of genetic advance as per cent mean while deciding selection strategies and selection based on these characters may be useful in realizing better gain by selection.

Mahantashivayogayya *et al.* (2016) carried out experiment to assess the genetic variability, heritability, genetic advance for yield and yield component characters in four hundred mutant lines of Rice. 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 chaffyness. Biological yield, number of grains per panicle.

Pathak *et al.* (2016) conducted the study on rice germplasm and observed considerable genetic variation in different quality characters analyzed. The grain length varied from 5.10 to 8.03 mm, grain width from 2.00 to 3.17 mm, cooked grain length from 7.40 to 12.37 mm, cooked grain width from 3.30 to 7.17 mm, grain elongation ratio from 1.29 to 2.02 and grain widening ratio from 1.37 to 3.32. On dry weight basis, starch contents of genotypes ranged from 70.37 to 82.83 per cent, GC from 53 to 100.03 mm, GT from 2 to 7, crude fat content from 2.64 to 3.76 per cent, crude protein content 8.10 to 10.32 and lysine content from 2.71 to 3.39 (g/100 g of protein). The difference between GCV and PCV was less for all characters except GT, which indicate greater correspondence between phenotype and genotype and less environmental influence and greater role of genetic factors on expression of grain quality traits. Based on above results amylose content trait would be highly effective to be used in breeding programmes for improving cooking and eating quality

2.2 Association of traits in saline tolerant mutant line

Shashidhar *et al.* (2005) reported grain yield showed positive association with plant height, productive tillers per plant, dry matter per plant, leaf weight per plant and harvest index both at phenotypic and genotypic levels.

Sivakumar and Kannan (2005) assessed the nature and magnitude of association between grain yield and its component characters of wide compatible gene involving inter sub-specific rice hybrids. Most of the characters studied (number of tillers per plant, panicle length, pollen fertility, grains per panicle and 100 grain weight) exhibited positive correlation with grain yield at both phenotypic as well as genotypic levels.

Borbora *et al.* (2005) studied correlation and path analysis for 11 characters in 30 genotypes of rice comprising 16 local varieties and 14 high yielding varieties per advanced lines under two sowing dates. The highest positive direct effect on grain yield per plant was recorded for grain yield per panicle followed by secondary branch number per panicle and plant height under both the environments. Chaffy grain number per panicle showed the highest negative direct effect on grain yield per plant followed by

panicle number per plant, days to 50 per cent flowering, primary branch number per panicle and 1000 grain weight. The characters filled grain number per panicle, primary branch number per panicle and 1000 grain weight showed highest indirect effects on grain yield per plant in twenty five indigenous aromatic rice genotypes were estimated and reported high heritability (broad sense) coupled with high genetic advance for yield plant⁻¹, number of panicle bearing tillers and number of grains panicle⁻¹. Number of panicle bearing tillers and days to 50 % flowering exhibited highest positive direct effect along with positive association with yield plant⁻¹. Kernel length after cooking showed highest positive direct effect on kernel length.

Neelima *et al.* (2007) investigated the correlation and path coefficient analysis for various growth characters (plant height, tiller number and total dry matter production) and yield attributes (productive tillers, length of panicle, grains per panicle, filled grains per panicle and test weight), the systematic inter-relationship between the variables can be understood. Path coefficient analysis helps in separating the direct effect from indirect effect by partitioning the correlation coefficients. It clearly showed that all the characters except number of leaves, productive tillers, length of panicle and grains per panicle were highly significant ($p=0.01$) and found to be positively correlated with grain yield of rice. Straw yield ($r=0.91$), plant height and dry matter production ($r=0.88$) and LAI ($r = 0.84$) had higher correlation coefficients but their direct effects varied. The direct effect was highest for straw yield (0.589). Though number of leaves and productive tillers showed a positive correlation with seed yield of rice their correlation coefficients were less ($r = 0.40$ and 0.37 , respectively). The information on correlation and path coefficient studies in regular agronomic experiments is meagre. Hence, this investigation was undertaken to assess and measure the magnitude of relationship between grain yield of rice and other characters.

Jayasudha and Sharma (2010) conducted studies on character association and path-coefficient analysis on forty seven (47) rice genotypes including thirty three hybrids and fourteen parents for grain yield and some physiological traits. Analysis of variance revealed considerable variability among the genotypes for all the characters. A high genotypic and phenotypic coefficient of variation was observed for grain yield per plant, harvest index, pollen fertility (%) and spikelet fertility (%). Characters like pollen fertility (%), spikelet fertility (%), days to 50 per cent flowering and grain yield per plant showed

high value of heritability coupled with high genetic advance. Spikelet fertility (%) and harvest index showed positive and significant correlation with seed yield per plant both at genotypic and phenotypic levels.

Idris *et al.* (2011) studied correlation between yield and yield components in some rice genotypes. Seven characters were measured including yield, yield components. Phenotypic (PCV) % and genotypic variances (GCV) %, coefficients of variation were estimated. Phenotypic and genotypic correlation between characters was determined. There were highly significant differences ($p = 0.01$) between the most of the character, except for percentage of unfilled grains per panicle (%). The highest values of phenotypic and genotypic variance were recorded by yield kg per ha. Also grain yield was attained the highest values of phenotypic and genotypic coefficients of variation. Positive phenotypic and genotypic correlation coefficient was detected between grain yield and number of filled grains per panicle, harvest index, panicle length and number of grains per panicle. This revealed that there was high genetic variability among the tested genotypes, indicating that it could be used for further improvement in rice breeding.

Rashid *et al.* (2013) studied variation and correlation on twenty diverse cultivars of rice. Highly significant differences were presented among the genotypes for all the traits. Among the traits days to heading, days to maturity, number of productive tillers, 1000-grain weight showed highly significant positive correlation with grain yield per plant whereas, flag leaf area, plant height and panicle length showed highly significant negative correlation with grain yield per plant. Number of grains per panicle was non-significant positively correlated with grain yield per plant. Cluster analysis revealed that maximum genetic diversity was present between Cluster I and Cluster VI. Minimum genetic diversity was found between Cluster III and Cluster IV. It was concluded that traits like number of productive tillers, number of grains per panicle and 1000-grain weight was useful for direct selection criteria for higher grain yield. Cultivars like IRRI-3, IRRI-4, KSK-133, SR-57, IRRI5, SRS-64 might be used for rice hybridization and improve programs for developing new rice varieties

Naseem *et al.* (2014) evaluated twenty genotypes of rice (*Oryza sativa* L.) were evaluated for genetic variability and correlation. The experiment was conducted in the research area of department of Plant Breeding and Genetics, University of Agriculture Faisalabad, following randomized complete block design with three replications. The data

was recorded on yield and different yield components. The results pertaining to analysis of variance showed highly significant differences among all genotypes for all the yield traits. Flag leaf area, number of productive tillers per plant, number of spikelets per panicle, number of grains per panicle and 1000 grain weight had a highly positive significant genotypic correlation with grain yield per plant. Same results were obtained for the phenotypic correlation. The study of path analysis for yield related traits revealed that number of productive tillers per plant, number of spikelets per panicle, number of grains per panicle and days to maturity had positive direct effect on grain yield per plant. In view of the results obtained from this experiment, it may be concluded that the characters like number of productive tillers per plant, number of spikelets per panicle could be used as a direct selection criteria for higher grain yield. Genotypes like Sr1 -57, Basmati-385, Srs-505, Ksk-133, Sr1 -13 and DM-2-25-9-2002 may be used to bring about improvement in rice grain yield by including these in rice breeding programs for development of commercial varieties.

Ghosh *et al.*, (2016) shown that Salinity has been a key abiotic constraint devastating crop production worldwide. Attempts in understanding salt tolerance mechanisms has revealed several key enzymes and altered biochemical pathways inferring resistance to crop plants against salt stress. The past decades have witnessed extensive research in development of salt tolerant cultivars via conventional means, improvised by modern era molecular tools and techniques. Rice (*Oryza sativa* L.) is the staple food crop across several countries worldwide. Being a glycophyte by nature, its growth is severely imparted in presence of excess salt. Rice is susceptible to salinity specifically at the early vegetative and later reproductive stages and the response of the crop to excessive salt toxicity at biochemical and molecular level as well as physiological level is well studied and documented. An understanding of the specific response of rice to ion accumulation at the toxic level can aid in identifying the key factors responsible for retarded growth and limited production of rice with the future scope of mitigating the same. The present review summarizes the differential responses of rice, in particular, to salt toxicity enumerating the detailed morphological, physiological, biochemical and molecular changes occurring in the plant.

2.3 Screening of rice mutants for salinity tolerance

Lee *et al.* (2003) selected sodium chloride (NaCl) tolerant cell lines from gamma-irradiated calli that were generated from seed culture. Multiplication of tolerant lines was done by culturing in callus induction medium for 120 days. Regenerants (M₁) were obtained from the tolerant calli and were cultured for 40 days on the hormone-free medium. Out of 5000 M₃ lines from M₂, 350 were screened from the germination stage to the 2-3 leaf stage with 1 per cent NaCl. Of the 350 M₃ lines, 12 were selected at the saline field near the sea coast (10-14 dSm⁻¹). Two of these lines had better agronomic traits. It was concluded that, the combination of radiation techniques with in vitro culture methods may be a valid approach in selecting salt tolerant lines.

Ali *et al.* (2004) screened ten advanced rice lines were screened for salinity tolerance at seedling stage using a rapid screening technique. Out of the lines tested, five were found tolerant, four were graded as moderately tolerant and one as susceptible. It appeared that tolerant lines had higher root and shoot ratio at seedling stage thus providing a clue about salt tolerance potential of a genotype. Further, comparative studies for salt tolerance in these rice genotypes in artificially saline conditions showed that salinity in general caused a marked reduction in yield and yield components in all the genotypes except in NR-2, whereas little negative effect was observed. Thus, it seems to possess better potential than Pokkali a recognized salt tolerant variety, and may boost up the rice production in salt affected areas.

Natarajan *et al.* (2005) studied the screening of rice accessions for growth and yield attributes contributing to salinity tolerance. Fifteen rice accessions from International Rice Soil Stress Tolerance Screening Nursery Trails (IRSSTN) of IRRI were used for the study. Based on the grouping, the rice accessions were grouped in to High Yielding Tolerant (HYT), High Yielding susceptible (HYS), Low Yielding Tolerant (LYT) and Low Yielding susceptible (LYT). Results revealed that the rice accessions of the high yielding and tolerant group recorded a higher value for the yield characters like number of productive tillers per plant, number of filled grains per panicle and thousand grain weight. It clearly indicates the direct effect of growth and yield attributes on higher yield of rice accessions for salinity tolerance.

Uddin *et al.* (2007) identified four salt tolerant rice mutant lines by screening four hundred M₂ families derived from the tropical japonica cultivar 'Drew' after gamma irradiation. The selected lines had significantly higher number of filled grains, lower grain

sterility, and higher grain yield as compared with their parent 'Drew' when grown under the NaCl stress of 10 dSm⁻¹ ECe. The mutant lines gave 8-9 times as much grain yield as the parent under salt stress and yielded 45-60 per cent of the grain yield of the parent without salt stress. The activity of anti-oxidant enzymes was determined in the salt tolerant lines as well as their parent under 200 mMNaCl stress. Increased antioxidant enzyme activity was one of the NaCl-stress tolerance mechanisms of the salt tolerant rice mutants obtained in this study.

Rao *et al.* (2008) screened rice genotypes of varying tolerance (tolerant, semi-tolerant and sensitive) in saline soil of electrical conductivity, ECe 4 and 8dSm⁻¹ and alkali soil of pH 9.5 and 9.8 in lysimeters. Vegetative growth events were less affected by both the stresses in comparison to reproductive stage. Grain yield was reduced by 26.7 per cent, 45.7 per cent and 50.3 per cent at ECe 8 dSm⁻¹ in three tolerance groups respectively. At pH 9.8 the reduction was 25.1 per cent, 37.2 per cent and 67.6 per cent in the three groups respectively. Higher floret fertility contributed to higher seed set and grain yields in tolerant genotypes whereas higher spikelet sterility led to poor seed set and lower grain yields in sensitive genotypes. The 1000 grains weight was also significantly reduced at ECe 4 or pH 9.8. Screening at reproductive stage for morphological traits like floret fertility is thus more useful to identify rice genotypes tolerant to both salinity and alkalinity stress. Genotypic (G) and environmental (E) effects and GE interactions were highly significant for the growth attributes and grain yield. Based on analysis of variance, genotypes tolerant to salinity and alkalinity as well to both the stresses were identified.

Mirza *et al.* (2009) carried out an experiment at the research field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh with the objective of verifying the effects of different salinity levels on the germination, growth and yield of four irrigated rice (*Oryza sativa* L.) cultivars. The experiment was performed with 6 NaCl concentrations viz. 0, 30, 60, 90, 120 and 150 mM. It was observed that seed germination, plant height, tiller number and leaf area index are negatively influenced by different salinity levels in all the rice varieties. All the yield components that is number of panicles, panicle length, spikelets per panicle, filled grain and grain weight also significantly decrease with the increased salinity stress. An increase of NaCl concentration up to 150 mM decreased 36-50 per cent of the grain yield of all the four rice varieties. Among the varieties BRRI dhan41 showed better performance at salinity stress up to a certain level.

Latif *et al.*, (2009) studied about the three rice genotypes for salinity tolerance in the gravel culture through addition of sodium chloride (NaCl) to create salinity level of <1 dS m^{-1} (control) and 7 dS m^{-1} . They observed that $K^+ : Na^+$ ratio and all growth parameters including number of tillers and roots and shoot (fresh and dry) weight decreased at 7 dS m^{-1} salinity compared to control. Among the three genotypes, KS-282 and BG-402 were rated as tolerant to semi tolerant whereas IR-28 was rated as salt sensitive genotype. The tolerant genotype (KS-282 and BG402-4) maintained low Na^+ and Cl^- but were higher in $K^+ : Na^+$ ratio. BG-402-4 was found to be tolerant in early stages of growth but becomes sensitive to salinity at later stages. K^+ decreased steeply at higher level of salt stress and the decrease in the concentration of K^+ in leaf at higher salinity level might be due to competition between K^+ and Na^+ which resulted in increased uptake of Na^+ at the cost of K^+ .

Bhowmik *et al.* (2009) opined selection of the salinity tolerance genotypes of rice based on phenotypic performance alone is less reliable and will delay progress in breeding. Recent advent of molecular markers, microsatellites or simple sequence repeats (SSRs) are used to find out salt tolerant rice genotypes. Three selected SSR markers; RM7075, RM336 and RM253 were used to evaluate rice genotypes for salt tolerance. Phenotypic and genotypic evaluation for salinity tolerance was done at the seedling stage. Phenotyping of 11 genotypes was done in hydroponic system using salinized (EC 12 dS m^{-1}) nutrient solution. IRRI standard protocol was followed to evaluate salinity tolerance. Large variation in salinity tolerance among the rice germplasm was detected. Plant height and total dry matter of tolerant lines were reduced by 19.0 and 40.6 per cent, respectively under salt stress (EC 12 dS m^{-1}), whereas those of susceptible lines were reduced by 46.0 and 73.5%, respectively. The markers showed polymorphism and were able to discriminate salt tolerant genotypes from susceptible. The genotypes having similar banding pattern with Pokkali were considered as salt tolerant. The SSR markers (RM7075, RM336 and RM253) identified 8, 9 and 7 salt tolerant genotypes, respectively. Through phenotypic and genotypic study, three genotypes viz., Pokkali, TNDB-100 and THDB were identified as salt tolerant rice cultivar. These SSR markers might have sequence homology with salt tolerant rice genotypes and consequently the markers could be able to identify salt tolerant rice genotypes from susceptible ones.

Islam and Karim (2010) studied the rice (*Oryza sativa* L.) genotypes for their tolerance to salinity. One hundred rice genotypes and two check cultivars (Pokkali as tolerant and IR29 as susceptible) were exposed to solution of electrical conductivity (EC) of 10, 15, and 20 dS m⁻¹ (5:1 molar concentration of NaCl and CaCl₂ solution) at germination and early seedling stage. Based on visual salt injury symptoms at 15dSm⁻¹, 13 genotypes were found fairly tolerant to salinity. However, among the 13 genotypes, only Patnai23 showed higher germination index and seedling relative dry weight than the check salt tolerant Pokkali at 15 dSm⁻¹. Beside these, performance of Awned-1, Nonasail and Soloi was also well at this level. The genotypes Patnai23, Awned-1, Nonasail and Soloi showed the best performance under saline condition.

Senguttuvel *et al.* (2010) revealed that the selection of genetically diverse and resistant genotypes based on association of Na⁺/K⁺ ratio with molecular markers is reliable. These markers can also be used to screen large set of germplasm collection to identify and discriminate more salt tolerant rice genotypes from susceptible based on sequence homology with already identified salt tolerant rice genotypes. The cluster and principal component analysis allowed a clear grouping of 25 genotypes grouped into 8 distinct clusters of resistant and susceptible genotypes with high and low level of 52 Na⁺ / K⁺ ratio. There was a highly significant correlation (R² = 88.75; p =5%) between the SSR markers and physiological trait based on ion analysis.

Mohammadi-Nejad *et al.* (2010) conducted a study to assess the role of saltol QTL in regards to effects of salinity on plant growth and yield components of different genotypes of rice at different growth stages. A greenhouse study was conducted to evaluate the response of 30 rice genotypes to three levels of salt stresses (0, 60, 100 mMNaCl) at reproductive stage. The seedling stage response of these genotypes to salinity with electrical conductivity at 12dSm⁻¹ also investigated. Pollen viability, number of unfilled and filled grain and grain yield per plant were evaluated. The rice genotypes differed significantly for salt tolerance at seedling stage. The genotypes were also significantly varied for the traits measured at the reproductive stage. The interactions of genotypes × salinity treatments were significant for pollen viability, number of unfilled grain and grain yield. Grain yield reduction due to salinity was more severe for control to 60 mM than for 60 mM to 100 mM. Pollen viability was found to be a robust criterion to screen the genotypes for salt tolerance at the reproductive stage.

Hakim *et al.* (2010) studied the response of twelve rice varieties against six salinity levels (0, 4, 8, 12, 16 and 20 dS m⁻¹) at germination and early seedling stages. Rice varieties MR211, IR20, BR40 and MR232 showed greater salt tolerance during germination (germinated at 12 dS m⁻¹ salinity). However, MR211, MR232 and IR20 performed better based on dry matter yield reduction. The result suggested that MR211, MR232 and IR20 might be used for further study of salinity effect on growth processes and physiological consequences at advanced stage of growth, since salt tolerance of a crop at germination and early seedling stage may not correspond to that at advanced stage.

Razzaque *et al.* (2011) studied the effects of salinity on mineral nutrient distribution along roots and shoots of seven selected rice (*Oryza sativa* L.) genotypes, namely Pokkali, PVSB9, PVSB19, PNR381, PNR519, NS15 and Iratom24 differing in salt tolerance. The rice plants were grown in pots and subjected to varying levels of salinity stress (0, 3, 6, 9, 12 and 15 dSm⁻¹). Mineral nutrients distribution in shoots and roots were measured after harvesting the plants at 95 days after transplanting. The responses of salt stress on mineral nutrient uptake and distribution along plant organs significantly differed among the rice genotypes. The contents of Na⁺ and Cl⁻ in the roots and shoots of resistant genotypes (PVSB9, PNR381 and Pokkali) were significantly lower than the susceptible rice genotype (NS15). The concentrations of Na⁺ and Na⁺/K⁺ in shoots of sensitive rice genotype (NS15) sharply increased with increasing salinity above 6 dS m⁻¹ than those of tolerant genotypes. The highest concentration of K⁺ was obtained in shoots of resistant genotype PVSB9 and this K⁺ content decreased more slowly with increasing salinity than those of other genotypes.

Hosseini *et al.* (2012) studied on Rice improvement for salt tolerance, which requires reliable assessment of salt tolerance variability among segregation genotypes. Sixty five genotypes of rice (traditional, improved and promising lines grown in north of Iran conditions) were evaluated under salt condition containing 0, 3, 6 and 8dSm⁻¹ levels during 2010. Five salt tolerance indices comprising: stress tolerances (TOL), mean productivity (MP), geometric mean productivity (GMP), stress tolerance index (STI) and stress susceptibility index (SSI) were used. The indices were adjusted based on shoot length and root dry weight under normal and salt conditions. Analysis of variance for shoot length and root dry weight showed that there was a significant genetic variation

among genotypes. Cluster analysis of genotypes using Y_s , Y_p and five other indices categorized genotypes into five groups for both shoot length and root dry weight. Results of cluster analysis distinguished tolerance and susceptible genotypes. It was concluded that the potential of these genotypes to tolerate salt stress was found to high MP, STI and low SSI for both shoot length and root dry weight. Also, based on broad-sense heritability Y_s , TOL and MP for shoot length and Y_s , TOL and STI for root dry weight can be used as the best indices for breeding program. Also, by cluster analysis based on tolerant indices, all genotypes were segregated into 4 and 3 groups based on both Y_p , Y_s , MP, GMP and STI and TOL or SSI, respectively. Therefore, genotypes such as IR56, Yosen, 8803, IR58, R3, 8802 and 8810 as tolerant and AbjiBoji, IR30, Amol 2, Neda and 8805 as susceptible can be used in breeding programs.

Wang *et al.* (2012) studied on plant survival under NaCl salt stress is maintaining a low Na^+ level or Na^+/K^+ ratio in the cells. A population of recombinant inbred lines derived from a cross between the salt-tolerant japonica rice variety Jiucailing and the salt-sensitive indica variety IR26, was used to determine Na^+ and K^+ concentrations in the roots and shoots under three different NaCl stress conditions (0, 100 and 120 mMNaCl). A total of nine additive QTLs were identified by QTL Cartographer program using single-environment phenotypic values, whereas eight additive QTLs were identified by QTL Ici Mapping program. Among these additive QTLs, five were identified by both programs. Epistatic QTLs and QTL-by-environment interactions were detected by QTL Network program in the joint analyses of multi-environment phenotypic values, and one additive QTL and nine epistatic QTLs were identified. There were three epistatic QTLs identified for Na^+ in roots (RNC), three additive QTLs and two epistatic QTLs identified for Na^+ in shoots (SNC), four additive QTLs identified for K^+ in roots (RKC), four additive QTLs and three epistatic QTLs identified for K^+ in shoots (SKC) and one additive QTL and one epistatic QTL for salt tolerance rating (STR). The phenotypic variation explained by each additive, epistatic QTL and QTL $\times$ environment interaction ranged from 8.5 to 18.9%, 0.5 to 5.3% and 0.7 to 7.5%, respectively. By comparing the chromosomal positions of these additive QTLs with those previously identified, five additive QTLs, qSNC9, qSKC1, qSKC9, qRKC4 and qSTR7, might represent novel salt tolerance loci. The identification of salt tolerance in selected RILs showed that a major QTL qSNC11 played a significant role in rice salt tolerance, and could be used to

improve salt tolerance of commercial rice varieties with marker-assisted selection (MAS) approach.

Nakhoda *et al.* (2012) evaluated three hundred forty two synthetic lines of bread wheat with three ones of control (Arg, Bam, Kavir) at salinity and normal conditions was carried out during the 2009-2010 in Iran. Salt tolerance indices including: Stress Tolerance Index (STI), Stress Susceptibility Index (SSI), Tolerance Index (TOL), Mean Productivity (MP) and Geometric Mean Productivity (GMP) were calculated. Result of tolerance indices showed that GMP and STI indices were appropriate indices to identify tolerant lines in salinity stress. On the basis of these indices, 12 lines were identified as the most tolerance lines. There were significant differences among evaluated lines and control lines for seed yield. The highest values for seed yield were observed in Arg and 22 lines in saline condition. This showed that salinity stress had significant effect on seed yield reduction of some genotypes. Therefore, selection of salt tolerance genotypes with consideration of their indices (e.g. GMP and STI) could be a good strategy for improvement of salt tolerance genotypes in bread wheat. It could be resulted that synthetic lines of 10, 32, 74, 86, 92, 98, 114, 188, 191, 297, 300, 326 that had more seed yield than control varieties of Arg, Bam and Kavir, were identified as the promising lines for wheat breeding programs.

Siddiqui *et al.* (2014) studied phenotyping of rice (*Oryza sativa* L.) in salt stress environment using infrared imaging. Results were correlated with the most frequently used physiological parameters such as stomatal conductance, relative water content and photosynthetic parameters. It was observed that stomatal conductance ($R^2 = -0.618$) and relative water content ($R^2 = -0.852$) were significantly negatively correlated with average plant temperature (thermal images), while dark-adapted quantum yield (F_v/F_m , $R^2 = -0.325$) and performance index ($R^2 = -0.315$) were not consistent with plant temperature. Advantages of infrared thermography and utilization of this technology for the selection of stress tolerance phenotypes are discussed.

Krishnamurthy *et al.* (2016) investigated the relationship between various morphological, physiological traits and stress indices. A set of 131 rice accessions were evaluated in two levels namely, non stress ($EC \sim 1.2 \text{ dSm}^{-1}$) and saline stress ($EC \sim 10 \text{ dSm}^{-1}$) in hydroponics at seedling stage. Root length and shoot lengths were reduced by 52 and 50 per cent, respectively in saline stress compared to non-stress conditions. There

was a significant correlation between various morphological and physiological parameters in non-saline in addition to saline stress as well as non-stress. The effect of the increased Na^+ concentration in the medium is detrimental to root length and shoot length as observed by reduction in root length and a concomitant reduction in shoot length. Increased concentration of Na^+ led to augmented Na^+/K^+ ratio with increased stress in the medium and decreased expression of traits. A significant positive correlation ($r=0.60$) was noticed between stress tolerance index (STI) of root and shoot length. The stress susceptibility index (SSI) for root length was expressed significant positive correlation with SSI for shoot length ($r=0.43$). SSI for K^+ content was registered significant negative correlation with STI for Na^+ content ($r=-0.43$). The three accessions namely, IC 545004, IC 545486 and IC 545215 were found to be the best performers adjudged on the morphological and physiological criteria in saline stress situation. These three rice accessions could be used as a donor parent or for genotypic studies in future breeding programs

Ching (2015) studied the mechanisms of salt tolerance in rice plants. There is evidence showing that Na^+ transporters play an important role in reducing Na^+ toxicity by excluding Na^+ from the cytosol or preventing Na^+ transport to the leaves. Evidence is provided to show that Na^+ transporters play regulatory roles in the tolerance of rice plants to salt stress.

2.4 Molecular characterization of salinity tolerant mutant lines

Seetharam *et al.* (2009) revealed that out of 35 primers of SSR markers, 28 were found to be polymorphic. The PIC value ranged from 0.064 (RM 274) to 0.72 (RM 580) with an average of 0.46. The Jaccard's similarity coefficient ranged from 0.42 to 0.90. The clustering pattern clearly grouped the genotypes based on their response to salinity and clustering was not based on their geographical origin. PCA components explained 38.4percent of variation.

Lang *et al.* (2009) conducted the mapping & MAS for salt tolerance genes in rice. SSR technique combined with selective genotyping was used for salt tolerance in rice. Salt tolerant cultivars AS996 was crossed to IR50404 & 229 recombinant inbred lines were produced by single seed descent. Highly significant associations were detected at the SSR locus RM223 on chromosome 8 to examine the power of the identified SSR

markers in predicting phenotype of the salt locus; they determined the genotypes of 93 improved varieties at RM223 locus. The results indicated an accuracy of more than 95 per cent in identifying the resistant plants which was similar to that using RM223.

Islam *et al.* (2008) used one hundred polymorphic SSR markers to characterize twenty one rice genotypes. These genotypes comprised of nine salt tolerant genotypes including five Pokkali accessions. The materials also included two improved varieties with a major QTL for submergence (*Sub1*) in Swarna background, *i.e.*, IR82810-407 and IR82809-237. The rest were popular or moderately salt tolerant rice varieties of Bangladesh, India, IRRI, or Philippines origin. The highest number of alleles (12) were found for RM418 followed by RM10793 (11), RM3412, RM400, and RM26809 (10). The highest PIC value (0.86) was found for RM10793 followed by RM418 and RM3412 (0.85), RM26809, RM490 and RM287 (0.84), RM16 (0.83), RM493, RM562, and RM253 (0.82). These suggested their greater usefulness for characterizing rice varieties. Pokkali and PSBRc82 were found to be the most genetically distant (78.65%) varieties. The Swarna+*Sub1* genotypes (IR82810-407 and IR82809-237) had the same genetic background; hence, they had highest genetic similarity between them (90%) and also with Swarna (>70%). Two main distinct clusters/groups were identified from cluster analysis. One cluster consists of mostly improved and adapted genotypes while the second cluster had mostly salt tolerant donors with few exceptions.

Bibi *et al.* (2009) exposed rice cultivars IR6 and IR8 to different doses of gamma radiation and stable mutants along with parents were studied for genetic diversity on the basis of morphological traits and molecular marker (RAPD). Morphological data showed that mutants of IR6 and IR8 performed well as compared to their parents. The genetic variation was determined through RAPD. A total of 74 scorable bands were observed, out of which 47 (63.6%) were polymorphic and 27 (36.5%) were monomorphic. The size of fragments ranged from 201bp–3.2 kbp. The number of fragments produced by various primers ranged from 1-12 with an average of 4.93 fragments per primer. Maximum 12 bands were amplified with primer A-03 and minimum one band was amplified with primer A-15, A-19 and B-10. Some specific RAPD bands were also identified reflecting the RAPDs application for the identification of rice cultivars/genotypes. Results revealed that variety Sarshar and IR8-178 contain a specific segment of 451bp amplified with primer A-19. The highest similarity was observed between IR8-15A and IR8-178 (96%)

and the least similarity was recorded between IR-8 and IR6-15/B (69%). On the basis of RAPD studies, genotypes were grouped on the basis of their similarities and distinctness.

Prabakaran *et al.* (2010) investigated the genetic divergence of 12 rice land races using five SSR markers. A total of 11 alleles were detected in 12 land races and the number of alleles per locus ranged from 2 to 3 with an average of 2.2 per locus. Among the primers used RM 481 identified more number of alleles and average PIC was 0.43. The dendrogram based on SSR marker analysis grouped the 12 rice accession into six clusters, where cluster VI was the largest with three accessions. The similarity coefficient through Jaccard's revealed that Anna samba and Chettivirippu were ascertained to be the genetically diverse from the other land races. The study also highlighted use of more number of markers for efficient characterizing the land races used for the present study.

Singh *et al.* (2010) used two different DNA-based techniques viz, simple sequence repeat (SSR) and inter simple sequence repeat (ISSR) markers to estimate genetic diversity among 20 rice genotypes possessing different physiological mechanisms contributing to salt tolerance. A total of 11 clear and repeatable bands were amplified from ten selected SSR primers pairs and 43 fragments were detected from nine ISSR primers. The level of polymorphism was 1.1 per cent with SSR compared to 90.7 per cent with ISSRs. Mean genetic similarity of 0.88 based on SSRs and 0.85 using ISSRs was observed. A total of 43 (39 polymorphic) and 11 bands were detected using 9 ISSR primers and 10 well distributed mapped SSR markers, respectively. Estimates of genetic similarity of ISSRs based on the 39 polymorphic markers between 20 rice cultivars ranged from 0.55 for PR108/CSR19 to 0.94 for Pokkali/CSR20 with an average of 0.81. The estimates revealed by the 11 polymorphic SSR bands showed the average value (0.94) and also the range of genetic similarity (from 0.86 to 1.00 for CSR22/CSR18 and CSR24/CSR20, respectively) reflecting their hyper variability and their high resolution power. The findings are likely to expedite breeding new salt tolerant cultivars by involving parents from diverse molecular clusters.

Senguttuvel *et al.* (2010) revealed that the selection of genetically diverse and resistant genotypes based on association of Na^+/K^+ ratio with molecular markers is reliable. These markers can also be used to screen large set of germplasm collection to identify and discriminate more salt tolerant rice genotypes from susceptible based on sequence homology with already identified salt tolerant rice genotypes, The cluster and

principal component analysis allowed a clear grouping of 25 genotypes grouped into 8 distinct clusters of resistant and susceptible genotypes with high and low level of Na^+/K^+ ratio. There was a highly significant correlation ($R^2=88.75$; $p = 5 \%$) between the SSR markers and physiological trait based on ion analysis.

Nantawan *et al.* (2011) evaluated thirty rice cultivars for salinity tolerance during the seedling stage. Genetic diversity of all rice cultivars was evaluated using RAPD and SSR markers. The cultivars were evaluated for polymorphisms after amplification with 20 random decamer primers and 20 SSR primer pairs. Mean genetic similarity coefficient was 0.82 for RAPD and 0.70 for SSR. Cluster analysis based on RAPD markers was effective in grouping cultivars based on their salt tolerance ability. Group IA1, IB and IV contained three T, three S and two HS rice cultivars respectively. The MT and MS cultivars which showed similar physiological responses to salinity were resolved into two groups: Group IA2 and Group II comprising ten and eight MT/MS cultivars respectively. Cluster analysis based on SSR markers separated rice cultivars into groups based on genetic relatedness which did not correspond to salinity tolerance level.

Islam *et al.* (2011) detected QTLs for salinity tolerance at the seedling stage in a F_2 breeding population derived from the cross between BRRI dhan40, a moderately tolerant female parent with IR61920-3B-22-2-1 (NSIC Rc106), a highly tolerant male parent. Out of total 300 F_2 segregating plants, 93 plants with extreme phenotype for salinity stress response were used for selective genotyping based on of visual seedling stage salt tolerance symptom. A total of 260 SSR and two EST markers evenly spread throughout the whole rice genome at 5 Mb intervals were used for parental polymorphism survey. The 90 polymorphic makers were used for QTL mapping for salinity tolerance at seedling stage. QTL analysis using single marker, interval mapping and composite interval mapping detected three major QTLs on chromosome 1, 8 and 10 with phenotypic variances (R^2) of 12.50, 29.0 and 20.20 per cent, respectively.

Ashrafuzzaman *et al.* (2012) used six selected SSR markers viz., RM10701, RM304, RM11757, RM336, RM7075, and RM152 for identification of salt tolerant genotypes. The band obtain from reaction with different markers were compared to the selected genotypes (BINAdhan-8 and AYT SL-3). Assessment of genetic diversity is an essential component in germplasm characterization and conservation. In DNA profiling, a total of 60 alleles were detected with an average number of alleles of 10 per locus (range

8 to 12 per locus) and the PIC values ranged from a low of the 0.7459 (RM152) to a high of 0.8908 (RM10701) and averaged 0.857. Positive correlations were found between gene diversity, PIC value and number of allele. The Unweighted Pair Group Method of Arithmetic Means (UPGMA) dendrogram constructed from (Nei's, 1972) genetic distance produced two main clusters of 26 rice germplasms. The lowest genetic distance (0.200) was found in CSR-28 vs. CSR90-IR-2 genotype pair indicating that they are genetically much closer among the genotypes. A cluster was consisted with a moderate salt tolerant due to higher similarity, while the mostly susceptible germplasms in the second cluster due to lower genetic distance between germplasms.

Berilus *et al.* (2013) evaluated twenty four genotypes of rice for polymorphisms after amplification with 30 SSR primer pairs. The results obtained depicted a wide range of variation among the varieties. The diversity parameters confirmed that Bordungsha F₁, S5 and Baodhan Bordungsha (deep water rice) were most diverse and were distinctly different from the rests of the genotype and the dissimilarity coefficient ranged from 0.06 to 0.94. This study provides a clear picture of the genetic diversity of rice. Among the set of SSR primers tested, RM44 (0.942), RM495 (0.932), RM125 (0.998) and OSR13 (0.970) were more informative in comparison to other primers.

Rabey *et al.* (2013) selected the microsatellite markers to estimate the genetic diversity of eight rice cultivars and to fingerprint the rice cultivars under study. These markers were precisely selected in order to represent the entire rice genome. These SSR generated 46 markers; twelve out of them were polymorphic. The number of SSRs alleles per locus varied from 2 for RM133, RM 215 and RM433 to six for RM271, with a mean of 3.83 alleles per locus. Whereas, 245 polymorphic AFLP markers (nearly 87.21 % of the total AFLP markers produced) were generated using five AFLP primer combinations. The polymorphism information content value for the two types of assays was 0.825 and 0.967 for SSR and AFLP markers, respectively. Pair-wise genetic similarity ranged from 0.393 to 0.783 and from 0.103 to 0.682 for AFLP and SSR, respectively. Cluster analysis was achieved based on SSRs and AFLP data and the relationship between the studied rice cultivars were addressed.

Islam *et al.* (2013) investigated the fourteen rice genotypes, composed of six salt tolerant, three submergence tolerant, two drought tolerant genotypes along with three high yielding genotypes, released from Bangladesh Rice Research Institute (BRRI) for

genetic diversity analysis using 40 simple sequence repeats (SSR) markers. All of the used SSR markers were found polymorphic among the 14 rice genotypes. The amplicon size ranged from 75 bp (RM436) to 330 bp (RM26360). A total of 168 alleles were detected, the number of alleles per locus ranged from 2 (RM252, S03120) to 6 (RM570, S12055, S11033) with an average of 4.2 alleles per locus. Polymorphic information content (PIC) value varied from 0.21 (RM252) to 0.76 (S07024) with an average of 0.57. From genetic distance co-efficient, the highest and lowest genetic distant varieties were found for BRRI dhan28 viz., BRRI dhan43 (0.82 %) and BRRI dhan40 vs. BRRI dhan44 (0.37 %) respectively. Unweight pair group method with arithmetic mean (UPGMA)-cluster analysis divided the rice genotypes into four distinct clusters. The information obtained from this study would be useful for planning the breeding program to develop stress tolerant rice variety with high yielding ability and fine grain quality.

Hani *et al.* (2017) studied four indigenous rice genotypes collected at Coastal Saline Research Centre, Ramanathapuram, Tamil Nadu, India, to screen under saline and non-saline conditions using the microsatellite markers for the identification of salt tolerant genotypes at the seedling and reproductive stages. Two selected SSR markers were used to determine salinity tolerance in rice genotypes. SSR based marker identified three genotypes as tolerant at least tolerant to one of the two SOS markers but one variety was susceptible for both the markers. The detected salt tolerant genotypes can be a probable germplasm resource for prospective breeding program.

MATERIAL AND METHODS

III. MATERIAL AND METHODS

The present investigation “Genetic and Molecular Assessment of Saline Tolerant rice mutants for yield and quality attributes” was conducted with the prime objective to study the extent of variability, heritability, genetic advance, association of characters, nature and magnitude of direct and indirect effects of different characters towards yield besides molecular characterization of mutants. The details of the experimental material used, the methodology followed, the protocols and statistical tools used for analysis during the course of study are presented under the respective experiments.

3.1 Experimental location

The experiment was conducted during *kharif* 2016 at Agricultural Research Station (ARS), Gangavathi, located at latitude of 15.43° North and longitude 76.53° East and an altitude of 406 meters above mean sea level (MSL). Gangavathi comes under the Northern Dry Zone of Karnataka with the annual rainfall of 523 mm. The data on weather parameters such as rainfall, temperature and relative humidity recorded at the Agro-meteorological observatory, Agricultural Research Station (ARS), Gangavathi, during crop growth period are furnished in Appendix IV. Agricultural Research Station, Gangavathi comes under Tungabhadra Project area, where natural salinity gradient have been maintained to carry out experiments.

Soil analysis

Representative soil samples from surface (0-15 cm) were collected from the experimental sites before transplanting. The collected samples were then air dried and passed through a 2 mm sieve. The processed soil samples were analysed for selected basic properties like pH and electrical conductivity (ECe).

Soil pH and electrical conductivity of the samples were measured on a 1:2.5 soil: water suspension separately using Systronic digital pH meter and Elico digital conductivity meter CM180, respectively. The EC (1:2.5) values were converted to ECe by multiplying a common factor of 2.66 which was derived for such soils at ARS,

In surface soil pH range from 8.03-8.5 with mean of 8.17. soil salinity as expressed by ECe ranged from 10-14 dS/m with mean of 11.15 dS/m before transplanting. Similarly

pH and ECe was calculated at the maturity, pH ranged from 8.0-8.42 and mean was 8.16 with ECe ranged from 10-14.9 dS/m with mean of 12.87 dS/m.

3.2 Experimental Material

The experimental material for the present study consists of mutant genotypes derived from the two rice varieties BPT-5204 and Rp-Bio-226. The cultivar Rp - Bio 226 is a improved version of BPT-5204 for BLB resistance as it has been introgressed with Xa21, xa13 and xa5 resistance or R genes by Directorate of Rice research (DRR), Hyderabad, India. The seeds of both the varieties were exposed to gamma rays treatment from Cobolt 60 source at Bhabha Atomic Research Centre (BARC), Trombay, Mumbai, at equilibrium moisture content of eight per cent. The handling of mutagen treated material had been indicated already (Archana,. 2015), M₆mutants comprised of 29 mutant genotypes of BPT-5204 and 28 mutant genotypes of RP-Bio 226 were selected from the M₅ generation, studied by Archana (2015) based on yield and yield attributing characters under saline condition. The selected 57 mutant genotypes were grown in the saline and normal soil conditions along with the checks viz., BPT-5204 (parent), RP-Bio-226 (parent), IRRI-154 (sensitive at seedling stage), Swarna Sub 1 (sensitive check), CSR-22 (local check), Pokkali (tolerance check) and FL-478 (tolerance at seedling stage) evaluated during *kharif* 2016. The details of selected lines are furnished in Table 1. General view of experimental field is shown in Plate 1.

3.3 Experimental method

3.3.1 Experimental layout and crop management

Evaluation of 57 mutant rice genotypes along with seven checks was carried out using randomized block design with two replications. Each entry was planted in six rows of four meter row length with spacing of 20 cm between the rows and 15 cm between the plants.

The seedlings were raised in wet nursery method under normal soil condition and 35 days old seedlings were transplanted in the respective normal and saline soil experimental field on 18th October 2016. The standard agronomic practices and plant protection measures were adopted to ensure uniform and healthy crop growth as per the package of practice recommended by the University of Agricultural Sciences, Raichur.



Plate 01. General view of soil salinity stress experimental plot

3.3.2 Sampling

During the different crop growth stages, observations on various agro-morphological and quality traits were recorded as per the set objectives. From each mutant line in each replication five plants were randomly selected in a net plot area in order to avoid the border effect and tagged for recording observations. The different observations were recorded mean data from sampled plants for different characters were used for statistical analysis.

3.4 Recording of observations

The details of the observations recorded on the mutants for various traits are presented below.

3.4.1 Agro-morphological characters

3.4.1.1 Days to 50 per cent flowering

The total number of days taken by each entry from date sowing to opening of first flower in 50 per cent of the plants was counted and recorded as days to 50 per cent flowering.

3.4.1.2 Plant height (cm)

The plant height at maturity was measured from base of the plant to the tip of the panicle and expressed in cm.

3.4.1.3 Panicle length (cm)

The length of the panicle from its base to the tip of last spikelet prior to harvest was measured and expressed in cm.

3.4.1.4 Number of grains per panicle

Number of grains per panicle was counted using AIDEX waver IC-VA ver.3.0 seed counter both filled and chaffy ones in five panicles were recorded and data was averaged.

Table 1 List of mutant rice genotypes used for the study during *kharif* 2016

Line number	Line number
BPT-5204-10	RP Bio-226-37
BPT-5204-15	RP Bio-226-41
BPT-5204-16	RP Bio-226-45
BPT-5204-22	RP Bio-226-57
BPT-5204-29	RP Bio-226-63
BPT-5204-37	RP Bio-226-65
BPT-5204-38	RP Bio-226-78
BPT-5204-42	RP Bio-226-83
BPT-5204-46	RP Bio-226-90
BPT-5204-57	RP Bio-226-103
BPT-5204-60	RP Bio-226-109
BPT-5204-67	RP Bio-226-115
BPT-5204-69	RP Bio-226-120
BPT-5204-77	RP Bio-226-130
BPT-5204-88	RP Bio-226-131
BPT-5204-94	RP Bio-226-147
BPT-5204-96	RP Bio-226-151
BPT-5204-98	RP Bio-226-152
BPT-5204-103	RP Bio-226-153
BPT-5204-115	RP Bio-226-159
BPT-5204-128	RP Bio-226-168

BPT-5204-130	RP Bio-226-172
BPT-5204-134	RP Bio-226-190
BPT-5204-139	RP Bio-226-191
BPT-5204-149	RP Bio-226-199
BPT-5204-158	BPT 5204
BPT-5204-165	RP -BIO 226
BPT-5204-166	Pokkali
BPT-5204-183	CSR 22
RP Bio-226-18	FL 478
RP Bio-226-23	Swarna Sub 1
RP Bio-226-29	IRRI 154

3.4.1.5 Panicle weight (g)

The fully dried panicle before separation of seeds was weighed and average data was recorded in grams.

3.4.1.6 Number of panicles (Productive tillers)

The total number of panicles per plant was counted at the time of harvest which represents the number of productive tillers.

3.4.1.7 Number of tillers per plant

The total number of tillers per plant including both productive and unproductive tillers were counted and recorded at maturity stage.

3.4.1.8 Length of flag leaf (cm)

The uppermost leaf below the panicle is the flag leaf. It generally differs from other leaves in shape, size and angle. Its length was measured from base to the tip of the leaf and expressed in cm.

3.4.1.9 Per cent chaffyness

Per cent chaffyness was calculated by counting of unfilled grains at the time of harvest in proportion to total number of well-developed and filled grains.

$$\text{Per cent chaffyness} = \frac{\text{Total No. of unfilled grains per panicle}}{\text{Total No. of filled grains per panicle}} \times 100$$

3.4.1.10 Grain yield per plant (g)

Total weight of all the grains from five plants in each entry was recorded in grams after harvest and 5 - 6 days sun drying and converted to grain yield per plant

3.4.1.11 Test weight (g)

One thousand seeds were counted using AIDEX waver IC-VA ver.3.0 seed counter and weight of thousand seeds was expressed in grams.

3.4.1.12 Panicle exertion

Degree of panicle exertion was measured at near maturity stage as the distance from the flag leaf ligule to the panicle node and the data was expressed in cm.

3.4.2 Quality parameters

Physico-chemical assessment of all the genotypes was carried out at laboratory of Plant Molecular Biology, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Raichur.

The observations on various physico-chemical traits were recorded. The stored grains of 57 rice genotypes were used for further study on quality analysis. The following observations were recorded for the physico-chemical quality assessment.

3.4.2.1 Grain size Classification

The length and breadth of the grain was measured using Grain Shape Tester. The genotypes were categorized based on classification given by Ramaiah (1969).

State	Kernel length (mm)	Length/breadth ratio
Short Slender	< 6.0	< 3.0
Short Bold	< 6.0	< 2.5
Medium Slender	< 6.0	2.5 - 3.0
Long slender	> 6.0	> 3.0
Long Bold	>6.0	< 3.0

3.4.2.2 Amylose content (%)

Starch makes up about 90% of the dry matter content of milled rice. Starch is a polymer of glucose and amylose is a linear polymer of glucose. Amylose has a major influence on cooking and eating quality characteristics of rice. It also plays an important role in determining the texture of cooked rice. The amylose content of starches usually ranges from 15 to 35%. High amylose content rice shows high volume expansion (not necessarily elongation) and high degree of flakiness. The grains cooked dry, are less tender and become hard upon cooling. In contrast low-amylose rice cooks moist and sticky. Intermediate amylose rice is preferred in most rice-growing areas of the world, except where low-amylose japonicas are grown. The amylose content in each rice sample was determined by using spectrophotometrical techniques according to modified method of Juliano (1971).

1. Weigh 100 mg well powdered milled rice into 100ml of volumetric flask.
2. Add 1 ml of 95 per cent ethanol and 9 ml of 1N NaOH.
3. Heat the sample for 10 mins in boiling water bath, cool it and make up the volume to 100 ml.
4. Pipette 5 ml from the 100 ml into another 100 ml of volumetric flask.
5. Add 1ml 1N acetic acid and then 2 ml iodide solution and makeup the volume to 100 ml.

6. Shake, stand for 20 min and determine the percent Transmittance at 620 nm using a colorimeter.
7. Prepare a series of standard starch solution containing 0, 20, 40, 60, 80 and 100 per cent amylose as in the steps 1 to 5.
8. Read the transmittance of the standards at 620 nm and plot a standard graph.
9. Amylose content of the sample is determined in reference to the standard curve and expressed on present basis.
10. Making of amylose standard
 - a. Pipette out 1, 2, 3, 4 and 5 ml of the standard amylose into 100 ml of volumetric flasks in three reactions.
 - b. Keep one flask as blank without adding anything.
 - c. Add 1.0 ml 1N acetic acid and 2.0 ml I-KI solution to all the flasks including blank.
 - d. Make up all the flasks to 100 ml using distilled water and cover all the flasks with a blank cloth or aluminium foil to prevent direct light.
 - e. Keep for 20 min and take reading at 620 nm in a spectrophotometer.
 - f. The standards including blank, correspond to 0, 4, 8, 12, 16 and 20 per cent of amylose.
 - g. Draw a standard curve using the absorbance reading.

Amylose content was determined by the following formula and expressed on dry weight basis.

$$\text{Amylose content} = \text{Optical density} \times \text{Slope of the curve} \times \text{Dilution factor}$$

Based on the amylose percentage genotypes can be grouped as follows:

Category	Amylose content (%)
Waxy	1-2
Very low amylase	2-3
Low	10-20
Intermediate	20-25
High	25-30

3.4.3 Screening of selected M₆ mutant lines for salinity tolerance

3.4.3.1 Phenotypic study of salinity tolerance based on yield and yield attributing characters (Stress Susceptibility Index)

The plants were screened for the salinity tolerance using Stress Susceptibility Index (SSI) (Fischer and Maurer, 1978). In Saline and normal soil conditions (ECe less than 4 dS/m) the mutant genotypes were screened based on the yield and yield attributing characters. Stress susceptibility index (SSI) was calculated by using formula:

$$SSI = \frac{1 - \frac{Y_s}{Y_p}}{SI} SI = 1 - \frac{\bar{Y}_s}{\bar{Y}_p}$$

Where,

Y_s -the yield of lines under stress

Y_p - the yield of lines under normal conditions

$\bar{Y}_s$ - the mean yields of all genotypes in stress (Y_s)

$\bar{Y}_p$ - the mean yields of all genotypes in non-stress conditions (Y_p)

SI - the stability index

3.4.3.2 Salinity tolerance at seedling stage

The mutants were screened for salt tolerance at seedling stage using IRRI standard protocol in in-situ saline soil condition. The evaluation was done using the modified standard evaluation system (SES) rating the visual symptoms of salt toxicity (IRRI, 1997). This scoring discriminated the susceptible from the tolerant and the moderately tolerant genotypes. The scoring was done at 30 days after transplanting.

Standard evaluation system (SES)

Score	Observation	Tolerance
1	Normal growth on leaf symptoms	Highly tolerant
3	Nearly normal growth, but leaf tips or few leaves whitish and rolled	Tolerant
5	Growth severely retarded; most leaves rolled; only a few are elongating	Moderately tolerant

7	Complete cessation of growth; most leaves dry; some plants dying	Susceptible
9	Almost all plants dead or dying	Highly susceptible

3.4.3.3 Na⁺:K⁺ ratio

Plant sampling and processing

All the lines grown undersaline conditions were selected and they were subjected to the estimation of Na⁺: K⁺. Third leaf from the apex was collected from the plant at the panicle initiation stage. The leaf samples were oven-dried at 60 °C to a constant weight and were ground in Willey mill and later were subjected for sodium and potassium analysis.

Digestion of the sample

A known quantity of plant sample was digested with diacid mixture (HNO₃:HClO₄) until white residue was developed. The residue was dissolved in 6N HCl and made up the volume to 50 ml in volumetric flask.

Determination of Total Na⁺ and K⁺

Total K and Na content in the digested plant sample was determined by flame photometer after making proper dilution (Jackson, 1973).

Singh *et al.* (2014) has grouped the genotypes into tolerant and susceptible based on the Na and K ratio and same has been adopted to categorize the genotypes in present study.

Na ⁺ : K ⁺ ratio	Scale of tolerance
0 – 0.2	Highly tolerant
0.2 – 0.5	Tolerant
0.5 – 0.8	Susceptible
≥ 0.8	Highly susceptible

3.5 Molecular characterization of rice genotypes using SSR markers

Among 57 mutant rice genotypes, 22 genotypes were selected based on salinity stress tolerance on yield and yield attributing traits. These 22 genotypes were subjected to molecular characterization using SSR markers for salinity stress tolerance. The detailed procedures followed are elaborated as below.

3.5.1 DNA Extraction

The genomic DNA was isolated from fresh leaves following C-TAB (Dellaporta *et al.*, 1983) procedure with minor modifications as explained below. Preparation of stocks for CTAB method of DNA Extraction is furnished in Appendix IV.

- Two grams of fresh young leaves were harvested and the surface was cleaned with wet paper towel. The sample was ground to fine powder using liquid nitrogen with pre-chilled pestle and mortar.
- The powder was transferred into a sterile 2.0 ml eppendorf tube. Then 1 ml of pre-warmed (65 °C) extraction buffer (0.35 M sorbitol, 100 µM Tris and 5 µM EDTA) was added. Before using, 0.4 g/100 ml of Sodium dodecyl sulfate, 1g/100 ml of Polyvinylpyrrolidone (1% PVP) was added in to the extraction buffer.
- The solution was kept in water bath at 65 °C for 10-15 min with intermittent mixing.
- The tubes were kept for 10 min to allow them to return to room temperature.
- Equal volume of chloroform: Isoamyl alcohol (CIA) (24:1) solution was added to the tubes and gently mixed by inverting.
- The solution was centrifuged at 15000 rpm for 10-15 min at room temperature.
- The aqueous supernatant solution was pipetted out and transferred to a fresh tube.
- DNA was precipitated by adding equal volume of ice cold isopropanol to the aqueous phase.

- The solution was left for overnight incubation at freezing temperature to enhance precipitation
- Solution was centrifuged at 15000 rpm for 5-10 minutes at 4°C.
- Supernatant was discarded (keeping pellet undisturbed).
- The DNA pellet was washed with 70 per cent alcohol (400 µl) for 30 min and the tubes were allowed to drain and dried at room temperature for 2-3 h.
- Then DNA was suspended in 50 µl TE (Tris EDTA) buffer (10 mM TrisHCl + 1mM EDTA + 2M NaCl, pH 7.5) in sterile eppendorf tube and kept for 45 min at room temperature.
- When DNA was fully dissolved, 1 µl of RNase (10 mg/ml) was added and incubated at 37 °C for one hour at room temperature.

3.5.2 DNA quantity and quality estimation

The concentration of DNA was assessed spectrophotometrically and also by gel electrophoresis using 0.8 per cent agarose with known concentration of uncut DNA. A good DNA preparation generally exhibits the spectral property of A_{260} / A_{280} values 1.7 - 2.0 (< 1.7- more protein, > 2.0 more RNA)

Concentration of DNA (µl/ml) = O.D at 260 x 50. To test the quality of DNA, samples were run on 0.8 per cent agarose gel 1x TAE (Tris acetic acid EDTA) buffer and stained with ethidium bromide and checked for contamination by RNA (which usually runs a head) and the DNA was evaluated by comparing it with a standard undigested DNA sample.

3.5.3 Polymerase chain reaction

- Random primers: The decamers were used for the study
- Template DNA: crude genomic DNA extracts of different genotypes.

- dNTPs: The four individual dNTPs viz., dATP, dGTP, dCTP and dTTP were obtained from xcelris genomics private ltd Ahmedabad, Gujarat, India and were used at a concentration of 2.5 mM each.
- Taq DNA polymerase: Taq DNA polymerase (5U/μl) and 10 X Taq assay buffer were obtained from xcelris genomics private ltd. Ahmedabad, Gujarat, India.
- Chemicals: Analytical grade chemicals were obtained locally
- Thermocycler - Eppendorf thermal cycler gradient was used for cyclic amplification of DNA.
- **3.5.4 Amplification reaction mixture for SSR marker**

Amplification reaction mixture for SSR marker was prepared in 0.5 ml PCR tubes containing following components in a total volume of 15 μl.

Sl. No.	Components		Quantity (μl/reaction)
1	10X Assay buffer with 17.5 mM MgCl ₂		2
2	NTPs mix (2.5 mM each)		1
3	Primer (10 pm/μl)	Forward (5pm/ μl)	0.6
		Reverse (5pm/ μl)	0.6
4	Template (15 ng/μl)		2
5	Sterile distilled water		9
6	Taq DNA polymerase (5 U/μl)		0.30

Except template, the master mix was distributed to PCR tubes (15μl/tube) and later 1.5μl of template DNA from the respective genotypes was added making the final volume of 15 μl.

SSR Markers used for characterization of rice

Marker	Primer s	Forward	Reverse
SSR	RM-336	CTTACAGAGAAACGGCATCG	GCTGGTTTGTTTCAGGTTCG
	RM-7075	TATGGACTGGAGCAAACCTC	GGCACAGCACCAATGTCTC

3.5.5 The PCR amplification profile for SSR marker

Sl. No.	Step	Temperature (°C)	Duration (min.)	Number of cycles
1	Initial denaturation	94	5.00	1
2	Denaturation	94	1.00	} 40
3	Annealing	55	0.45	
4	Extension	72	1.00	
5	Final extension	72	5.00	1
6	Dump	4	-	-

After the completion of the PCR, the products were stored at 4 °C until the gel electrophoresis was done.

3.5.6 Separation of amplified products by Agarose Gel

The amplified products from each tube along with 2 µl of loading dye (bromophenol blue) were separated on 2.5 per cent agarose gel containing ethidium bromide at 70 volts (<5volts per cm of gel) using 1X TAE buffer of pH 8.0. Lambda DNA double digest was used as DNA molecular weight marker. The gel was photographed by using documentation system (Bio Rad).

3.5.7 Scoring the amplified fragments

The amplified fragments were scored as '1' for presence of single band, and '0' for the absence of a band generating the 0 and 1 matrix and per cent polymorphism was calculated by using the following formula.

$$\text{Per cent polymorphism} = \frac{\text{Number of polymorphic bands}}{\text{Total number of bands}}$$

3.5.8 Analysis of the profiles of the amplified fragments

Pair wise genetic similarities (S_{ij}) between genotypes were estimated by Jaccard similarity coefficient. Clustering was done using the symmetric matrix of similarity coefficient and cluster obtained based on unweighted pair group arithmetic mean (UPGMA) using NTSYS-PC. The similarity measurements were converted to genetic distance measurements as $(1 - S_{ij}) \times 100$ (Spooner *et al.*, 1996).

Polymorphic information content values for primers were calculated by using the formula (Nei, 1973)

$$PIC_j = \sum_{i=1}^n 1 - P_{ij}^2$$

Where,

P_i = the frequency for the j^{th} allele for marker i and summation extends over n alleles.

3.6 Statistical analysis

The statistical analysis of the data on individual character was carried out on the mean values of each genotypes using WINDOSTAT. Different statistical methods employed for the analysis are presented below:

3.6.1 Mean, Range and Co-efficient of variation

On the basis of individual plant observations, the population mean from each character was computed as below.

$$\text{General mean } (\bar{x}) = \frac{\text{Sum of observations of all the plants for each genotype}}{\text{Total number of plants}}$$

The minimum and maximum values on the basis of individual plant observations were used to indicate the range of given character.

$$\text{Co-efficient of variation (\%)} = \frac{\text{SD}}{(\bar{x})} \times 100$$

Where,

SD = Standard deviation

$\bar{x}$ = General mean of the character

3.6.2 Analysis of variance (ANOVA)

The mean values of five plants in each replication for each character were used for analysis of variances. The differences among the genotypes were tested by 'F' test as given below.

Source of variation	Degrees of Freedom	Mean sum of square	Cal. F
Replication	r-1	RMS	RMS/EMS
Treatment	t-1	TMS	TMS/EMS
Error	(r-1)(t-1)	EMS	-
Total	rt-1	-	-

Where,

r = Number of replication

t = Number of treatment

RMS = Replication mean sum of square

Tr MS = Treatment mean sum of square

EMS = Error mean sum of square

The Standard error was calculated as,

$$S.E.m. = \sqrt{\frac{EMS}{r}}$$

The significance of difference among all the genotypes was tested by 'F' test using the error variance by comparing the calculated 'F' value with the Table 'F' value at 5 per cent and 1 per cent probability levels. After testing for significance of the difference among the means of different genotypes for each character, further computations were done as detailed below.

3.6.3 Estimation of genetic variability parameters

In order to identify and ascertain the genetic variability among genotypes and to assess the extent of environmental effect on various characters, different genetic parameters were estimated as described below.

3.6.3.1 Estimation of variance components

Phenotypic and genotypic variances were estimated using the formula given by Lush (1949).

$$\text{Phenotypic variance } (\sigma_p^2) = \text{Genotypic variance } (\sigma_g^2) + \text{Error variance } (\sigma_e^2)$$

$$\text{Genotypic variance} = \frac{TMS - EMS}{r}$$

$$\text{Error variance } (\sigma_e^2) = EMS$$

Where,

TMS = MS for treatment (genotype)

EMS = MS for error

r = Number of replications

3.6.3.2 Coefficient of variation

The genotypic and phenotypic coefficient of variation was computed as per the method suggested by Burton and Devane (1953) and expressed as percentage.

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\bar{X}$ = General mean of the character

PCV and GCV values were categorized as low, moderate and high values as suggested by Sivasubramanian and Menon (1973). Which is as follow

0 – 10 % : Low

10 – 20 % : Moderate

20 % and above: High'

3.5.3.3 Heritability (h_b^2)

Heritability in broad sense (h_b^2) was computed as the ratio of genotypic variance to the total phenotypic variance as suggested by Hanson *et al.* (1953) and expressed as percentage.

$$\text{Heritability in broadsense } (h_b^2) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

The heritability percentage was categorized as low, moderate and high as given by Robinson *et al.* (1949).

0 – 30 % : Low

30 – 60 % : Moderate

> 60 % : High

3.5.3.4 Genetic advance (GA, expected response)

Genetic advance was estimated by using the formula given by Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = K h^2 \sigma_p$$

Where,

K = Selection intensity which is equal to 2.06 at 5% intensity of selection

h_b^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.5.3.5 Genetic advance as per cent mean (GAM)

This was estimated by using the formula given by Johnson *et al.* (1955).

$$\text{GAM} = \frac{\text{GA}}{\bar{x}} \times 100$$

Where,

GA = Genetic advance

$\bar{x}$ = General mean of character

Genetic advance as per cent mean was categorized as low, moderate and high as given by Johnson *et al.* (1955).

0 – 10 % : Low

10 – 20 % : Moderate

> 20 % : High

3.6.4 Correlation analysis

The correlation coefficients were worked out to determine the degree of association of a character with yield and yield attributing components.

To estimate the degree of association between the traits studied, phenotypic correlation was computed by using the formula given by Webber and Moorthy (1952).

$$r_p = \frac{\text{Cov}(x, y)}{[V(x) V(y)]^{1/2}}$$

Where,

r_p = Phenotypic correlation co-efficient

$\text{COV}(X, Y)$ = Phenotypic covariance between trait X and Y

$V(X)$ and $V(Y)$ = Phenotypic variances of the traits X and Y

The significance of correlation co-efficient was tested by referring to the Table value at $n-2$ df given by Snedecor (1961).

3.6.5 Path Coefficient analysis

Path coefficient analysis was carried out using phenotypic correlation values of yield components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Path coefficients were obtained by solving the simultaneous equation, which express the basic relationship between correlation and path coefficients. The equations were as follows.

$$r_{1,y} = p_{1,y} + r_{1,2}p_{2,y} + r_{1,3}p_{3,y} + \dots + r_{1,7}p_{7,y}$$

$$r_{2,y} = p_{2,y} + r_{2,1}p_{1,y} + r_{2,3}p_{3,y} + \dots + r_{2,7}p_{7,y}$$

$$r_{3,y} = p_{3,y} + r_{3,1}p_{1,y} + r_{3,2}p_{2,y} + \dots + r_{3,7}p_{7,y}$$

$$r_{6,y} = p_{6,y} + r_{6,2}p_{2,y} + r_{6,3}p_{3,y} + \dots + r_{6,7}p_{7,y}$$

Where,

$r_{1,y}$ to $r_{7,y}$ denote the correlation coefficients between independent characters

1 to 6 and dependent characters 'y', $r_{1, 2 \text{ to } 5, 6}$ denote the correlation coefficients between all possible combinations of independent characters. $P_{1, y}$ to $P_{6, y}$ denote the effects of characters 1 to 6 on character y.

Scale for path coefficients (Lenka and Mishra, 1973)

Value of direct or indirect effects	Scale
0.0 To 0.09	Negligible
0.10 to 0.19	low
0.20 to 0.29	Moderate
0.30 to 0.99	High
More then 1.00	Very high

EXPERIMENTAL RESULTS

IV. EXPERIMENTAL RESULTS

The prime objective of conducting these experiments were to study the extent of variability, heritability, genetic advance, association between the characters, nature and magnitude of direct and indirect effects of different characters towards yield. Further molecular characterization of these genotypes was also carried out using trait specific SSR markers.

A total of 57 M₆ mutants of rice were evaluated under saline stress and normal soil conditions, during *kharif* 2016. Observations on quantitative characters were recorded on selected individuals in each mutant line and the results obtained are presented under different headings as below;

4.1 Analysis of variance

4.2 Genetic variability, heritability and genetic advance

4.3 association of trait under saline and normal soil in mutants

4.4 Salinity tolerance of mutants

4.5 Molecular characterization using SSR markers

4.1 Analysis of Variance

The analysis of variance for different characters under normal condition is presented in Table 2. The genotype mean sum of squares due to genotypes showed significant differences for all the characters viz., days to 50 per cent flowering, plant height, panicle length, number of grains per panicle, panicle weight, productive tillers per plant, length of flag leaf, per cent chaffyness, test weight, panicle exertion, grain yield per plant and yield per hectare suggesting that the genotypes were genetically diverse for majority of the characters under study.

The analysis of variance for different characters under saline condition is presented in Table 3. The genotype mean sum of squares due to genotypes showed

Table 2 Analysis of Variance for yield, yield attributing traits of rice mutant genotypes under normal soil

Source of variation	df	DFF	PH	PL	NGP	PW	NPT	TNT	LF	% CH	GYP	TW	PE	YIELD
Replication	1.00	8.77	16.97	3.71	132.03	0.50	1.01	1.17	0.83	0.05	0.45	0.13	0.30	33904.05
Genotype	63.00	62.26**	239.54**	4.95**	3866.03**	24.54**	10.14**	13.10**	19.36**	59.51**	51.76**	16.13**	3.91**	1731818.29**
Error	63.00	31.52	26.99	1.83	205.05	2.02	2.73	2.86	2.91	0.50	2.20	0.51	0.08	164340.95
CV		5.58	5.44	5.93	6.74	9.97	12.16	10.07	6.45	10.71	4.75	5.24	11	6.04

Table 3 Analysis of Variance for yield, yield attributing traits of rice mutant in saline soil

Source of variation	df	DFF	PH	PL	NGP	PW	NPT	TNT	LF	% CH	GYP	TW	PE	YIELD
Replication	1.00	75.03	31.94	5.39	270.28	0.50	0.00	1.20	4.10	12.50	0.13	0.13	0.59	4174.13
Genotype	63.00	60.01**	209.42**	3.97**	3153.31**	15.68**	10.73**	13.24**	19.97**	234.72**	61.03**	12.13**	4.90**	1120895..93**
Error	63.00	31.08	24.03	1.71	196.39	0.50	2.63	2.29	2.70	7.93	2.03	0.51	0.41	123520.00
CV		5.13	5.98	5.80	7.14	6.65	11.69	8.73	6.12	12.22	5.67	5.40	18.08	8.52

* - Significant at 5%, ** - Significant at 1%

significant differences for all the characters viz., day to 50 per cent flowering, plant height, panicle length, number of grains per panicle, panicle weight, productive tillers per plant, length of flag leaf, per cent chaffyness, test weight, panicle exertion, grain yield per plant and yield per hectare, suggesting that the genotypes were genetically diverse for majority of the characters under study.

4.2 Genetic variability parameters

In both normal and saline soil conditions range, mean, phenotypic and genotypic coefficients of variability (Fig. 1 and Fig. 2), heritability estimates in broad sense and genetic advance as per cent mean (Fig. 3 and Fig.4) for these characters is presented in Table 4 and Table 5 respectively. Morphological variation in the mutants is shown in plate.02 (upper).

4.2.1 Days to 50 per cent flowering

In normal soil condition, days to 50 per cent flowering varied from 91 to 125 days with an overall mean of 100.51 days. The line RP-Bio-226-120 was observed as earliest to days to 50 per cent flowering (91 days).Whereas, the check IRRI-154 line was observed late to 50% flowering (125 days) followed by BPT-5204-67 (105 days) and BPT-5204-183 (104 days). Similarly in saline soil condition days to 50 per cent flowering varied from 99.5 days to 128 days with overall mean of 108.54 days. Line RP-Bio-226-190 recorded as early (99.5 days) to days to 50 per cent flowering. Whereas the FL-478 was recorded the late to 50 per cent flowering (128 days) followed by the line BPT-5204-183 (125 days) and BPT-5204-15 (116 days).

In normal soil condition, the genotypic and phenotypic coefficients of variation were 3.9 and 6.81, respectively. This trait had moderate heritability (32.8) with low genetic advance (4.62) and per cent mean genetic advance was low (4.6) whereas in the saline soil condition the genotypic and phenotypic coefficients of variation was 3.50 and 6.21 respectively. This trait had moderate heritability (31.8) with low genetic advance (4.41) and per cent mean genetic advance (4.06). The desirable early grain maturing genotype is shown in plate 03 (upper).

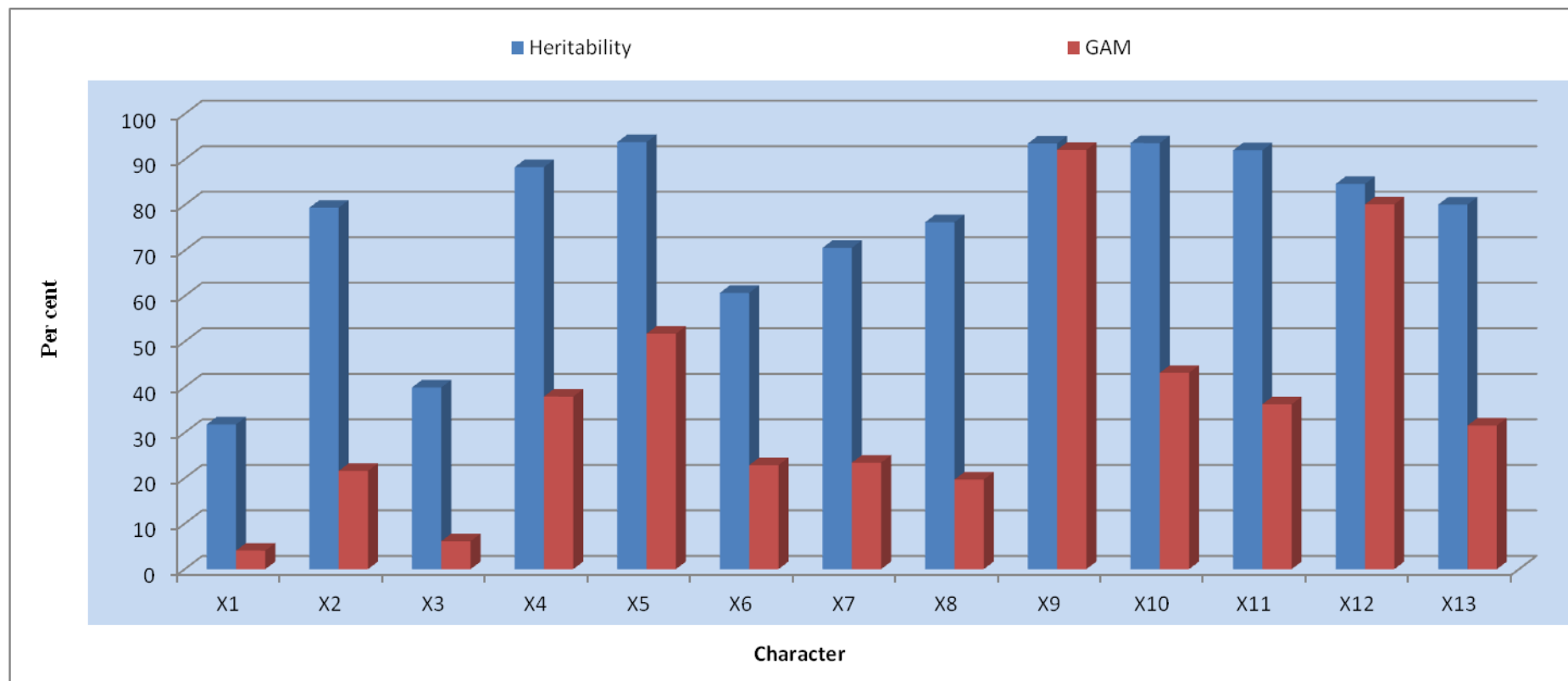


Fig.4 Heritability and genetic advance as per cent mean for yield and yield attributing traits in mutant rice genotypes in saline condition

X1 : Days to 50 per cent flowering, X2 : Plant height (cm), X3 : Panicle length (cm), X4 : Number of grains per panicle, X5 : Panicle weight (g), X6: Number of productive tillers per plant, X7 : Total number of tillers, X8 : Length of flag leaf (cm), X9 : Per cent chaffyness (%), X10 : Grain yield per plant, X11 : Test weight (g), X12: Panicle exertion (cm), X13: Yield per hectare

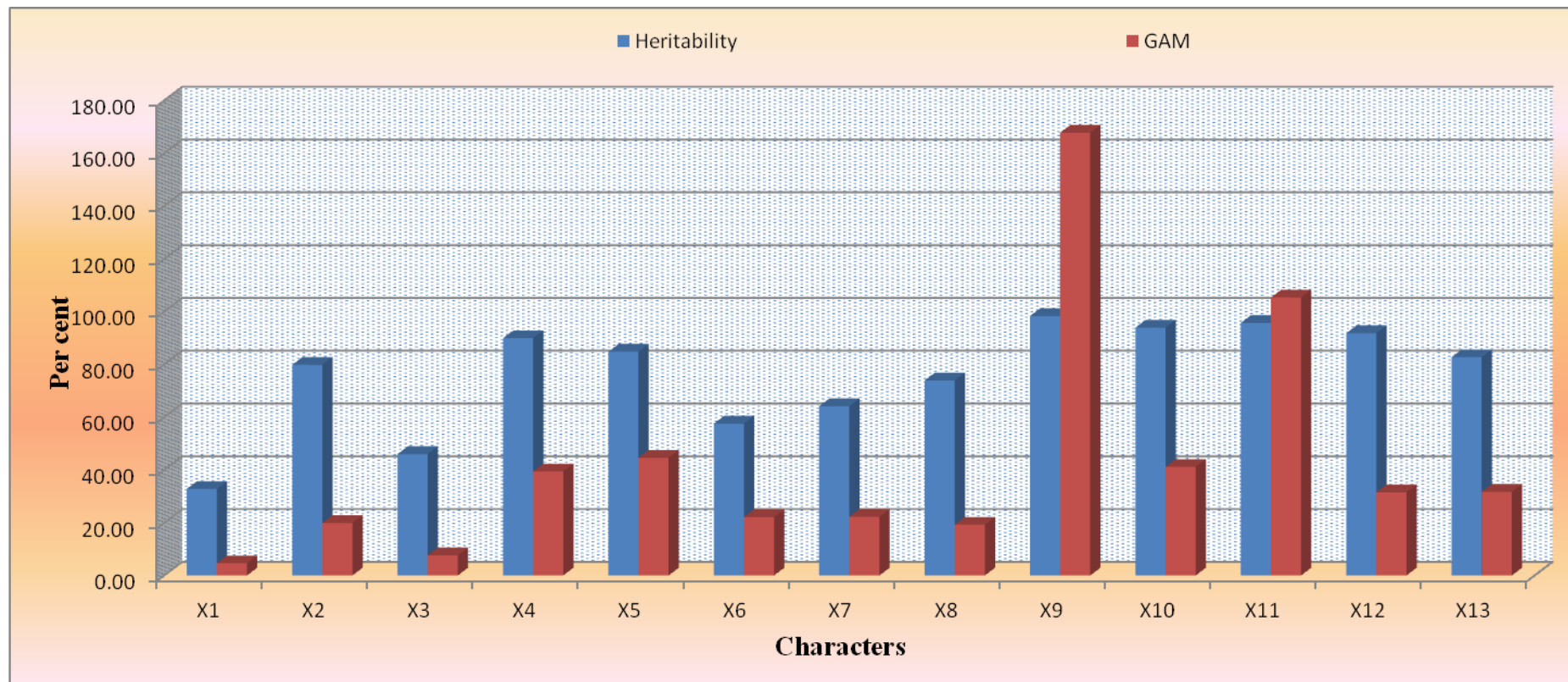


Fig.3 Heritability and genetic advance as per cent mean for yield and yield attributing traits in mutant rice genotypes in normal condition

X1 : Days to 50 per cent flowering, X2 : Plant height (cm), X3 : Panicle length (cm), X4 : Number of grains per panicle, X5 : Panicle weight (g), X6: Number of productive tillers per plant, X7 : Total number of tillers, X8 : Length of flag leaf (cm), X9 : Per cent chaffyness (%), X10 : Grain yield per plant, X11 : Test weight (g), X12: Panicle exertion (cm), X13: Yield per hectare

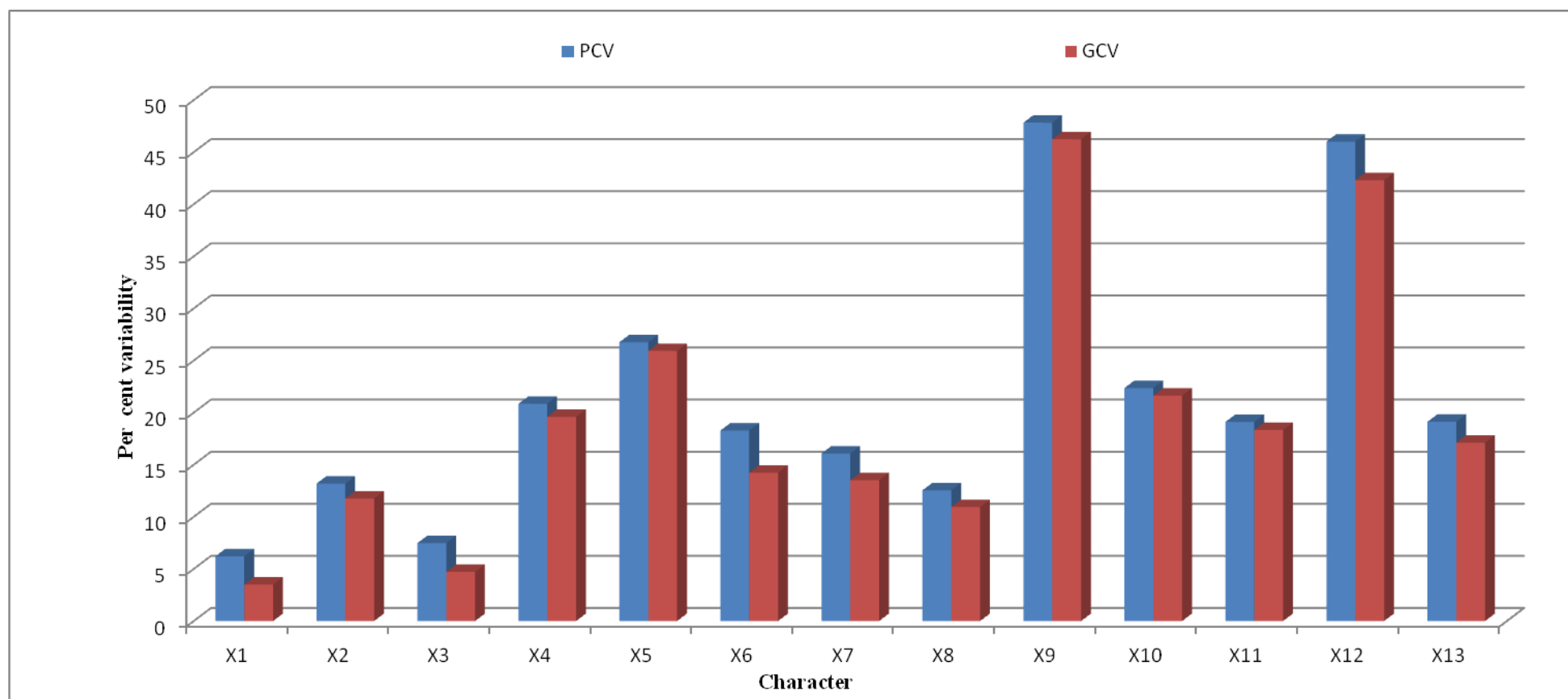


Fig 2. Phenotypic (PCV) and genotypic (GCV) coefficient of variation of yield and yield attributed traits in mutant rice genotypes in saline condition

X1 : Days to50 per cent flowering, X2 : Plant height (cm), X3 : Panicle length (cm), X4 : Number of grains per panicle, X5 : Panicle weight (g), X6: Number of productive tillers per plant, X7 : Total number of tillers, X8 : Length of flag leaf (cm), X9 : Per cent chaffyness (%), X10 : Grain yield per plant, X11 : Test weight (g), X12: Panicle exsertion (cm), X13: Yield per hectare

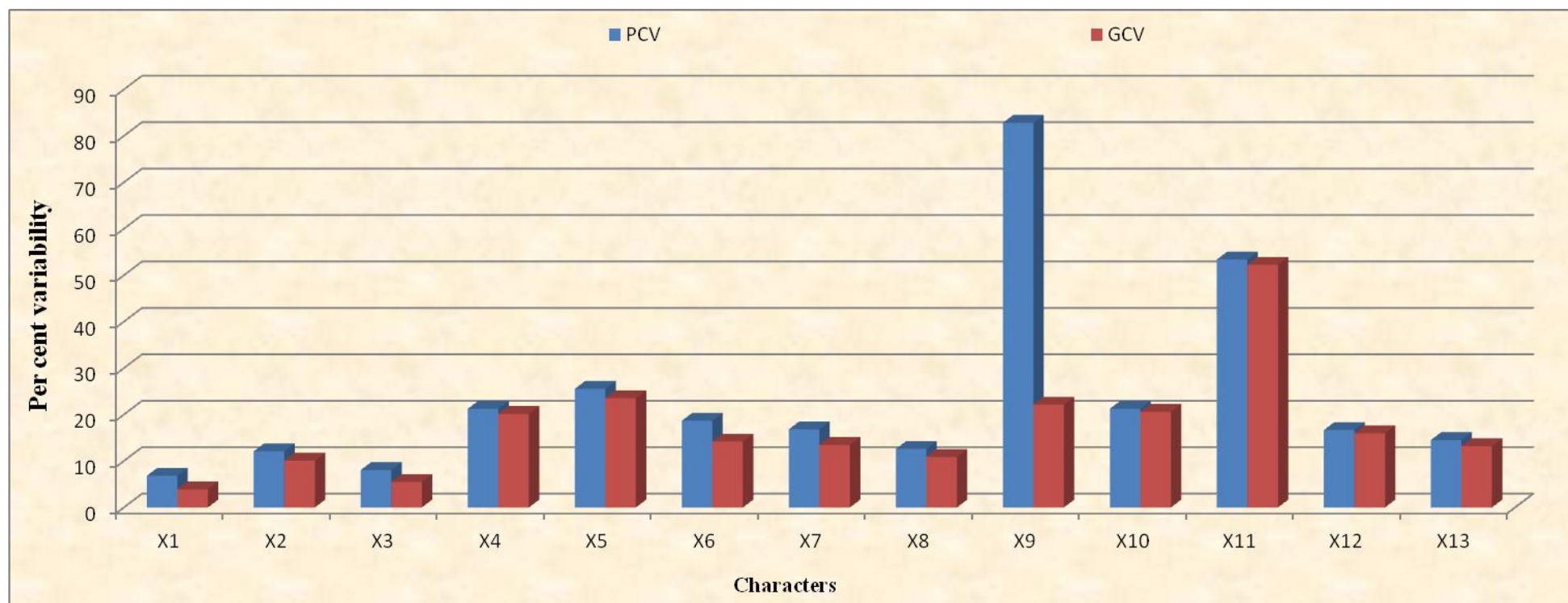


Fig 1. Phenotypic (PCV) and genotypic (GCV) coefficient of variation of yield and yield attributed traits in mutant rice genotypes in normal condition

X1 : Days to 50 per cent flowering, X2 : Plant height (cm), X3 : Panicle length (cm), X4 : Number of grains per panicle, X5 : Panicle weight (g), X6 : Number of productive tillers per plant, X7 : Total number of tillers, X8 : Length of flag leaf (cm), X9 : Per cent chaffyness (%), X10 : Grain yield per plant, X11 : Test weight (g), X12 : Panicle exertion (cm), X13 : Yield per hectare.



Morphological comparison of desirable mutants over BPT-5204



Plate 02. Promising mutants having high number of grains per panicle over the checks (BPT-5204, CSR-22 and Pokkali)



**Desirable early grain maturing mutant
(BPT-5204 Mutant 16) over the check BPT-5204**



**Plate 03. Desirable mutant (BPT-5204 Mutant 42)
showing complete panicle exertion compared
to check BPT-5204**

4.2.2 Plant Height

In normal soil condition, plant height varied from 71.5 to 159 cm with an overall mean of 95.38 cm. IRRI-154 was dwarfest (71.5cm) followed by the line RP-Bio-226-131 was (79.7 cm) and Pokkali was tallest (159 cm) followed by the line BPT-5204-183 (120.5 cm) and RP-Bio-226-120 (86.9cm). Similarly, in saline soil condition, the plant height varied from 56.5 to 136.9 cm with an overall mean of 81.92 cm. The IRRI-154 was dwarfest (56.5 cm) followed by BPT-5204-165 (73.5 cm) and BPT-5204-130 (73.5 cm) and Pokkali was tallest (136.9 cm) followed by the BPT-5204-183 (112.4 cm) and BPT-5204-139 (97.5 cm).

In normal soil condition, the genotypic and phenotypic coefficients of variation were 10.08 and 12.10 per cent respectively. This trait exhibited high heritability (79.8%) with moderate genetic advance (18.96) and per cent mean genetic advance (19.88). Similarly in case of saline soil condition the genotypic and phenotypic coefficients of variation were 11.75 and 13.18 per cent, respectively. This trait exhibited high heritability (79.4%) with moderate genetic advance (17.67) and high per cent mean genetic advance (21.57).

4.2.3 Panicle length

In normal soil condition, panicle length varied from 17.0 to 28.0cm with an overall mean of 22.79 cm. Pokkali produced largest panicle length (28 cm) followed by BPT-5204-139 (25.8 cm) and BPT 5204 produced shortest panicle length (17 cm). Whereas, in saline soil condition panicle length varied from 16.55 to 26.0 cm with an overall mean of 22.50 cm. RP-Bio-226-37 produced largest panicle length (26 cm) and FL 478 produced shortest panicle length (16.55 cm) followed by IRRI 154 (17.605 cm) and BPT-5204-29 (20.99 cm).

In normal soil condition, the genotypic and phenotypic coefficients of variation were 5.48 and 8.07 per cent respectively. This trait exhibited moderate heritability (46%) with low genetic advance (1.74). The per cent mean genetic advance (7.65). Similarly in case of saline soil condition the genotypic and phenotypic coefficients of variation were 4.7 and 7.48 per cent, respectively. This trait exhibited moderate heritability (39.9%) with low genetic advance (1.38). The per cent mean genetic advance was high (6.14). Variation in panicle length is shown in plate 2 (lower).

Table 4 Estimation of range, mean and different genetic parameters for yield and yield attributing characters in mutant rice genotypes under normal soil

Characters	Min.	Max.	Mean	PCV	GCV	h_b^2	GA	GAM
DDF	91.00	125.00	100.50	6.81	3.90	32.80	4.62	4.60
PH	71.50	159.00	95.38	12.10	10.08	79.80	18.97	19.88
PL	17.00	28.00	22.79	8.07	5.48	46.00	1.74	7.65
NGP	135.60	360.00	212.20	21.25	20.15	89.90	83.58	39.37
PW	7.50	25.20	14.26	25.54	23.51	84.80	6.37	44.59
NPT	8.50	20.50	13.60	18.66	14.16	57.55	3.01	22.12
TNT	11.50	24.20	16.80	16.82	13.47	64.14	3.73	22.23
LF	21.05	40.50	26.41	12.60	10.86	73.90	5.08	19.23
%CH	1.50	31.50	6.61	82.82	22.12	98.30	11.10	167.76
GYP	18.10	45.80	31.16	16.66	15.97	91.80	9.83	31.53
TW	12.30	30.80	13.56	21.26	20.60	93.90	5.59	41.14
PE	0.00	5.80	2.64	53.40	52.25	95.70	2.79	105.32
YLD	3653.85	9714.00	6702.00	14.52	13.20	82.70	1658.12	31.70

GCV - Genotypic coefficient of variation, PCV - Phenotypic coefficient of variation, h_b^2 – Heritability in broad sense, GA – Genetic advance and GAM - Genetic advance as per

DDF : Days to 50 per cent flowering, NPT : Number of productive tillers per plant, TW : Test weight (g), PE : Panicle exertion (cm), YLD : Yield per hectare, TNT : Total number of tillers, LF : Length of flag leaf (cm), %CH : Per cent chaffyness (%), GYP : Grain yield per plant, PH : Plant height (cm), PL : Panicle length (cm), NGP: Number of grains per panicle, PW : Panicle weight (g)

Table 5 Estimation of range, mean and different genetic parameters for yield and yield attributing characters in mutant rice genotypes under saline soil

Characters	Min.	Max.	Mean	PCV	GCV	h_b^2	GA	GAM
DFE	99.50	128.00	108.54	6.21	3.50	31.80	4.41	4.07
PH	56.50	136.95	81.92	13.18	11.75	79.40	17.67	21.57
PL	16.55	26.00	22.50	7.48	4.72	39.90	1.38	6.14
NGP	123.60	287.40	196.26	20.85	19.59	88.30	74.42	37.91
PW	6.00	18.77	10.62	26.76	25.92	93.80	5.50	51.72
NPT	9.00	19.00	14.14	18.28	14.24	60.68	3.23	22.85
TNT	10.80	23.00	17.32	16.07	13.51	70.57	4.05	23.38
LF	17.00	38.50	26.85	12.54	10.94	76.20	5.28	19.67
%CH	2.50	50.14	23.02	47.83	46.24	93.50	21.21	92.10
GYP	8.80	38.20	25.10	22.36	21.63	93.60	10.82	43.11
TW	9.60	26.70	13.15	19.11	18.33	92.00	4.77	36.22
PE	0.00	6.84	3.54	46.01	42.30	84.60	2.84	80.14
YLD	1762.00	6165.00	4124.00	19.12	17.12	80.10	1302.35	31.57

GCV - Genotypic coefficient of variation, PCV - Phenotypic coefficient of variation, h_b^2 – Heritability in broad sense, GA – Genetic advance and GAM - Genetic advance as per cent over mean

DFE : Days to 50 per cent flowering, NPT : Number of productive tillers per plant, TW : Test weight (g), PE : Panicle exertion (cm), (%), YLD : Yield per hectare, TNT : Total number of tillers, LF : Length of flag leaf (cm), %CH : Per cent chaffyness (%), GYP : Grain yield per plant, PH : Plant height (cm), PL : Panicle length (cm), NGP : Number of grains per panicle, PW : Panicle weight (g)

4.2.4 Total number of tillers per plant

In normal soil condition, the total number of tillers varied from 11.5 to 24.2 with an overall mean of 16.79. BPT-5204-139 produced the minimum total number of tillers (11.5) and BPT-5204-166 produced the maximum total number of tillers (23.8). In case of saline soil condition the total number of tillers varied from 10.8 to 23 with an overall mean of 17.32. BPT-5204-77 produced the minimum total numbers of tillers (10.8) and BPT-5204-158 produced the maximum total number of tillers (22.89).

In normal soil condition, the genotypic and phenotypic coefficients of variation were 13.47 and 16.82 per cent respectively. This trait exhibited high heritability (64.14%) with low genetic advance (3.73). The per cent mean genetic advance was high (22.22). Similarly in saline soil condition the genotypic and phenotypic coefficients of variation were 13.51 and 16.06 per cent, respectively. This trait also exhibited high heritability (70.56%) with genetic advance of 4.05. The per cent mean genetic advance was high (23.38).

4.2.5 Number of productive tillers per plant

In normal soil condition, number of productive tiller ranged from 8.5 to 20.5 with a mean value of 13.59. Highest number of productive tillers per plant was recorded by BPT-5204-166 (20.5) and BPT-5204-139 (8.5) recorded the lowest number of productive tillers. In case of saline soil condition number of productive tiller ranged from 9 to 19 with a mean value of 14.13. Highest number of productive tillers per plant recorded by line RP-Bio-226-103 (19) and RP-Bio-226 and BPT-5204-77 recorded the lowest number of productive tillers per plant (9).

In normal soil condition, the genotypic and phenotypic coefficients of variability observed were 14.15 and 18.66 per cent, respectively. High heritability of 57.55 per cent with low genetic advance of 3.0 was recorded. The per cent mean genetic advance was high (22.12). Similarly in saline soil condition the genotypic and phenotypic coefficients of variability observed were 14.24 and 18.28 per cent, respectively. High heritability of 60.68 per cent with low genetic advance of 3.23 was recorded. The per cent mean genetic advance was high (22.85).

4.2.6 Length of flag leaf

In normal soil condition, flag leaf length varied from 21.05 to 40.50 cm with an overall mean of 26.41 cm. Maximum flag leaf length was observed in Pokkali and minimum flag leaf length was observed in RP-Bio-226-131. Similarly, in saline soil condition the flag leaf length varied from 17 to 38.50 cm with an overall mean of 26.85 cm. Pokkali exhibited maximum flag leaf length whereas, RP-Bio-226-153 showed minimum flag leaf length.

In normal soil condition, the genotypic and phenotypic coefficients of variation were 10.86 and 12.60 per cent respectively. This trait exhibited high heritability (73.9%) with low genetic advance (5.07) and per cent mean genetic advance (19.23) similarly in case of saline soil condition the genotypic and phenotypic coefficients of variation were 10.94 and 12.54 per cent, respectively. This trait exhibited high heritability (76%) with low genetic advance (5.28) and moderate per cent mean genetic advance (19.67).

4.2.7 Panicle weight

In normal soil condition, the significant difference among the mutants for panicle weight was noticed. It ranged from 7.5 to 25.20 g with a mean value of 14.26 g. Maximum panicle weight was recorded by Pokkali and BPT-5204-149 showed the minimum panicle weight. In case of saline soil significant difference among the mutants for panicle weight was noticed. It ranged from 6.0 to 18.77 g with a mean value of 10.62 g. Maximum panicle weight was recorded by BPT-5204-139 and RP-Bio-226-45 recorded the minimum panicle weight.

In normal soil condition, the genotypic and phenotypic coefficients of variability observed 23.51 and 25.54 per cent, respectively. High heritability 84.80 per cent with genetic advance of 6.36 was recorded. The per cent mean genetic advance was 44.59. In case of saline soil the genotypic and phenotypic coefficients of variability observed were 25.92 and 26.76 per cent, respectively. High heritability of 93.80 per cent with genetic advance of 5.49 was recorded. The per cent mean genetic advance was 51.72

4.2.8 Number of grains per panicle

Significant difference among the mutants for number of grains per panicle in the normal soil was noticed. The number of grains per panicle ranged from 135.60 to 360.0

with a mean value of 212.20. Highest number of grains per panicle was recorded by line FL-478 and BPT-5204-38 showed the lowest number of spikelet per panicle. In the saline soil also significant difference among the mutants for number of grains per panicle was noticed. The number of grains per panicle ranged from 123.6 to 287 with a mean value of 196.26. Highest number of grains per panicle was recorded by line RP-Bio-226-134 and Pokkali showed the lowest number of spikelet per panicle.

In the normal soil condition, the genotypic and phenotypic coefficients of variability under the normal condition observed were 20.15 and 21.25 per cent, respectively. High heritability of 89 per cent with high genetic advance of 83.57 and high (39.37) per cent mean genetic advance was exhibited by this trait. In the saline soil condition the genotypic and phenotypic coefficients of variability observed were 19.59 and 20.85 per cent, respectively. High heritability of 88.30 per cent with high genetic advance of 74.42 and high (37.91) per cent mean genetic advance was exhibited by this character.

4.2.9 Per cent chaffyness (%)

Per cent chaffyness in the normal soil condition ranged from 1.5 to 31.5 with a mean of 6.61. The maximum per cent chaffyness was observed in line BPT-5204-183 and the minimum per cent chaffyness was noticed in line RP-Bio-226-78. In saline soil condition per cent chaffyness ranged from 2.5 to 50.14 with a mean of 23.02. The maximum per cent chaffyness was observed in line BPT-5204-69 and the minimum per cent chaffyness was noticed in CSR-22.

In normal soil condition the genotypic and phenotypic coefficients of variability for this character were 22.12 and 82.82 per cent respectively. High heritability of 98.3 per cent with a moderate genetic advance of 11.09 per cent and high (167.75) per cent mean genetic advance was exhibited by this character. In saline soil condition the genotypic and phenotypic coefficients of variability for this character were 46.24 and 47.83 per cent, respectively. High heritability of 93.50 per cent with a genetic advance of 21.20 per cent and high (92.10) per cent mean genetic advance was exhibited by this character.

4.2.10 Test Weight (g)

Significant difference among the mutants for test weight in normal soil was ranged from 12.3 to 30.8 g with a mean of 13.56 g. The maximum and minimum test weight was observed in line Pokkali and RP-Bio-226-152 respectively. Significant difference among the mutants for test weight in saline soil ranged from 9.6 g to 26.70 g with a mean of 13.15 g. The maximum and minimum test weight was observed in Pokkali and IRRI-154.

The genotypic and phenotypic coefficients of variability for this character in normal soil condition were 20.60 and 21.26 per cent respectively. High heritability of 93.90 per cent with low genetic advance of 5.587 per cent and 41.14 per cent mean genetic advance was exhibited by this character. In case of saline soil condition the genotypic and phenotypic coefficients of variability for this character were 18.33 and 19.11 per cent, respectively. High heritability of 92 per cent with a low genetic advance of 4.76 per cent and high per cent mean genetic advance (36.22) was exhibited by this character.

4.2.11 Panicle exertion

Significant difference among the mutants for panicle exertion in normal soil was ranged from 0 to 5.8 cm with a mean of 2.64 cm. The maximum panicle exertion observed in line RP-Bio-226-45 and minimum was observed in FL-478, BPT-5204, RP-Bio-226, CSR-22 and pokkali. Significant difference among the mutants for panicle exertion in saline soil ranged from 0 cm to 6.8 cm with a mean of 3.54. The maximum panicle exertion was observed in BPT-5204-42 and minimum was observed in BPT-5204-139,103, pokkali, BPT-5204, FL-478, IRRI-154 respectively.

The genotypic and phenotypic coefficients of variability for this character in normal soil condition were 52.25 and 53.40 per cent respectively. High heritability of 95.7 per cent with low genetic advance of 2.78 per cent and (105.32) per cent mean genetic advance was exhibited by this trait. In case of saline soil condition the genotypic and phenotypic coefficients of variability for this character were 42.30 and 46.01 per cent respectively. High heritability of 84.6 per cent with a low genetic advance of 2.84 per cent and high per cent mean genetic advance (80.14) was exhibited by this character.

Desirable mutant showing complete panicle exertion over the BPT-5204 is shown in plate 03 (lower).

4.2.12 Grain yield per plant

In the normal soil condition, grain yield per plant varied significantly from 18.10 to 45.80 g with a mean of 31.16 g. The lowest grain yield was recorded by RP -BIO 226 and RP-Bio-226-168 had the highest grain yield of 45.08 g. In case of saline soil condition grain yield per plant varied significantly from 8.8 to 38.2 g with a mean of 25.1 g. The lowest grain yield was recorded by RP-Bio-226-18 and RP-Bio-226-57 had the highest grain yield followed by RP-Bio-226-168, BPT-5204-166 and BPT-5204-67.

The genotypic and phenotypic coefficients of variability for this trait in the normal soil were 15.97 and 16.66 per cent respectively. High heritability of 91.8 per cent with an low genetic advance of 9.83 per cent and the per cent mean genetic advance was high (31.53). In the saline soil condition the genotypic and phenotypic coefficients of variability for this character were 21.63 and 22.36 per cent, respectively. High heritability of 93 per cent with a moderate genetic advance (10.82) and the per cent mean genetic advance was high (43.11).

4.2.13 Grain Yield per hectare

In normal soil the significant difference among the mutants for grain yield per hectares was noticed. It ranged from 3653 to 9714 kg per hectares with a mean value of 6702 kg per hectares. Maximum yield was recorded by BPT-5204-134 followed by RP-Bio-226-172 (7,900 kg per hectares) and BPT 5204 showed the minimum grain yield. In case of saline soil too significant difference among the mutants for yield was noticed. It ranged from 1762 to 6165 kg with a mean value of 4125 kg per hectares. Maximum grain yield was recorded by RP-Bio-226-120 followed by RP-Bio-226-37 and IRRI 154 showed the minimum grain yield per plant.

In normal soil condition, the genotypic and phenotypic coefficients of variability observed 13.20 and 14.52 per cent respectively. High heritability 82.5 per cent with genetic advance of 1658.12 was recorded. The per cent mean genetic advance was 24.73. In case of saline soil the genotypic and phenotypic coefficients of variability observed were 17.12 and 19.12 per cent, respectively. High heritability of 80.1 per cent with genetic advance of 1302.35 was recorded. The per cent mean genetic advance was 31.57.

4.2.14 Grain size

Variation in grain size was observed *i.e.*, short bold, short slender, medium slender and long slender. In the population, grain size of CSR-22 and Swarna Sub 1 genotypes observed long slender, pokkali observed short bold grain size, 4 lines observed short slender and 57 lines observed medium slender grain size.

4.2.15 Grain length

In normal condition, range of grain length varied from 5.03 to 6.6 cm with an average of 5.31 cm. whereas, CSR-22 observed maximum grain length and FL-478 as minimum grain length. Similarly in saline condition grain length varied from 5 to 6.5 cm with an average of 5.25 cm, Swarna Sub 1 observed maximum grain length and FL-478 as minimum grain length.

4.2.16 Amylose content

Highest amylose content 26.35 per cent was observed in genotype BPT-5204-115 and majority of the genotypes falls under intermediate (20-25 %) amylose content along with check BPT-5204 (24.10%). The lowest amylose content observed was 21.38 per cent in the RP-Bio-226-190. Overall mean of the genotypes for amylose content was 23.51 per cent in normal condition. Similarly in saline condition BPT-5204-115 genotype observed maximum amylose content 25.9 per cent, RP-Bio-226-190 observed minimum amylose content and mean obtained was 21 per cent.

4.3 Association of traits

Correlation coefficient (r) values range from -1 to 1. The magnitude and direction of correlation coefficient have relevance only when these values are significantly different from zero. Otherwise, the values are indicating absence of correlation. In the present context, the correlation coefficient was referred to as negative or positive only if it is significant, whereas non-significant values were been considered to indicate the absence of association between the characters. Phenotypic and genotypic correlations were worked out among 12 characters for saline and normal conditions to know the nature of association existing among the characters.

4.3.1 Phenotypic correlation for yield and yield attributing characters

The phenotypic correlation coefficient among yield and yield attributing traits worked out are presented in Table 6 and 7 for normal and saline soil.

4.3.1.1 Association of grain yield with other traits

In normal condition, out of 12 characters, the grain yield showed significantly positive association with number of grains per panicle (0.453) and panicle exertion (0.252) and panicle length (0.134). While, days to 50 per cent flowering (-0.299) observed negatively associated with grain yield.

In saline condition, out of 12 characters, the grain yield showed significantly positive association with panicle length (0.400), number of grains per panicle (0.240), Panicle weight (0.175). Days to 50 per cent flowering (-0.409) observed significant negative association.

4.3.1.2 Days to 50 per cent flowering

In normal soil condition, days to 50 per cent flowering had significant and positive association with test weight (0.341). High significant but negative association recorded for panicle exertion (-0.328). In saline soil condition, the trait showed negative significant association with panicle length (0.381), length of flag leaf (-0.216), panicle exertion (-0.382).

4.3.2.2 Plant height

In normal soil condition, plant height showed positive significant association with panicle length (0.481), panicle weight (0.353), length of flag leaf (0.554) and test weight (0.389) and negative significant association with number of grains per panicle (-0.259), number of productive tillers per plant (-0.257) and total number of tillers (-0.296). In saline soil condition, the trait showed positive significant association with panicle length (0.202), length of flag leaf (0.393) and test weight (0.405) and negative significant association with panicle length (-0.381), length of flag leaf (-0.216), panicle exertion (-0.382) and yield (-0.409).

4.3.2.3 Panicle length

In normal soil condition, the panicle length showed positive significant association with panicle weight (0.332) and length of flag leaf (0.554) and negative significant association with number of grains per panicle (-0.259), number of productive tillers per plant (-0.257) and total number of tillers per plant (-0.296). In saline soil condition, the trait showed positive significant association with panicle weight (0.272), length of flag leaf (0.231) and panicle exertion (0.232).

4.3.2.4 Number of grains per panicle

In normal soil condition, the number of grains per panicle showed positive significant association with number of productive tillers per plant (0.187) and total number of tillers (0.320) and negative significant association with length of flag leaf (-0.322) and per cent chaffyness (-0.209). In saline soil condition, the trait showed negative significant association with test weight (-0.241).

4.3.2.5 Panicle weight

In normal soil condition, the panicle weight showed positive significant association with length of flag leaf (0.183), per cent chaffyness (0.206) and test weight (0.267). In saline soil condition, the trait showed positive significant association with grain yield per panicle (0.254) and negative significant association with test weight (-0.209).

4.3.2.6 Number of productive tillers per plant

In normal soil condition, the number of productive tillers per plant showed positive significant association with total number of tillers (0.930) and showed negative and non-significant association for rest of the characters. In saline soil condition, the trait showed positive significant association with total number of tillers (0.925) and negative significant association with length of flag leaf (-0.251) and test weight (-0.200).

4.3.2.7 Total number of tillers

In normal soil condition, the total number of tillers showed positive significant association with grain yield per panicle (0.192) and negative significant association with

Table 6 Estimates of Phenotypic correlation coefficients for yield and yield attributing characters in mutant rice genotypes under normal soil

	DFE	PH	PL	NGP	PW	NPT	TNT	LF	%CH	GYP	TW	PE	YLD
DFE	1.000												
PH	-0.117	1.000											
PL	-0.171	0.481**	1.000										
NGP	0.073	-0.259**	-0.191*	1.000									
PW	-0.144	0.353**	0.332**	-0.027	1.000								
NPT	0.109	-0.257**	-0.184*	0.187*	-0.114	1.000							
TNT	0.089	-0.296**	-0.212*	0.320**	-0.102	0.930**	1.000						
LF	0.110	0.554**	0.254**	-0.322**	0.183*	-0.091	-0.201*	1.000					
%CH	0.046	0.073	-0.171	-0.209*	0.206*	0.118	0.059	0.004	1.000				
GYP	-0.052	-0.161	-0.033	0.107	-0.094	0.169	0.192*	-0.077	-0.019	1.000			
TW	0.341**	0.389**	0.126	0.036	0.267**	-0.024	-0.071	0.327**	-0.031	-0.204*	1.000		
PE	-0.328**	0.031	0.075	-0.092	-0.108	0.113	0.051	0.024	0.100	0.211*	-0.352**	1.000	
YLD	-0.299**	-0.015	0.134	0.453**	-0.040	0.111	0.136	-0.204*	-0.031	0.075	-0.171	0.252**	1.000

* - Significant at 5% (r = 0.1736153) probability level, ** - Significant at 1% (r = 0.2269142) probability level

Table 7 Estimates of Phenotypic correlation coefficients for yield and yield attributing characters in mutant rice genotypes under saline soil

	DFE	PH	PL	NGP	PW	NPT	TNT	LF	%CH	GYP	TW	PE	YLD
DFE	1.000												
PH	-0.036	1.000											
PL	-0.381**	0.202*	1.000										
NGP	-0.137	-0.275**	0.006	1.000									
PW	-0.110	0.070	0.272**	0.128	1.000								
NPT	-0.021	-0.121	-0.094	0.086	-0.028	1.000							
TNT	-0.037	-0.119	-0.170	0.052	-0.096	0.925**	1.000						
LF	-0.216*	0.393**	0.231**	-0.038	0.078	-0.251**	-0.208*	1.000					
%CH	-0.162	-0.013	0.018	-0.053	0.021	0.002	0.008	-0.070	1.000				
GYP	-0.143	-0.117	0.099	0.169	0.254**	0.129	0.159	0.010	-0.069	1.000			
TW	0.061	0.405**	-0.049	-0.241**	-0.209*	-0.200*	-0.119	0.358**	-0.373**	-0.122	1.000		
PE	-0.382**	-0.066	0.232**	0.051	0.074	-0.059	-0.095	0.087	0.255**	0.156	-0.345**	1.000	
YLD	-0.409**	0.166	0.400**	0.240**	0.175*	0.162	0.061	-0.100	0.122	0.146	-0.213*	0.314**	1.000

* - Significant at 5% (r = 0.1736153) probability level, ** - Significant at 1% (r = 0.2269142) probability level

length of flag leaf (-0.201). In saline soil condition, the trait showed negative significant association with length of flag leaf (-0.208).

4.3.2.8 Length of flag leaf

In normal soil condition, the length of flag leaf showed positive significant association with test weight (0.327). In saline soil condition, the trait showed positive significant association with test weight (0.358).

4.3.2.9 Per cent chaffyness

In normal soil condition, the per cent chaffyness showed no positive or negative significant association with any of the traits. In saline soil condition, the trait showed positive significant association with panicle exertion (0.255) and negative significant association with test weight (-0.373).

4.3.2.10 Test weight

In normal soil condition, the test weight showed no positive significant association with any trait but showed negative significant association with panicle exertion (-0.352). In saline soil condition, the trait showed negative significant association with panicle exertion (-0.345).

4.3.2.11 Panicle exertion

In normal soil condition, the panicle exertion showed positive significant association with yield (0.252). In saline soil condition the trait showed positive significant association with yield (0.31).

4.3.2.12 Grain yield per plant

In normal soil condition, grain yield per panicle showed positive significant association with panicle exertion (0.211) and negative significant association with test weight (-0.204). In saline soil condition the trait showed no positive or negative significant association with any of the traits.

4.3.3 Genotypic associations for yield and yield attributing traits

The genotypic correlation coefficients among yield and yield attributing traits was worked out in order to determine the extent of association with each component is presented in Tables 8 and 9 for normal and saline soil.

4.3.3.1 Genotypic associations for yield

In normal condition, out of 12 characters, the grain yield showed significantly positive association with number of grains per panicle (0.550), panicle exertion (0.290) and total number of tillers (0.191). Days to 50 per cent flowering (-0.623), length of flag leaf (-0.204) and test weight (-0.210) observed negative significantly association.

In saline condition, out of 12 characters, the grain yield showed significantly positive association with panicle length (0.657) number of grains per panicle (0.318), panicle exertion (0.371), Panicle weight (0.192) plant height (0.216) grain yield per panicle (0.180). Days to fifty per cent flowering (-0.910) test weight (-0.236) observed significant negative association

4.3.3.2 Days to 50 per cent flowering

In normal soil condition, days to 50 per cent flowering showed positive significant association with number of productive tillers per plant (0.292), total number of tillers (0.185) and test weight (0.459) and a significant negative association with plant height (-0.225), panicle weight (-0.451) and panicle exertion (-0.639) has been observed. In saline soil condition, the trait showed positive significant association with test weight (0.254).whereas, it showed negative association with rest of the traits.

4.3.3.3 Plant height

In normal soil condition, plant height showed positive significant association with panicle length (0.760), panicle weight (0.424), length of flag leaf (0.734) and test weight (0.445).Number of grains per panicle (-0.334), number of productive tillers per plant (-0.379), total number of tillers (-0.425) and grain yield per panicle (-0.208) observed negative significant association. In saline soil condition, the trait showed positive significant association with panicle length (0.413), length of flag leaf (0.541) and test

weight (0.482) and a negative significant association with number of grains per panicle (-0.399).

4.3.3.4 Panicle length

In normal soil condition, the panicle length showed positive significant association with panicle weight (0.559), length of flag leaf (0.459) and test weight (0.216) and a negative significant association with number of grains per panicle (-0.397), number of productive tillers per plant (-0.282), total number of tillers (-0.303) and per cent chaffyness (-0.220). In saline soil condition, the trait showed significant positive association with panicle weight (0.432), length of flag leaf (0.537) and panicle exertion (0.404) and negative significant association with number of productive tillers per plant (-0.274) and total number of tillers (-0.333).

4.3.3.5 Number of grains per panicle

In normal soil condition, the number of grains per panicle showed positive significant association with number of productive tillers per plant (0.259), total number of tillers (0.417) and negative significant association with length of flag leaf (-0.444) and per cent chaffyness (-0.189). In saline soil condition the trait showed significant positive association with grain yield per panicle (0.199) and negative significant association with test weight (-0.292).

4.3.3.6 Panicle weight

In normal soil condition,, the panicle weight showed positive significant association with length of flag leaf (0.234), per cent chaffyness (0.224) and test weight (0.272). In saline soil condition, the trait showed significant positive association with grain yield per panicle (0.261) and negative significant association with test weight (-0.211).

4.3.3.7 Number of productive tillers

In normal soil condition, the number of productive tillers per plant showed positive significant association with total number of tillers (0.946) and grain yield per panicle (0.276). In saline soil condition, the trait showed significant positive association

Table 8 Estimation of genotypic correlation coefficient for yield and yield attributing characters in mutant rice genotypes under normal soil

	DFE	PH	PL	NGP	PW	NPT	TNT	LF	%CH	GYP	TW	PE	YLD
DFE	1.000												
PH	-0.225*	1.000											
PL	-0.873**	0.760**	1.000										
NGP	0.011	-0.334**	-0.397**	1.000									
PW	-0.451**	0.424**	0.559**	-0.036	1.000								
NPT	0.292**	-0.379**	-0.282**	0.259**	-0.122	1.000							
TNT	0.185*	-0.425**	-0.303**	0.417**	-0.083	0.946**	1.000						
LF	0.148	0.734**	0.459**	-0.444**	0.234*	-0.165	-0.272**	1.000					
%CH	0.128	0.091	-0.220*	-0.189*	0.224*	0.143	0.062	0.027	1.000				
GYP	-0.109	-0.208*	-0.133	0.102	-0.070	0.276**	0.283**	-0.066	-0.017	1.000			
TW	0.459**	0.445**	0.216*	0.038	0.272**	-0.021	-0.080	0.385**	-0.027	-0.213*	1.000		
PE	-0.639**	0.031	0.139	-0.109	-0.145	0.129	0.046	0.033	0.102	0.228**	-0.372**	1.000	
YLD	-0.623**	-0.023	0.132	0.550**	-0.003	0.145	0.191*	-0.226**	-0.043	0.079	-0.210*	0.290**	1.000

* - Significant at 5% ($r = 0.173$) probability level, ** - Significant at 1% ($r = 0.226$) probability level

DFF : Days to 50 per cent flowering, NPT : Number of productive tillers per plant, TW : Test weight (g), PE : Panicle exertion (cm), YLD : Yield per hectare, TNT : Total number of tillers, LF : Length of flag leaf (cm), %CH : Per cent chaffyness (%), GYP : Grain yield per plant, PH : Plant height (cm), PL : Panicle length (cm), NGP : Number of grains per panicle, PW : Panicle weight (g)

Table 9 Estimation of genotypic correlation coefficient for yield and yield attributing characters in mutant rice genotypes under saline soil

	DFE	PH	PL	NGP	PW	NPT	TNT	LF	%CH	GYP	TW	PE	YLD
DFE	1.000												
PH	-0.257**	1.000											
PL	-1.121**	0.413**	1.000										
NGP	-0.183*	-0.399**	0.086	1.000									
PW	-0.258**	0.060	0.432**	0.111	1.000								
NPT	-0.110	-0.163	-0.274**	0.093	-0.063	1.000							
TNT	-0.024	-0.149	-0.333**	0.017	-0.134	0.965**	1.000						
LF	-0.354**	0.541**	0.537**	-0.065	0.104	-0.430**	-0.330**	1.000					
%CH	-0.346**	-0.025	-0.002	-0.043	0.036	0.007	0.003	-0.101	1.000				
GYP	-0.104	-0.092	0.096	0.199*	0.261**	0.192*	0.203*	0.013	-0.066	1.000			
TW	0.254**	0.482**	-0.094	-0.292**	-0.211*	-0.251**	-0.14	0.406**	-0.380**	-0.144	1.000		
PE	-0.750**	-0.081	0.404**	0.069	0.065	-0.034	-0.108	0.065	0.274**	0.165	-0.393**	1.000	
YLD	-0.910**	0.216*	0.657**	0.318**	0.192*	0.151	0.033	-0.090	0.153	0.180*	-0.236**	0.371**	1.000

* - Significant at 5% ($r = 0.173$) probability level, ** - Significant at 1% ($r = 0.226$) probability level

DFF : Days to 50 per cent flowering, NPT : Number of productive tillers per plant, TW : Test weight (g), PE : Panicle exertion (cm), YLD : Yield per hectare, TNT : Total number of tillers, LF : Length of flag leaf (cm), %CH : Per cent chaffyness (%), GYP : Grain yield per plant, PH : Plant height (cm), PL : Panicle length (cm), NGP : Number of grains per panicle, PW : Panicle weight (g)

with total number of tillers (0.965) and grain yield per panicle (0.192) and negative significant association with length of flag leaf (-0.430) and test weight (-0.251).

4.3.3.8 Total number of tillers

In normal soil condition, the total number of tillers showed positive significant association with grain yield per panicle (0.283) and negative significant association with length of flag leaf (-0.272). In saline soil condition, the trait showed significant positive association with grain yield per panicle (0.203) and negative significant association with length of flag leaf (-0.330).

4.3.3.9 Length of flag leaf

In normal soil condition, the length of flag leaf showed positive significant association with test weight (0.385). In saline soil condition the trait showed significant positive association with test weight (0.406).

4.3.3.10 Per cent chaffyness

In normal soil condition, the per cent chaffyness doesn't showed positive or negative significant association with any traits. In saline soil condition, the trait showed significant positive association with panicle exertion (0.274) and negative significant association with test weight (-0.380).

4.3.3.11 Test weight

In normal soil condition, the test weight has showed negative significant association with panicle exertion (-0.372). In saline soil condition, the trait showed negative significant association with panicle exertion (-0.393).

4.3.3.12 Panicle exertion

In normal soil condition, panicle exertion showed positive significant association with yield (0.290). In saline soil condition, the trait showed significant positive association with yield (0.371).

4.3.3.13 Grain yield per panicle

In normal soil condition, the grain yield per panicle showed positive significant association with panicle exertion (0.228) and negative significant association with test weight (-0.213). In saline soil condition, the trait showed significant positive association with yield (0.180).

4.4 Path co-efficient analysis

Path co-efficient analysis was carried out at phenotypic levels taking the grain yield as a dependent character and such of the character found significantly correlated with grain yield (days to 50 per cent flowering, panicle length, test weight, number of grains per panicle, panicle weight, panicle exertion and length of flag leaf) as independent characters. The results obtained are given in the Tables 10 and 11 in normal and saline soil conditions, respectively. And the direct and indirect effects of different characters on grain yield are presented below.

4.4.1 Direct effects of yield contributing characters on yield at phenotypic level

In normal condition, plant height (0.093) recorded positive negligible effect on grain yield. Panicle length (0.250) observed moderately positive and direct effect. Number of grains per panicle (0.592) and number of productive tillers per plant (0.308) recorded high positive and direct effect on grain yield. Per cent chaffyness (0.134) and panicle exertion (0.137) exhibited low positive and direct effect. Days to 50 per cent flowering (-0.247) and total number of tillers (-0.283) recorded moderate negative and direct effect on grain yield. Panicle weight (-0.150) recorded negative low effect. Length of flag leaf (-0.084), grain yield per plant (-0.039) and test weight (-0.077) indicated negligible negative and direct effect on grain yield.

Similarly in saline condition, plant height (0.021), number of grains per panicle (0.097), panicle weight (0.069) per cent chaffyness (0.037) and grain yield per panicle (0.051) showed negligible effect on grain yield. Panicle length (0.126), test weight (0.128) and panicle exertion (0.110) showed low and positive direct effect. Number of productive tillers per plant (0.539) recorded high positive and direct effect on grain yield. Days to 50 per cent flowering (-0.148) observed low negative and direct effect. Total

number of tillers (-0.459) recorded high and negative effect, Length of flag leaf (0.250) recorded moderate negative direct effect.

4.4.2 Indirect effects of yield contributing characters on yield at phenotypic level

. In normal and saline condition the traits which showed significance difference among the traits are only considered,

4.4.2.1 Days to fifty per cent flowering

In normal condition, positive and negligible indirect effect for grain yield via plant height (0.005), panicle length (0.056), Number of grains per panicle (0.020) and panicle exertion (0.081). Negative and negligible indirect effect for grain yield was recorded via test weight (-0.084).

In saline condition, positive and negligible indirect effect for grain yield was recorded via panicle length (0.056), length of flag leaf (0.032), and panicle exertion (0.057).

4.4.2.2 Number of grains per panicle

In normal condition, the positive and low indirect effect for grain yield recorded via number of productive tillers per plant (0.111) and total number of tillers (0.190). Negative and low indirect effect recorded for grain yield via plant height (-0.153), panicle length (-0.133), length of flag leaf (-0.191) and per cent chaffyness (-0.123). In saline soil condition, the positive and negligible indirect effect for grain yield was recorded via panicle weight (0.012). Negative and negligible indirect effect observed through plant height (-0.027) and test weight (-0.023) for grain yield.

4.4.2.3 Length of flag leaf

In normal condition, the positive and negligible indirect effect for grain yield recorded via number of grains per panicle (0.027) and total number of tillers (0.017). The negative and negligible indirect effect for grain yield recorded via Plant height (-0.046), panicle length (-0.021), panicle weight (-0.015) and test weight (-0.028).

Table 10 Estimation of phenotypic path coefficient for yield and yield attributing characters in mutant rice genotypes under normal soil

	DFF	PH	PL	NGP	PW	NPT	TNT	LF	%CH	GYP	TW	PE	YLD
DFF	-0.247	0.029	0.042	-0.018	0.036	-0.027	-0.022	-0.027	-0.011	0.013	-0.084	0.081	-0.299
PH	-0.011	0.093	0.045	-0.024	0.033	-0.024	-0.028	0.052	0.007	-0.015	0.036	0.003	-0.015
PL	-0.042	0.120	0.250	-0.048	0.082	-0.046	-0.053	0.063	-0.043	-0.008	0.032	0.018	0.134
NGP	0.043	-0.153	-0.113	0.592	-0.016	0.111	0.190	-0.191	-0.123	0.063	0.021	-0.054	0.453
PW	0.022	-0.053	-0.050	0.004	-0.150	0.017	0.015	-0.027	-0.031	0.014	-0.040	0.016	-0.041
NPT	0.034	-0.079	-0.057	0.058	-0.035	0.308	0.287	-0.028	0.036	0.052	-0.007	0.035	0.111
TNT	-0.025	0.084	0.060	-0.091	0.029	-0.263	-0.283	0.057	-0.017	-0.054	0.020	-0.014	0.136
LF	-0.009	-0.046	-0.021	0.027	-0.015	0.008	0.017	-0.084	0.000	0.006	-0.028	-0.002	-0.204
%CH	0.006	0.010	-0.023	-0.028	0.028	0.016	0.008	0.001	0.134	-0.002	-0.004	0.013	-0.031
GYP	0.002	0.006	0.001	-0.004	0.004	-0.007	-0.007	0.003	0.001	-0.039	0.008	-0.008	0.075
TW	-0.026	-0.030	-0.010	-0.003	-0.021	0.002	0.005	-0.025	0.002	0.016	-0.077	0.027	-0.172
PE	-0.045	0.004	0.010	-0.013	-0.015	0.015	0.007	0.003	0.014	0.029	-0.048	0.137	0.252

Residual effect = 0.7527

DFF : Days to 50 per cent flowering, NPT : Number of productive tillers per plant, TW : Test weight (g), PE : Panicle exertion (cm), YLD : Yield per hectare, TNT : Total number of tillers, LF : Length of flag leaf (cm), %CH : Per cent chaffyness (%), GYP : Grain yield per plant, PH : Plant height (cm), PL : Panicle length (cm), NGP : Number of grains per panicle, PW : Panicle weight (g)

Table 11 Estimation of phenotypic path coefficient for yield and yield attributing characters in mutant rice genotypes under saline soil

	DFF	PH	PL	NGP	PW	NPT	TNT	LF	%CH	GYP	TW	PE	YLD
DFF	-0.148	0.005	0.056	0.020	0.016	0.003	0.006	0.032	0.024	0.021	-0.009	0.057	-0.409
PH	-0.001	0.021	0.004	-0.006	0.001	-0.002	-0.002	0.008	0.000	-0.002	0.008	-0.001	0.166
PL	-0.048	0.025	0.126	0.001	0.034	-0.012	-0.021	0.029	0.002	0.012	-0.006	0.029	0.400
NGP	-0.013	-0.027	0.001	0.097	0.012	0.008	0.005	-0.004	-0.005	0.016	-0.023	0.005	0.240
PW	-0.008	0.005	0.019	0.009	0.069	-0.002	-0.007	0.005	0.001	0.018	-0.014	0.005	0.175
NPT	-0.012	-0.065	-0.051	0.047	-0.015	0.539	0.499	-0.135	0.001	0.069	-0.108	-0.032	0.162
TNT	0.017	0.055	0.078	-0.024	0.044	-0.425	-0.459	0.095	-0.003	-0.073	0.054	0.044	0.061
LF	0.054	-0.098	-0.058	0.010	-0.020	0.063	0.052	-0.250	0.018	-0.003	-0.090	-0.022	-0.100
%CH	-0.006	0.000	0.001	-0.002	0.001	0.000	0.000	-0.003	0.037	-0.003	-0.014	0.009	0.122
GYP	-0.007	-0.006	0.005	0.009	0.013	0.007	0.008	0.001	-0.004	0.051	-0.006	0.008	0.146
TW	0.008	0.052	-0.006	-0.031	-0.027	-0.026	-0.015	0.046	-0.048	-0.016	0.128	-0.044	-0.213
PE	-0.042	-0.007	0.026	0.006	0.008	-0.007	-0.011	0.010	0.028	0.017	-0.038	0.110	0.314

Residual effect = 0.6111

DFE : Days to 50 per cent flowering, NPT : Number of productive tillers per plant, TW : Test weight (g), PE : Panicle exertion (cm), YLD : Yield per hectare, TNT : Total number of tillers, LF : Length of flag leaf (cm), %CH : Per cent chaffyness (%), GYP : Grain yield per plant, PH : Plant height (cm), PL : Panicle length (cm), NGP : Number of grains per panicle, PW : Panicle weight (g)

In saline condition, the positive and negligible indirect effect for grain yield recorded via days to 50 per cent flowering (0.054), number of productive tillers per plant (0.063) and total number of tillers (0.052). Negative and negligible indirect effect observed through Plant height (-0.098), panicle length (-0.058) and test weight (-0.090).

4.4.2.4 Panicle exertion

In normal condition, the positive and negligible indirect effect for grain yield recorded via plant height (0.004) and grain yield per panicle (0.029). Test weight (-0.048) observed negative and negligible indirect effect. In saline condition, positive and negligible indirect effect for grain yield via panicle length (0.026) and per cent chaffyness (0.028) observed. Days to fifty per cent flowering (-0.042) and test weight (-0.038) observed negative and negligible indirect effect.

4.4.2.5 Panicle length

In normal condition, the positive and low indirect effect for grain yield recorded via plant height (0.120). Panicle weight (0.082) and length of flag leaf (0.063) observed positive and negligible indirect effect. Number of grains per panicle (-0.048), number of productive tiller (-0.047) and total number of tillers (-0.053) observed negative and negligible indirect effect. In saline condition, the positive and negligible indirect effect for grain yield recorded via panicle weight (0.001) and length of flag leaf (0.008). Days to 50 per cent flowering (-0.001) observed negative and negligible indirect effect.

4.4.2.6 Panicle weight

In normal condition, the positive and negligible indirect effect for grain yield recorded via plant height (-0.053), panicle length (0.050), length of flag leaf (-0.027), per cent chaffyness (-0.031) and test weight (-0.040). Days to 50 per cent flowering (0.022) observed positive and negligible indirect effect. In saline condition, the positive and negligible indirect effect for grain yield recorded via panicle length (0.019) and grain yield per panicle (0.018). Test weight (-0.014) observed negative and negligible indirect effect for grain yield

4.4.2.7 Test weight:

In normal condition, the positive and negligible indirect effect for grain yield recorded via panicle exertion (0.027) and grain yield per panicle (0.016). Days to 50 per

cent flowering (-0.026), plant height(-0.030), panicle weight (-0.021) and length of flag leaf (-0.025) observed negative and negligible indirect effect. In saline condition, the positive and negligible indirect effect for grain yield recorded via plant height (0.052) and length of flag leaf (0.046). Number of grains per panicle (-0.031), panicle weight (-0.027), number of productive tillers per plant (-0.026), per cent chaffyness (-0.048) and panicle exsertion (-0.044) observed negative and negligible indirect effect.

4.5 Salinity tolerance of mutants

Salinity tolerance of mutants was assessed and salinity tolerant mutants were identified as per Stress Susceptibility Index (SSI), Na^+/K^+ in shoot and Standard Evaluation System (SES).

4.6 Stress Susceptibility Index

Although, salt stress affects all growth stages of a plant but seedling growth stages are known to be more sensitive for most of the plant species. The indices are either based on stress resistance or susceptibility of genotypes. Some researchers believe in selection under non-stress conditions, others in stress condition while others yet have chosen a mid-point and believe in selection under both non-stress and stress conditions. Fischer and Maurer suggested the stress susceptibility index (SSI) for measurement of yield stability that apprehended the changes in both potential and actual yields in variable environments. As larger value of SSI represents relatively more sensitivity to stress, thus a smaller value SSI are favored. Selection based on these criteria favors genotypes with low yield potential under non-stress conditions and high yield under stress conditions. Guttieri *et al.*, (2001) using SSI criterion suggested that $\text{SSI} > 1$ indicated above-average susceptibility and $\text{SSI} < 1$ indicated below average susceptibility to stress.

The results pertaining to SSI were furnished in the Table 14. The mutant lines which recorded lesser values for stress susceptibility index for yield and yield attributing traits are indicated below.

Among the mutants of RP-Bio-226, line Rp-Bio-226-120 showed lesser SSI value for number of productive tillers per plant per plant (0.283), plant height (0.118), grain yield per plant (0.652), panicle length (0.351), number of grains per panicle (0.513), per cent chaffynesss (0.744) and test weight (-2.230) indicating its salt tolerance.

The line Rp-Bio-226-37 recorded lesser SSI value for plant height (-0.020), grain yield per plant (-0.709), panicle length (-0.947) and test weight (-1.443) the salt tolerance.

The Rp-Bio-226-23 showed lesser SSI value for total number of productive tillers per plant per plant (-1.845), plant height (0.297), grain yield per plant (0.208), test weight (-0.763), panicle length (-1.637), number of grains per panicle (-3.218) and per cent chaffyness (0.766).

The Rp-Bio-226-191 showed lesser SSI value for plant height (1.432), panicle length (1.392), number of grains per panicle (-1.443), number of productive tillers per plant (-0.778), per cent chaffyness (2.711), grain yield per panicle (-0.580) and test weight (1.741).

Among the mutants of BPT-5204 lines, BPT-5204-166 observed lesser SSI values for plant height (0.364), panicle length (1.336), number of grains per panicle (-5.535), number of productive tillers per plant (-2.903), per cent chaffyness (2.465), grain yield per plant (0.955) and test weight (2.083).

The BPT-5204-37 observed lesser SSI values for plant height (1.509), panicle length (-1.091), number of grains per panicle (-1.197), number of productive tillers per plant (-0.628), per cent chaffyness (0.117), grain yield per plant (-0.488) and test weight (1.388).

The BPT-5204-67 observed lesser SSI values for plant height (0.764), panicle length (0.723), number of grains per panicle (7.565), number of productive tillers per plant (3.967), per cent chaffyness (1.938), grain yield per plant (-0.097) and test weight (-0.403).

The CSR 22 observed lesser SSI values for plant height (0.858), panicle length (9.933), number of grains per panicle (-4.782), number of productive tillers per plant (8.208), per cent chaffyness (-0.241), grain yield per plant (-0.307) and test weight (-0.246).

The BPT-5204 observed SSI values for plant height (0.586), panicle length (-13.123), number of grains per panicle (-5.122), number of productive tillers per plant (0.826), per cent chaffyness (3.296), grain yield (4.33) and test weight (0.7527)

The IRRI-154 observed higher SSI values for plant height (1.448), panicle length (7.884), number of grains per panicle (1.164), number of productive tillers per plant (-1.841), per cent chaffyness (0.914), grain yield per plant (2.861) and test weight (10.472).

4.5.2 Na⁺/K⁺ in shoot

Sodium is not essential for plant growth. High cytosolic Na⁺ concentrations can damage the plants. High potassium concentrations in relation to that of sodium concentrations also helps the plants to survive under saline conditions, since there is an evidence that high affinity potassium transporters are involved in the exclusion of excessive Na⁺ from the cells. Therefore, an analysis of Na-K concentrations in the plants was done and then Na/K ratio was calculated and the lines were identified as tolerant or sensitivity based on this ratio. Based on reports of Singh *et al.* (2014), the Na⁺ and K⁺ ratio was calculated for all the rice mutant genotypes and six genotypes viz., The Rp-Bio-226-103, BPT-5204-158, Swarna Sub-1, IRRI-154, BPT-5204 and RP-Bio-226 were grouped as sensitivity and remaining genotypes were grouped as tolerance, of which twenty nine genotypes were highly tolerant.

4.5.3 Standard Evaluation System (SES)

The mutants were screened for salt tolerance at seedling stage using IRRI standard protocol (Gregorio *et al.*, 1997) in Saline soil. The evaluation was done using the modified standard evaluation system (SES) rating the visual symptoms of salt toxicity (IRRI, 1997). This scoring discriminated the sensitivity from the tolerant and the moderately tolerant genotypes.

The six genotypes shown sensitivity and remaining all shown tolerance. The line RP-Bio-226-103, BPT-5204, RP-Bio-226, Swarna Sub 1, IRRI-154 and BPT-5204-158 scored five, Pokkali, CSR-22 and FL-478 scored three, and remaining all genotypes scored one. Table 16.

Table 12 Stress Susceptibility Index (%) of mutant rice genotypes

Sl. no.	Genotypes	PH	PL	NGP	NPT	%CH	GYP	TW	YLD
1	BPT-5204-10	0.95	-1.74	-5.93	-3.11	2.89	1.09	1.04	10.79
2	BPT-5204-15	1.54	-4.46	3.60	1.89	1.18	-0.34	-0.26	13.03
3	BPT-5204-16	1.06	-5.80	1.77	0.93	0.10	1.59	-0.48	9.78
4	BPT-5204-22	1.43	-0.33	10.32	5.41	0.46	0.57	0.29	11.90
5	BPT-5204-29	1.29	-3.40	4.39	2.30	2.08	0.31	-0.25	14.14
6	BPT-5204-37	1.51	-1.09	-1.20	-0.63	0.12	-0.49	1.39	13.62
7	BPT-5204-38	0.64	0.38	1.51	0.77	2.99	1.55	-0.95	7.50
8	BPT-5204-42	0.99	-1.05	-1.44	-0.75	3.04	1.47	0.19	10.02
9	BPT-5204-46	1.35	-0.16	-0.18	-0.10	2.70	0.26	0.40	9.57
10	BPT-5204-57	1.52	-1.03	-7.96	-4.18	-0.04	2.36	0.52	12.08
11	BPT-5204-60	1.23	10.48	-2.54	-1.33	2.17	-0.51	-1.56	12.29
12	BPT-5204-67	0.76	0.72	7.57	3.97	1.94	-0.10	-0.40	11.13
13	BPT-5204-69	0.91	-1.21	3.83	2.01	2.44	1.81	0.27	6.58
14	BPT-5204-77	1.45	0.19	-7.06	-3.70	1.83	2.66	0.66	9.71

15	BPT-5204-88	1.37	0.75	-2.69	-1.41	0.11	1.16	0.83	10.11
16	BPT-5204-94	1.12	4.71	9.43	5.88	2.58	0.82	0.98	9.50
17	BPT-5204-96	1.52	4.59	-1.12	-0.59	3.32	0.59	-0.40	10.53
18	BPT-5204-98	1.63	0.36	-2.34	-1.23	1.80	2.18	1.10	11.51
19	BPT-5204-103	1.75	0.37	-0.18	-0.10	0.97	1.28	-0.50	12.60
20	BPT-5204-115	0.84	1.76	2.24	1.18	1.04	1.29	0.19	10.33
21	BPT-5204-128	1.11	-4.11	0.31	0.13	2.16	1.19	0.52	11.47
22	BPT-5204-130	1.69	-4.18	-6.10	-3.20	1.27	1.70	1.94	11.90
23	BPT-5204-134	1.55	-0.36	-7.30	-3.83	1.22	1.40	3.79	14.93
24	BPT-5204-139	0.95	0.02	12.61	6.61	1.59	0.79	0.45	10.43
25	BPT-5204-149	1.58	1.05	-1.01	-0.51	4.63	1.12	0.28	13.65
26	BPT-5204-158	0.69	1.67	15.24	10.22	0.84	-3.23	1.82	10.03
27	BPT-5204-165	1.52	3.85	3.81	2.00	0.78	0.78	1.77	12.09
28	BPT-5204-166	0.36	1.34	-5.54	-2.90	2.47	0.96	2.08	11.99
29	BPT-5204-183	0.48	-2.08	6.30	3.31	-0.04	-0.16	-0.13	9.62
30	RP-Bio-226-18	0.64	2.17	10.81	5.67	0.41	3.32	0.96	9.49

31	RP-Bio-226-23	0.30	-1.64	-3.52	-1.85	0.77	0.21	-0.76	6.34
32	RP-Bio-226-29	0.62	0.02	6.54	3.43	1.69	1.68	0.36	5.90
33	RP-Bio-226-37	-0.02	-0.95	8.07	4.23	3.07	-0.71	-1.44	3.71
34	RP-Bio-226-41	1.16	1.10	0.08	0.04	2.96	1.85	0.38	8.60
35	RP-Bio-226-45	0.81	-0.33	-2.10	-1.10	-0.27	1.06	0.69	9.58
36	RP-Bio-226-57	0.85	-0.53	6.54	3.43	0.97	-1.32	2.36	10.48

PH : Plant height (cm), PL : Panicle length (cm), NGP : Number of grains per panicle, NPT : Number of productive tillers per plant, %CH : Per cent chaffyness (%), TW : Test weight(g), GYP : Grain yield per plant YLD : Yield per hectare

Table 12 contd..

37	RP-Bio-226-63	1.11	0.70	5.79	4.90	3.57	0.82	2.11	10.44
38	RP-Bio-226-65	1.16	0.00	4.67	2.45	0.20	0.82	0.89	8.39
39	RP-Bio-226-78	0.45	1.72	5.04	2.65	4.40	1.51	1.73	7.23
40	RP-Bio-226-83	0.60	4.67	-1.22	-0.66	2.35	0.55	2.52	10.08
41	RP-Bio-226-90	1.05	8.02	1.09	0.60	2.21	0.58	1.33	6.55
42	RP-Bio-226-103	1.33	0.91	13.11	6.88	0.35	-0.35	0.27	2.51

43	RP-Bio-226-109	1.33	0.02	4.03	2.12	4.11	1.22	0.88	9.49
44	RP-Bio-226-115	0.48	0.87	-2.33	-1.21	1.56	1.23	1.50	9.85
45	RP-Bio-226-120	0.12	0.35	0.51	0.28	0.74	0.65	-2.23	2.09
46	RP-Bio-226-130	1.29	-2.18	3.69	1.94	1.94	1.74	1.12	10.06
47	RP-Bio-226-131	-0.42	0.38	-0.49	-0.26	0.27	0.76	1.92	8.86
48	RP-Bio-226-147	0.59	2.86	4.95	2.57	2.05	3.81	-0.25	9.86
49	RP-Bio-226-151	1.78	2.89	0.11	0.06	1.02	0.28	1.49	10.26
50	RP-Bio-226-152	0.62	-0.16	-2.70	-1.42	1.17	1.03	-0.41	5.48
51	RP-Bio-226-153	0.82	0.37	6.09	7.30	1.22	-0.15	-0.92	6.03
52	RP-Bio-226-159	1.04	-0.51	1.61	0.84	0.40	1.24	1.35	9.40
53	RP-Bio-226-168	0.48	1.25	-3.47	-1.82	1.29	1.36	0.27	7.27
54	RP-Bio-226-172	0.86	2.59	-2.98	-1.58	1.07	1.68	1.70	9.97
55	RP-Bio-226-190	0.77	0.73	0.81	0.42	2.31	2.10	0.58	9.48
56	RP-Bio-226-191	1.43	1.39	-1.44	-0.78	2.71	-0.58	1.74	10.16
57	RP-Bio-226-199	0.46	-0.54	8.83	8.65	0.68	-0.14	-2.20	7.15
58	BPT 5204	0.59	-13.12	-5.12	0.83	3.29	1.63	0.76	4.33

59	Rp -Bio 226	1.90	6.98	4.73	5.79	2.51	-0.88	1.73	14.65
60	Pokkali	0.98	15.21	-1.21	-0.64	1.77	2.81	4.44	8.67
61	CSR 22	0.86	9.93	-4.78	8.21	-0.24	-0.31	-0.25	11.38
62	FL 478	-0.32	10.46	0.58	1.56	0.17	1.27	5.36	11.03
63	Swarna Sub 1	1.18	-10.14	-2.23	-1.16	-0.27	-0.03	0.29	15.87
64	IRRI 154	1.49	7.88	1.16	-1.84	0.91	2.86	10.47	17.02

PH : Plant height (cm), PL : Panicle length (cm), NGP : Number of grains per panicle, NPT : Number of productive tillers per plant, %CH : Per cent chaffyness (%), TW : Test weight(g), GYP : Grain yield per plant YLD : Yield per hectare

Table 13 Na⁺ and K⁺ concentration in shoot of mutant rice genotypes

genotype	% Na⁺	% K⁺	Na⁺ / K⁺	Designation
BPT-5204-10	0.613	2.484	0.247	Tolerant
BPT-5204-15	0.230	2.210	0.104	Tolerant
BPT-5204-16	0.364	2.143	0.170	Tolerant
BPT-5204-22	0.258	2.277	0.113	Tolerant
BPT-5204-29	0.256	2.310	0.111	Tolerant
BPT-5204-37	0.654	1.970	0.332	Tolerant
BPT-5204-38	0.614	2.298	0.267	Tolerant
BPT-5204-42	0.256	2.456	0.104	Tolerant
BPT-5204-46	0.309	2.089	0.148	Tolerant
BPT-5204-57	0.317	2.593	0.122	Tolerant
BPT-5204-60	0.253	2.155	0.117	Tolerant
BPT-5204-67	0.245	1.761	0.139	Tolerant
BPT-5204-69	0.688	2.526	0.272	Tolerant
BPT-5204-77	0.299	2.210	0.135	Tolerant
BPT-5204-88	0.293	2.841	0.103	Tolerant
BPT-5204-94	0.479	2.592	0.185	Tolerant
BPT-5204-96	0.289	2.340	0.124	Tolerant
BPT-5204-98	0.273	2.358	0.116	Tolerant
BPT-5204-103	0.296	2.310	0.128	Tolerant
BPT-5204-115	0.122	1.041	0.118	Tolerant
BPT-5204-128	0.392	2.326	0.169	Tolerant
BPT-5204-130	0.312	2.500	0.125	Tolerant
BPT-5204-134	0.557	2.229	0.250	Tolerant
BPT-5204-139	0.320	2.300	0.139	Tolerant

BPT-5204-149	0.213	2.010	0.106	Tolerant
BPT-5204-158	0.798	1.590	0.502	Sensitive
BPT-5204-165	0.302	2.479	0.122	Tolerant
BPT-5204-166	0.617	2.629	0.235	Tolerant
BPT-5204-183	0.237	2.259	0.105	Tolerant
RP-Bio-226-18	0.644	1.933	0.333	Tolerant
RP-Bio-226-23	0.441	2.519	0.175	Tolerant
RP-Bio-226-29	0.583	2.723	0.214	Tolerant
RP-Bio-226-37	0.578	2.421	0.239	Tolerant
RP-Bio-226-41	0.535	2.620	0.204	Tolerant
RP-Bio-226-45	0.474	2.300	0.206	Tolerant
RP-Bio-226-57	0.766	2.383	0.322	Tolerant
RP-Bio-226-63	0.608	2.852	0.213	Tolerant
RP-Bio-226-65	0.234	1.700	0.138	Tolerant
RP-Bio-226-78	0.853	3.535	0.241	Tolerant
RP-Bio-226-83	0.750	2.479	0.303	Tolerant
RP-Bio-226-90	1.203	2.409	0.499	Tolerant
RP-Bio-226-103	1.359	2.617	0.519	Sensitive
RP-Bio-226-109	1.018	2.617	0.389	Tolerant
RP-Bio-226-115	0.835	2.533	0.330	Tolerant

Table 13 contd...

RP-Bio-226-120	0.236	2.310	0.102	Tolerant
RP-Bio-226-130	0.596	2.310	0.258	Tolerant
RP-Bio-226-131	0.801	2.877	0.278	Tolerant
RP-Bio-226-147	0.663	2.662	0.249	Tolerant

RP-Bio-226-151	0.431	2.845	0.152	Tolerant
RP-Bio-226-152	0.732	2.910	0.252	Tolerant
RP-Bio-226-153	0.889	2.455	0.362	Tolerant
RP-Bio-226-159	0.772	2.646	0.292	Tolerant
RP-Bio-226-168	0.779	3.511	0.222	Tolerant
RP-Bio-226-172	0.792	2.118	0.374	Tolerant
RP-Bio-226-190	0.576	2.910	0.198	Tolerant
RP-Bio-226-191	0.804	2.482	0.324	Tolerant
RP-Bio-226-199	0.519	2.797	0.185	Tolerant
BPT 5204	0.745	1.251	0.596	Sensitive
Rp -BIO 226	0.654	1.200	0.545	Sensitive
Pokkali	0.641	1.798	0.356	Tolerant
CSR 22	0.179	1.738	0.103	Tolerant
FL 478	0.379	1.770	0.214	Tolerant
Swarna Sub 1	0.589	1.035	0.569	Sensitive
IRRI 154	0.654	1.045	0.626	Sensitive

Table 14 Standard Evaluation System (SES) of scoring rice mutants genotypes

Genotypes	SES	Designation	Genotypes	SES	Designation
BPT-5204-10	1	T	RP-Bio-226-37	1	T
BPT-5204-15	1	T	RP-Bio-226-41	1	T
BPT-5204-16	1	T	RP-Bio-226-45	1	T
BPT-5204-22	1	T	RP-Bio-226-57	1	T
BPT-5204-29	1	T	RP-Bio-226-63	1	T
BPT-5204-37	1	T	RP-Bio-226-65	1	T
BPT-5204-38	1	T	RP-Bio-226-78	1	T
BPT-5204-42	1	T	RP-Bio-226-83	5	S
BPT-5204-46	1	T	RP-Bio-226-90	5	S
BPT-5204-57	1	T	RP-Bio-226-103	5	S
BPT-5204-60	1	T	RP-Bio-226-109	1	T
BPT-5204-67	1	T	RP-Bio-226-115	1	T
BPT-5204-69	1	T	RP-Bio-226-120	1	T
BPT-5204-77	1	T	RP-Bio-226-130	1	T
BPT-5204-88	1	T	RP-Bio-226-131	1	T
BPT-5204-94	1	T	RP-Bio-226-147	1	T
BPT-5204-96	1	T	RP-Bio-226-151	1	T
BPT-5204-98	1	T	RP-Bio-226-152	1	T
BPT-5204-103	1	T	RP-Bio-226-153	1	T
BPT-5204-115	1	T	RP-Bio-226-159	1	T
BPT-5204-128	1	T	RP-Bio-226-168	1	T
BPT-5204-130	1	T	RP-Bio-226-172	1	T
BPT-5204-134	1	T	RP-Bio-226-190	1	T
BPT-5204-139	1	T	RP-Bio-226-191	1	T

BPT-5204-149	1	T	RP-Bio-226-199	1	T
BPT-5204-158	5	S	BPT 5204	7	S
BPT-5204-165	1	T	Rp -Bio 226	7	S
BPT-5204-166	1	T	Pokkali	3	T
BPT-5204-183	1	T	CSR 22	3	T
RP-Bio-226-18	5	S	FL 478	3	T
RP-Bio-226-23	1	T	Swarna Sub 1	7	S
RP-Bio-226-29	1	T	IRRI 154	7	S

T= Tolerant S= Sensitive

4.6 Molecular characterization using SSR markers

Molecular techniques are best employed to assess the genetic differences or similarity existing among the genotypes. DNA markers are more useful as they are precise and quick means of assessing salinity tolerance through DNA polymorphism. In the present study Simple Sequence Repeats (SSR) markers were used for the characterization of rice genotypes.

The two SSR primers used in present study produced scorable, unambiguous bands. A total of four alleles were detected with an average of 2 alleles for each marker. In RM-336 the allelic difference is at 154bp and 160bp based on the number of repeat motifs in (CT)₂₀ is shown in plate 04 (upper). In RM-7075 having band size of 155bp and 160bp based on the number of repeat motifs in (CT)₁₉, is shown in plate 04 (lower).

4.6.1 Cluster Analysis based on dendrogram

Cluster analysis was performed using the UPGMA method to group the rice genotypes. Based on simple matching similarity coefficient two clusters were formed at genetic similarity level of 0.50. Cluster I consists four genotypes viz., Swarna sub 1, IRRI-154, BPT-5204, RP-Bio-226. Cluster II consists twenty five genotypes viz., Pokkali, CSR-22, FL-478 and RP- Bio226-120, RP- Bio226-37, RP- Bio226-23 , RP- Bio226-29, RP- Bio226-153, RP- Bio226-199, RP- Bio226-41, RP- Bio226-63, RP- Bio226-172, RP- Bio226-109, RP- Bio226-191, RP- Bio226-131, RP- Bio226-151, RP- Bio226-130, RP-

Bio226-63. BPT-5204-69, BPT-5204-94, BPT-5204-134, BPT-5204-38, BPT-5204-77,
BPT-5204-10 and BPT-5204-166 (Fig. 5)



Molecular profiling of 29 mutants with SSR marker RM-7075

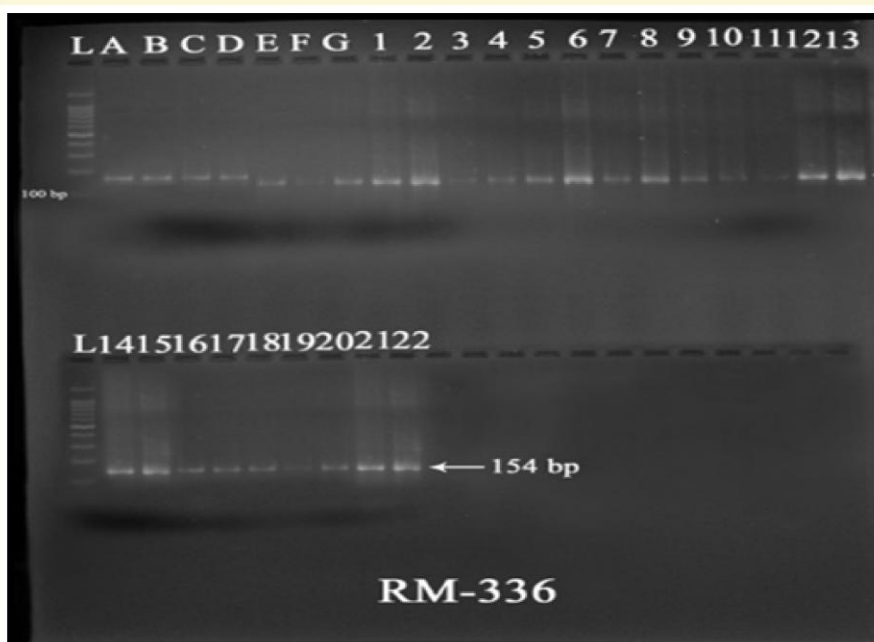


Plate 04. Molecular profiling of 29 mutants with SSR marker RM-336

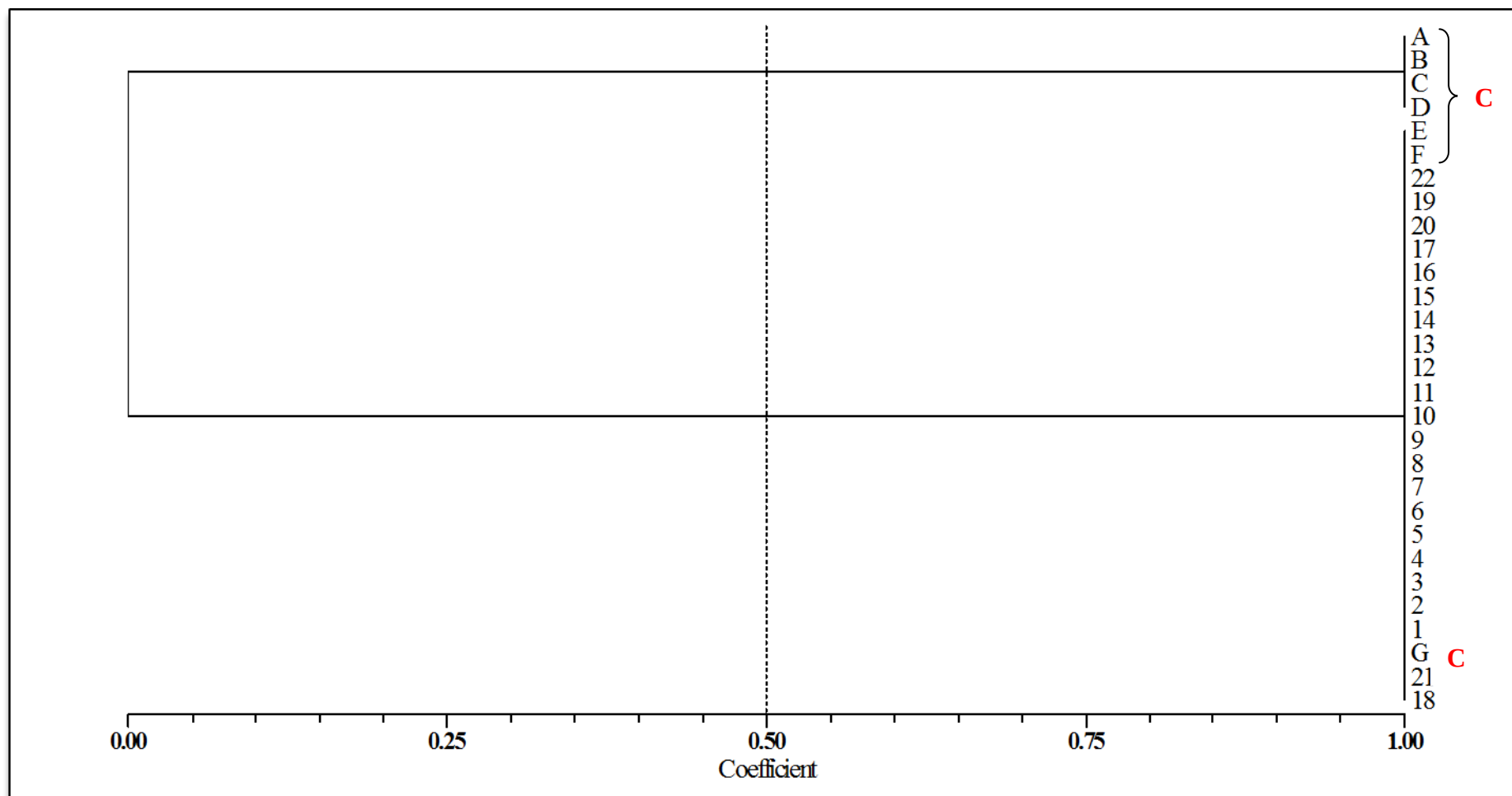


Fig.5 Dendrogram showing genetic similarity among 29 mutant rice genotypes using Jaccard Coefficient for SSR markers

(C – Checks , A - BPT-5204, B - RP-Bio-226, C - Swarna Sub 1, D - IRRI 154, E - Pokkali, F - CSR 22, G - FL 478)

DISCUSSION

V. DISCUSSION

For a crop improvement programme, plant breeding is pre-requisite to maintain the genetic variability that allows identification of promising genotypes in the study material that can be incorporated in the breeding programme to develop promising cultivars. The genetic material could be judged based on the knowledge of extent of variability, character association and direct and indirect effects influencing different characters.

The selected M₅ generation mutant lines of BPT-5204 and RP Bio-226 under saline stress soil were used for further evaluation in M₆ generation for salinity tolerance at Agricultural research station, Gangavati, this city is called rice bowl of Karnataka, where, 25 per cent of the Tungabhadra Project command area is reported to be affected by salinity hazard which is due to adaption of improper water, fertilizer and soil management practices. To address this problem an effort has been made through mutation breeding approach. Popular cultivars like BPT-5204 is well known for its quality and grain yield but are sensitive to salinity stress. These varieties were evaluated for variability under both normal and salinity condition.

The results obtained from the present investigation are discussed under the following headings.

5.1 Analysis of variance

5.2 Genetic variability, heritability and genetic advance

5.3 Correlation coefficient

5.4 Path analysis

5.5 Salinity screening

5.6 Molecular Characterization

5.1 Analysis of variance

The analysis of variance of different characters for both normal and saline condition for all the genotypes showed significant differences at 5% level of significance,

suggesting that the genotypes were genetically diverse for majority of the characters under study. Similar observation was noticed by Mahantashivayogayya *et al.* (2016).

5.2 Genetic variability parameters

Variability was measured by estimation of mean, coefficient of variation (genotypic and phenotypic), heritability, genetic advance and genetic gain. Environment plays an important role in the expression of phenotype and genotype factors, which are inferred, from phenotypic observations. Hence, variability can be observed through biometric parameters like genotypic coefficient of variation, heritability (broad sense) and genetic advance. This would be of great help to breeders in evolving a selection programme for suitable gene or genotype. The estimates of variance, coefficient of variation, heritability and genetic advance for all the characters under normal and saline condition are studied and discussed here.

5.2.1 Genetic variability parameters for yield and yield attributing characters

GCV and PCV were high for number of grains per panicle, panicle weight and panicle exertion, while these were moderate for total number of tillers per plant, number of productive tillers, plant height, length of flag leaf and grain yield, both in normal and saline soil condition which indicated that variability for these traits was high and less influence of environmental factors which suggested that selection would be effective. The present results are in conformity with findings of Mahantashivayogayya *et al.* (2016), Singh *et al.* (2005), Mamta *et al.* (2007), Jaiswal *et al.* (2007), Sharma and Sharma (2007) and Pillai *et al.* (2011), Pandey *et al.* (2012), Karim *et al.* (2007) and Babu *et al.* (2012). Basavaraj (2017) also observed high GCV and PCV for filled grain number per panicle, test weight, panicle weight, test weight and grain yield. Traits like days to 50 percent flowering and panicle length showed low GCV and PCV which is indicative of low variability for these characters and selection for these characters would not be effective indicating the need for creation of variability by hybridization or mutation followed by selection. Similarly Low GCV and PCV were observed by Rashid *et al.* (2017) for days to 50% flowering, days to maturity, panicle length, number of effective tillers per plant, fertility (%), 1000 Seed weight and yield per panicle these results can also be confirmed by the findings of Vaithiyalingan and Nadarajan (2006), Gangashetty *et al.* (2012) and Pandey *et al.* (2012).

Heritability estimates reveals the heritable portion of variability present in different characters. The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation. However, heritability values coupled with genetic advance would be more reliable (Johnson *et al.*, 1955) and useful in formulating selection procedure. In the present study, heritability estimates in broad sense and genetic advance as per cent of mean were estimated.

In the present study, high to moderate heritability coupled with high to moderate genetic advance as per cent of mean were observed in normal and saline condition, Plant height, number of grains per panicle, panicle weight, total number of tillers, flag leaf length, per cent chaffyness, grain yield per plant, test weight and panicle exertion observed high genetic advance over mean coupled with heritability, similar finding are observed by Mahantashivayogayya *et al.*(2016), under study which indicated the prevalence of additive gene action and the lesser influence of environment in expression of these characters, which provides good scope for further improvement by selection similar results were observed by Rashid *et al.* (2017) for number of filled grains per panicle number of unfilled grains per panicle and plant height. These results can also be confirmed by the results of Siddiqui and Sanjeeva (2010), Selvaraj *et al.* (2011), Singh *et al.* (2011), Pandey *et al.* (2012), Babu *et al.* (2012) and Satish *et al.* (2013).

In normal and saline conditions the grain size and shaped varied from short bold, long slender short slender and medium slender, which shows the variability, similar observation are found in Jaiswal and Srivastava (2007). Compare to the normal condition grain size and shape shows little variation in saline condition due to salinity stress, the reduced size and shape is mainly due to chaffyness or unfilled grains, due to the higher concentration of Na^+ , which abstracts the photosynthetic activity.

Highest amylose content 26.35 per cent was observed in genotype BPT-5204-115 and majority of the genotypes falls under intermediate (20-25 %) amylose content along with check BPT-5204 (24.14%). The lowest amylose content observed was 21.63 per cent in the RP Bio-226-115. Overall mean of the genotypes for Amylose Content was 23.5 per cent in normal condition. Similarly in saline condition BPT-5204-115 genotype observed maximum amylose content, RP Bio-226-190 observed minimum amylose content and mean obtained was 23.15 per cent. Similarly, Basavaraj *et al.*, (2017) also observed variation for the amylose content which ranged from 7.2 % to 31.02 %.

5.3 Correlation coefficient

5.3.1 Yield and yield components

The phenotype of a plant is result of interaction of large number of factors. Hence, final yield was the sum total effect of several component factors. Therefore, it was important to know the extent and nature of inter-relationship revealing between grain yield and its component characters and also among themselves. Also it becomes necessary to know the association of grain quality characters among themselves. This would be obtained from simple correlation coefficient which helps a breeder in determining the direction and number of characters to be considered in improving yield and grain quality. In the present investigation, correlation coefficient was worked out for grain yield and yield attributing traits.

In the present study correlations among quantitative characters of rice were computed. The grain yield had significantly high positive correlation with panicle exertion, number of grains per panicle in normal condition and in saline soil condition, panicle length, panicle exertion, number of grains per panicle and panicle weight had significantly high positive correlation. Similar significant positive magnitude of correlation was recorded by plant height, number of productive tillers, total number of tillers and grain yield per plant in both normal and saline soil condition which indicated that yield is a complex trait and it can be improved through indirect selection of these traits. Therefore, from the results significant positive correlation suggests that selection for one character could be used to indirectly select for another character. These results are in line with Kalyan *et al.* (2017). Similar finding are observed by Katoch *et al.* (2005), Akinwale *et al.* (2011), Mahantashivayogayya *et al.* (2016), Kiani *et al.* (2012), Bhattacharya and Sowbhagya (1980) and Neelima *et al.* (2007).

Whereas significant negative association with days to 50 per cent flowering, percentage of chaffyness in the saline soil condition, while days 50per cent flowering, seedling mortality and test weight in normal soil condition indicated that shorter duration genotypes coupled with more chaffy grains contributed for lower yields these results are supported by the results of Khan *et al.*, (2014).

5.3.2 Correlation among yield components

Study of association of yield components with yield assumes special importance and forms basis for selecting desired mutant line. Correlation coefficient measures the magnitude and direction of association among the characters. The genotypic correlations between different characters within a plant often arise because of either genetic linkages or pleiotropy (Herald, 1939). It is important to the breeders to establish and understand the existing relationship between the yield and yield contributing characters. It is intended to consider the issues concerning the significant inter relationships among yield character other than grain yield which might aid in conceiving an ideal plant type.

5.3.2.1 Days to 50 per cent flowering:

In normal soil condition test weight observed significantly high positive correlation. Panicle exertion and yield observed significantly high negatively correlation. These are the early maturing genotypes producing bolder grains, lesser yield as the short period for grain filling. These results are supported by finding of Kalyan *et al*, (2017) and Khan *et al*, (2014). In saline condition panicle length, length of flag leaf, panicle exertion and yield observed negatively correlated. Similar results are obtained by Hairmansis *et al*, (2013)

5.3.2.2 Plant height:

In normal condition panicle length, panicle weight, length of flag leaf and test weight observed significantly high positive correlation. As the length of flag leaf increased more assimilates transferred to grains that resulted in high panicle weight. Number of grains per panicle, number of productive tillers and total number of tillers observed negatively correlated with plant height indicated that dwarf to semi dwarf plants produced more yield rather than taller plants. Both in normal and saline condition plant height had negative correlation with yield. Amirthadevarathinam (1983) and Ratna *et al*, (2013) also found that grain yield was negatively correlated with plant height.

5.3.2.3 Panicle length

In normal soil condition panicle weight and flag leaf length observed significantly high positive correlation. Number of grains per panicle, number of productive tillers and

total number of tillers observed negatively correlated as observed by Hairmansis *et al.* (2013). In saline condition panicle weight, length of flag leaf and panicle exsertion observed significantly high positive correlation as noticed by Devi *et al.*, (2016).

5.3.2.4 Number of gains per panicle:

In normal soil condition number of productive tillers and total number of tillers observed significantly high positive correlation. These results are in line with Sravan *et al.*, (2012). Length of flag leaf and per cent chaffyness observed high negatively correlated as noticed by Rashid *et al.* (2014). In saline condition test weight observed high negatively correlated as noticed by Nagesh *et al.* (2012)

5.3.2.5 Panicle weight

In normal condition length of flag leaf and test weight observed significantly positive correlation with panicle weight this indicated that area of flag leaf and 1000 gains contributed to high panicle weight similar findings observed by Rashid *et al.*, (2013) were he observed positive correlation of panicle weight with flag leaf length.

5.3.2.6 Number of productive tillers

In normal and saline conditions total number of tillers observed significantly positive correlation with number of productive tillers which indicated that majority of the tillers produced by the genotypes was productive in nature (*i.e.* contributed toward higher yield). The present results are in line with the results obtained by Rashid *et al.* (2013). In saline condition length of flag leaf and test weight observed negatively correlated the reason would be saline soils adversely affected the production of productive tillers. Similar results are in-line with Rashid *et al.* (2013) were observed negative correlation between productive tillers and test weight.

5.3.2.7 Total number of tillers

In normal condition number of grains per panicle observed significantly positive correlation which is an indicated that all the tillers had more number of grains. Similar finding were observed by Rashid *et al.* (2013). In saline condition length of flag leaf observed high negatively correlated. Length of flag leaf observed high negatively

correlated which indicative that more of assimilates contributed for the vegetative growth rather than the productive parts. Similar finding were observed by Rashid *et al.* (2013).

5.3.2.8 Length of flag leaf

In normal and saline condition test weight observed significantly high positive correlation. As the length of flag leaf increased more assimilates transferred to grains that resulted in high test weight. These results are in accordance with Sravan *et al.* (2012).

5.3.2.9 Per cent chaffyness

In saline condition panicle exertion observed significantly high positive correlation. Test weight observed negatively correlated, more the chaffy grain lesser the test weight which is an indicative of desirableness of per cent chaffyness. Thus, in order to increase yield, it is important to reduce spikelet sterility or increase spikelet fertility. Luzikihupi *et al.* (1998) also reported negative correlation between unfilled grains and test weight.

5.3.2.10 Grain yield per plant

In normal condition panicle exertion observed significantly high positive correlation, fully exerted panicles from the flag leaf produced more number of grains which intern contributed for higher yields. Grain yield is a complex trait which can be improved through indirect selection of these traits. Therefore, from the results selection for one character could be used to indirectly select for another character. The present results are also supported by results of Chauhan and Chauhan (1994) and Murthy and Babu (1992). These studies can also be confirmed by Akinwale *et al.* (2011), who recorded significantly positive correlation of grain yield with the number of tillers per plant, panicle weight and number of grains per panicle.

5.3.2.11 Test weight:

Test weight observed negatively correlated the reason would be small sized grains resulted in lesser yields. In normal and saline condition panicle exertion observed negatively correlated with test weight contrasting results were obtained by Rajeswari and Nadarajan (2004). The reason would be though the panicles were not fully exerted the genotypes gave more yields this is because the genotypes are from BPT 5204 back

ground which is the high yielding genotype so the contrasting results were obtained in present study. Whereas seedling mortality observed positive correlation this is because lesser competition for nutrients with surrounding population that resulted in higher test weight.

5.4 Path coefficient analysis

Path analysis was first suggested by Wright (1921). It is standardized partial regression analysis based on cause and effect of relationship and is useful for analysis by sub dividing correlation in a causal scheme.

In normal soil condition direct effect on grain yield reveals that out of twelve characters four characters (days to 50 per cent flowering, length of flag leaf, number of grains per panicle and panicle exertion) considered for path analysis, number of grains per panicle exerted maximum direct effect on grain yield followed by panicle exertion. This indicates that, if other factors are held constant, an increase in number of grains per panicle individually will reflect in increased yield. The indirect effect of all these characters on grain yield was also high. Many other workers have also considered number of grains per panicle, panicle exertion and to be most important yield components having greatest direct effect. Similar results are observed by Naseem *et al.* (2014), Jaiswal *et al.* (2007), Jayasudha and Deepak (2010), Mustafa (2011) and Kole *et al.* (2008). The length of flag leaf and days to 50 per cent flowering observed negative direct effect, in case of the days to 50 per cent flowering because of the short duration, the lesser accumulation of assimilates hence lesser yield obtained. Similar results are obtained by Dhurai *et al.* (2016)

In saline condition based on the correlation significance days to 50 per cent flowering, panicle length, number of grains per panicle, panicle weight, test weight, seedling mortality and panicle exertion are under consideration. Days to 50 per cent flowering and seedling mortality observed negative direct effect on yield, in saline condition the sensitive genotypes observed high seedling mortality then tolerant genotypes hence sensitive genotypes could not sustain the saline stress situation as the results lower the plant population lower yields are obtained. Similar results are obtained by Dhurai *et al.* (2016).

Panicle exertion, test weight, panicle weight, number of grains per panicle and panicle length observed positive direct effect on yield. Similar results are conformed by Sivakumar and Kannan (2005), Eradasappa *et al.* (2007) and Rita *et al.* (2006).

In normal soil condition, number of grains per panicle showed positive and negligible indirect effect on grain yield via test weight and days to 50 per cent flowering, positive and low indirect effect are showed by number productive tillers and total number tillers, these results are in conformity with the observations made by Monalisa *et al.* (2006) and Neelima *et al.* (2007). Similarly in saline soil condition, number of productive tillers showed positive and high indirect effect on grain yield via total number of tillers. Grains yield per panicle and number of grains per panicle showed positive and negligible indirect effect on grain yield. The negative indirect effect was recorded by test weight and panicle exertion. These results are in conformity with the observations made by Sadeghi, (2011), Neelima *et al.* (2007), Sivakumar and Kannan, (2005) and Rita *et al.* (2006).

5.5 Screening for Salinity

Breeding for salinity tolerance of two staple crops in the world including rice and wheat is an important goal, especially for FAO. Evaluations for the effects of salinity stress on rice yield have an important necessity for rice breeding. Yield loss due to salinity is 30-50 per cent, for every increase in 1 ds/m there will be decrease in one tons per hectare. It is now realized that sustainability as well as productivity could be essential for rice breeding. Stress indices have been used for screening stress-tolerant genotypes. Salinity tolerance of mutants was assessed and salinity tolerant mutants were identified as per Stress Susceptibility Index (SSI), Na^+/K^+ in shoot and Standard Evaluation System (SES).

Fischer and Maurer (1978) suggested the stress susceptibility index (SSI) for measurement of yield stability that apprehended the changes in both potential and actual yields in variable environments, which can be used to identify genotypes that produce high yield under both stressed and non-stressed conditions. Guttieri *et al.* (2001) suggested that genotypes with larger SSI values had sensitivity to salinity stress in rice genotypes. SSI indices and seed yield were used as stability parameters for identification of salinity resistant genotypes.

Sodium and Potassium in shoot are negatively correlated, It was observed that the lines that showed the Na^+/K^+ ranging from 0-0.2 were grouped under highly tolerant, that showed a ratio of 0.2-0.5 were categorized as tolerant, 0.5-1 as sensitive and above 1 as highly sensitive. These designations were in accordance with the results of Singh *et al.* (2014), Krishnamurthy *et al.* (2016).

The mutants were screened for salt tolerance at seedling stage using IRRI standard protocol (Gregorio *et al.*, 1997) in Saline soil. The evaluation was done using the modified standard evaluation system (SES) rating the visual symptoms of salt toxicity (IRRI, 1997). This scoring discriminated the susceptible from the tolerant and the moderately tolerant genotypes, the one which shows normal growth on leaf symptoms are given one score because of Highly tolerant, Tolerant are genotypes even observed nearly normal growth, but leaf tips or few leaves whitish and rolled which scored three. Moderately tolerant genotype scored five, as they observed severely retarded in growth, most leaves rolled and only few are elongating. Complete cessation of growth, most leaves dry and some plants dying in case of susceptible with score of 7. Highly susceptible genotypes scored nine, with almost all plants dead or dying.

Based on SSI, SES, Na^+/K^+ and per se performance of the genotypes, the top lines are selected for saline condition (table 15).

In RP Bio-226 mutant lines, RP Bio-226-20, RP Bio-226-23, RP Bio-226-29, RP Bio-226-37, RP Bio-226-41, RP Bio-226-109, RP Bio-226-153, RP Bio-226-172 and RP Bio-226-199. Similarly in BPT-5204 mutant lines, BPT-5204-69, BPT-5204-94, BPT-5204-134 and BPT-5204-166 has recorded higher per cent gain in the yield with respect to per se performance with national check, Pokkali. These genotypes has recorded lesser SSI values for plant height, number of grains per panicle, panicle length, number of productive tillers per plant and grain yield per plant. Similar results are in line with Natarajan *et al.* (2005), Ali *et al.* (2004), Bhowmik *et al.* (2009) and Nakhoda *et al.* (2012), Siddiqui (2014), Farshadfar *et al.* (2014), Krishnamurthy *et al.* (2016) and Kumawat *et al.* (2017).

These genotypes has scored one in the standard Evaluation System, as they observed phenotypically high tolerance, similar results are noticed by Mondal and Borromeo (2016).

The sodium potassium ratio also explains these genotype are highly tolerant to salinity, lesser the value of Na^+ / K^+ in shoot higher the tolerance. The similar results were reported by Hani *et al*, (2017) The variety showed very low Na^+ / K^+ which may be an indication that this variety shows saline tolerance when compared with all other varieties. This is in line with the findings of Mishra *et al.*, (1997). This low Na^+ / K^+ of ion uptake is positively correlated with a high level of salt tolerance and can be taken into consideration as a desired characteristic while screening rice lines. Similar results were observed by Wang *et al*, (2012). Similar study carried out by Brady *et al.*, (1984). The high Na^+ / K^+ leads to metabolic disorders such as reduction in protein synthesis and enzyme activities. Presence of high K content in the tolerant genotypes observed in this study resulted in higher yielding ability. This is in accordance with Joshi *et al.*, (1980). The tissue concentration of sodium and potassium and the Na^+ / K^+ has been suggested as useful parameters for screening genotypes of any crop under salt stress condition. Hence these lines are tolerant to salinity.

5.6 Molecular characterization using SSR markers

Among the several classes of available DNA markers, microsatellite or simple sequence repeat (SSR) markers are considered the most suitable due to their multi allelic nature, high reproducibility, co-dominant inheritance, abundance and extensive genome coverage. A large number of SSR markers have been developed and mapped in rice (Temnykh *et al.*, 2000, McCouch *et al.*, 2002), which vary in the degree of polymorphism depending on their position in the coding or non-coding segments, nature of their repeat motifs and the genome wide abundance. Therefore, an ideal set of SSR markers providing genome wide coverage will facilitate an unbiased assay to screen the salinity tolerant genotypes.

5.6.1 Selection of rice genotypes for similarity studies

The present study involved a selected salinity tolerant total of 22 rice mutant lines based on yield and yield attributing traits in saline stress condition used for molecular profiling; These 22 rice mutant lines included check varieties viz., Pokkali, BPT-5204, RP-Bio 226, FL28, IRRI-154, Swarna Sub 1 and CSR-22.

DNA based molecular markers developed during the last two decades of molecular biology research has been utilized for various applications in the area of plant

genome analysis. They have acted as versatile tools and have found their own position in various fields like taxonomy, physiology, embryology, genetic engineering etc. In the last few years, microsatellites have become one of the most popular molecular markers used with application in many fields. High polymorphism and the relative ease of scoring represent the two major features that make microsatellite of large interest for many genetic studies. Hence SSR markers RM 336 and RM 7075 have been used in molecular profiling

5.6.2 Clustering of rice genotypes

Dendrogram was constructed from the genetic similarity matrix using Numerical Taxonomy System NTSYSpc-2.02j software. Sequential, agglomerative, hierarchical and nested clustering (SAHN) was used for building the cluster tree. The SSR markers were successful in revealing the presence of two broad groups among the genotypes. This dendrogram revealed that the genotypes derived from a genetically similar type and clustered together. Cluster I consist of Swarna sub1, IRRI -154, BPT-5204, Rp-Bio 226. cluster II consist of Pokkali, CSR-22,FL-478 and RP- Bio226-120,RP- Bio226-37,RP- Bio226-23, RP- Bio226-29,RP- Bio226-153,RP- Bio226-199,RP- Bio226-41,RP- Bio226-63,RP- Bio226-172,RP- Bio226-109,RP- Bio226-191,RP- Bio226-131,RP- Bio226-151,RP- Bio226-130,RP- Bio226-63, BPT-5204-69, BPT-5204-94, BPT-5204-134, BPT-5204-38, BPT-5204-77, BPT-5204-10 and BPT-5204-166.

The SSR marker RM 336 and RM 7075 data were able to differentiate the mutants into separate clusters; this elucidated the potentiality of SSR markers for the characterization of mutant lines. Only two clusters are formed because, these mutants are derived from the same back ground BPT-5204 and RP Bio-226 and only two markers were used.

The two clusters are formed through the SSR data revealed that the presence of saline sensitive genotypes in cluster I and presence of salinity tolerant genotypes in cluster II.indicated that the genotypes contained in their respective cluster shared more genomic regions, The results of the current study are in line with a study by Bhowmik (2009) which evaluated 11 rice genotypes using three SSR markers viz., RM7075, RM336 and RM253, found that markers were capable to distinguish the salt tolerant genotypes from the salt sensitive traits by exhibiting the polymorphism among them. The

SSR markers including RM7075, RM336 and RM253 used detected 8, 9 and 7 salt tolerant genotypes, respectively. As SSR or microsatellite markers are well known for constructing genetic maps, aiding in selection and studying genetic diversity in germplasm, they play a vital role in detecting salt tolerant gene to assist the plant breeder in developing new cultivars. Accordingly, these markers used in this study showed polymorphism for the rice genotypes. In addition, the detected salt tolerant rice genotypes can be considered as the potential source to improve the salt tolerant genotype. Similar results are found by Hani *et al*, (2017).

Table 15 Performance of selected mutants of BPT-5204 and RP Bio-226 under saline and normal soils

Genotypes	SES	SSI								LEAF Na ⁺ /K ⁺			Per se performance of yield			
	score	PH	PL	NGP	NPT	%CH	GYP	TW	YLD	% Na ⁺	% K ⁺	Na ⁺ / K ⁺	N	% R or %G	S	% R or G
BPT-5204-10	1	0.95	-1.74	-5.93	-3.11	2.89	1.09	1.04	10.79	0.613	2.484	0.247	7030	21.58	4,113	8.66
BPT-5204-15	1	1.54	-4.46	3.60	1.89	1.18	-0.34	-0.26	13.03	0.23	2.21	0.104	6838	19.66	3,411	1.64
BPT-5204-16	1	1.06	-5.80	1.77	0.93	0.10	1.59	-0.48	9.78	0.364	2.143	0.17	6507	16.35	4,060	8.12
BPT-5204-22	1	1.43	-0.33	10.32	5.41	0.46	0.57	0.29	11.90	0.258	2.277	0.113	6421	15.49	3,483	2.35
BPT-5204-29	1	1.29	-3.40	4.39	2.30	2.08	0.31	-0.25	14.14	0.256	2.31	0.111	7564	26.92	3,451	2.03
BPT-5204-37	1	1.51	-1.09	-1.20	-0.63	0.12	-0.49	1.39	13.62	0.654	1.97	0.332	7329	24.57	3,490	2.43
BPT-5204-38	1	0.64	0.38	1.51	0.77	2.99	1.55	-0.95	7.50	0.614	2.298	0.267	5737	8.65	4,081	8.34
BPT-5204-42	1	0.99	-1.05	-1.44	-0.75	3.04	1.47	0.19	10.02	0.256	2.456	0.104	6015	11.43	3,697	4.49

BPT-5204-46	1	1.35	-0.16	-0.18	-0.10	2.70	0.26	0.40	9.57	0.309	2.089	0.148	6410	15.38	4,049	8.02
BPT-5204-57	1	1.52	-1.03	-7.96	-4.18	-0.04	2.36	0.52	12.08	0.317	2.593	0.122	6987	21.15	3,739	4.92
BPT-5204-60	1	1.23	10.48	-2.54	-1.33	2.17	-0.51	-1.56	12.29	0.253	2.155	0.117	6870	19.98	3,622	3.75
BPT-5204-67	1	0.76	0.72	7.57	3.97	1.94	-0.10	-0.40	11.13	0.245	1.761	0.139	5738	8.66	3,280	0.32
BPT-5204-69	1	0.91	-1.21	3.83	2.01	2.44	1.81	0.27	6.58	0.688	2.526	0.272	5694	8.22	4,252	10.05
BPT-5204-77	1	1.45	0.19	-7.06	-3.70	1.83	2.66	0.66	9.71	0.299	2.21	0.135	6667	17.95	4,178	9.30
BPT-5204-88	1	1.37	0.75	-2.69	-1.41	0.11	1.16	0.83	10.11	0.293	2.841	0.103	6207	13.35	3,793	5.45
BPT-5204-94	1	1.12	4.71	9.43	5.88	2.58	0.82	0.98	9.50	0.479	2.592	0.185	6667	17.95	4,231	9.83
BPT-5204-96	1	1.52	4.59	-1.12	-0.59	3.32	0.59	-0.40	10.53	0.289	2.34	0.124	6069	11.97	3,611	3.64
BPT-5204-98	1	1.63	0.36	-2.34	-1.23	1.80	2.18	1.10	11.51	0.273	2.358	0.116	6806	19.34	3,793	5.45
BPT-5204-103	1	1.75	0.37	-0.18	-0.10	0.97	1.28	-0.50	12.60	0.296	2.31	0.128	6966	20.94	3,590	3.42
BPT-5204-115	1	0.84	1.76	2.24	1.18	1.04	1.29	0.19	10.33	0.122	1.041	0.118	5780	9.08	3,483	2.35
BPT-5204-128	1	1.11	-4.11	0.31	0.13	2.16	1.19	0.52	11.47	0.392	2.326	0.169	6912	20.40	3,862	6.15

BPT-5204-130	1	1.69	-4.18	-6.10	-3.20	1.27	1.70	1.94	11.90	0.312	2.5	0.125	7094	22.22	3,846	5.99
BPT-5204-134	1	1.55	-0.36	-7.30	-3.83	1.22	1.40	3.79	14.93	0.557	2.229	0.25	9715	48.43	4,135	8.87
BPT-5204-139	1	0.95	0.02	12.61	6.61	1.59	0.79	0.45	10.43	0.32	2.3	0.139	6816	19.44	4,081	8.34
BPT-5204-149	1	1.58	1.05	-1.01	-0.51	4.63	1.12	0.28	13.65	0.213	2.01	0.106	7318	24.46	3,475	2.28
BPT-5204-158	5	0.69	1.67	15.24	10.22	0.84	-3.23	1.82	10.03	0.798	1.59	0.502	6870	19.98	4,220	9.73
BPT-5204-165	1	1.52	3.85	3.81	2.00	0.78	0.78	1.77	12.09	0.302	2.479	0.122	7493	26.21	4,008	7.60
BPT-5204-166	1	0.36	1.34	-5.54	-2.90	2.47	0.96	2.08	11.99	0.617	2.629	0.235	7816	29.44	4,209	9.62
BPT-5204-183	1	0.48	-2.08	6.30	3.31	-0.04	-0.16	-0.13	9.62	0.237	2.259	0.105	5256	3.84	3,312	0.64
RP Bio-226-18	5	0.64	2.17	10.81	5.67	0.41	3.32	0.96	9.49	0.644	1.933	0.333	6998	21.26	4,444	11.97
RP Bio-226-23	1	0.30	-1.64	-3.52	-1.85	0.77	0.21	-0.76	6.34	0.441	2.519	0.175	7180	23.08	5,427	21.80
RP Bio-226-29	1	0.62	0.02	6.54	3.43	1.69	1.68	0.36	5.90	0.583	2.723	0.214	6978	21.06	5,395	21.48
RP Bio-226-37	1	-0.02	-0.95	8.07	4.23	3.07	-0.71	-1.44	3.71	0.578	2.421	0.239	6678	18.06	5,725	24.77
RP Bio-226-41	1	1.16	1.10	0.08	0.04	2.96	1.85	0.38	8.60	0.535	2.62	0.204	7393	25.21	4,947	16.99

RP Bio-226-45	1	0.81	-0.33	-2.10	-1.10	-0.27	1.06	0.69	9.58	0.474	2.3	0.206	7158	22.86	4,519	12.72
RP Bio-226-57	1	0.85	-0.53	6.54	3.43	0.97	-1.32	2.36	10.48	0.766	2.383	0.322	7554	26.82	4,509	12.61
RP Bio-226-63	1	1.11	0.70	5.79	4.90	3.57	0.82	2.11	10.44	0.608	2.852	0.213	7568	26.96	4,530	12.82
RP Bio-226-65	1	1.16	0.00	4.67	2.45	0.20	0.82	0.89	8.39	0.234	1.7	0.138	7274	24.02	4,926	16.78
RP Bio-226-78	1	0.45	1.72	5.04	2.65	4.40	1.51	1.73	7.23	0.853	3.535	0.241	6111	12.39	4,413	11.65
RP Bio-226-83	5	0.60	4.67	-1.22	-0.66	2.35	0.55	2.52	10.08	0.75	2.479	0.303	7329	24.57	4,487	12.40
RP Bio-226-90	5	1.05	8.02	1.09	0.60	2.21	0.58	1.33	6.55	1.203	2.409	0.499	5898	10.26	4,412	11.65
RP Bio-226-103	5	1.33	0.91	13.11	6.88	0.35	-0.35	0.27	2.51	1.359	2.617	0.519	4872	0.00	4,402	11.55
RP Bio-226-109	1	1.33	0.02	4.03	2.12	4.11	1.22	0.88	9.49	1.018	2.617	0.389	7489	26.17	4,755	15.07
RP Bio-226-115	1	0.48	0.87	-2.33	-1.21	1.56	1.23	1.50	9.85	0.835	2.533	0.33	7276	24.04	4,519	12.72
RP Bio-226-120	1	0.12	0.35	0.51	0.28	0.74	0.65	-2.23	2.09	0.236	2.31	0.102	6706	18.34	6,166	29.18
RP Bio-226-130	1	1.29	-2.18	3.69	1.94	1.94	1.74	1.12	10.06	0.596	2.31	0.258	7511	26.39	4,605	13.57
RP Bio-226-131	1	-0.42	0.38	-0.49	-0.26	0.27	0.76	1.92	8.86	0.801	2.877	0.278	7132	22.60	4,701	14.53

RP Bio-226-147	1	0.59	2.86	4.95	2.57	2.05	3.81	-0.25	9.86	0.663	2.662	0.249	7265	23.93	4,509	12.61
RP Bio-226-151	1	1.78	2.89	0.11	0.06	1.02	0.28	1.49	10.26	0.431	2.845	0.152	7607	27.35	4,605	13.57
RP Bio-226-152	1	0.62	-0.16	-2.70	-1.42	1.17	1.03	-0.41	5.48	0.732	2.91	0.252	5673	8.01	4,477	12.29
RP Bio-226-153	1	0.82	0.37	6.09	7.30	1.22	-0.15	-0.92	6.03	0.889	2.455	0.362	6774	19.02	5,203	19.56
RP Bio-226-159	1	1.04	-0.51	1.61	0.84	0.40	1.24	1.35	9.40	0.772	2.646	0.292	6934	20.62	4,428	11.81
RP Bio-226-168	1	0.48	1.25	-3.47	-1.82	1.29	1.36	0.27	7.27	0.779	3.511	0.222	5919	10.47	4,263	10.15
RP Bio-226-172	1	0.86	2.59	-2.98	-1.58	1.07	1.68	1.70	9.97	0.792	2.118	0.374	7901	30.29	4,872	16.24
RP Bio-226-190	1	0.77	0.73	0.81	0.42	2.31	2.10	0.58	9.48	0.576	2.91	0.198	6710	18.38	4,263	10.15
RP Bio-226-191	1	1.43	1.39	-1.44	-0.78	2.71	-0.58	1.74	10.16	0.804	2.482	0.324	7767	28.95	4,733	14.85
RP Bio-226-199	1	0.46	-0.54	8.83	8.65	0.68	-0.14	-2.20	7.15	0.519	2.797	0.185	7073	22.01	5,128	18.81
BPT 5204	7	0.59	-13.12	-5.12	0.83	3.29	1.63	0.76	4.33	0.745	1.251	0.596	3654	- 12.18	3,045	-2.03
RP Bio-226	7	1.90	6.98	4.73	5.79	2.51	-0.88	1.73	14.65	0.654	1.2	0.545	6881	20.09	3,002	-2.45
Pokkali	3	0.98	15.21	-1.21	-0.64	1.77	2.81	4.44	8.67	0.641	1.798	0.356	4872	0.00	3,248	0.00

CSR 22	3	0.86	9.93	-4.78	8.21	-0.24	-0.31	-0.25	11.38	0.179	1.738	0.103	5566	6.94	3,130	-1.17
FL 478	3	-0.32	10.46	0.58	1.56	0.17	1.27	5.36	11.03	0.379	1.77	0.214	5160	2.88	2,970	-2.77
Swarna Sub 1	7	1.18	-10.14	-2.23	-1.16	-0.27	-0.03	0.29	15.87	0.589	1.035	0.569	7435	25.63	2,895	-3.53
IRRI 154	7	1.49	7.88	1.16	-1.84	0.91	2.86	10.47	17.02	0.654	1.045	0.626	5108	2.36	1,763	- 14.85

SES: Standard Evaluation System, SSI: Stress Susceptibility Index, PH: Plant height, PL: Panicle length, NGP: Number of grains per panicle, NPT : number of productive tillers per plant, %CH: per cent chaffyness, GYP: grain yield per panicle, TW : Test weight, YLD: yield kg/ha, %Na⁺: per cent sodium, %K⁺: per cent potassium, N: Grain yield under normal condition, % R: percent reduction, %G: per cent gain, S: grain yield under saline condition, % R or G : per cent reduction or gain,

SUMMARY AND CONCLUSIONS

VI. SUMMARY AND CONCLUSIONS

Rice is the world's most important food crop and a primary source of food for more than half the world's population. As a cereal grain, it is the most widely consumed staple food for a large part of the world's human population, especially in Asia. Globally, rice is cultivated in an area of about 161.40 million hectares with a production of about 515 million tonnes and productivity of 3.14 tonnes per hectare (Anon, 2015). Rice occupies a pivotal place in Indian agriculture and it contributes to around 17 per cent annual Gross Domestic Product (GDP) and provides 43 per cent calorie requirement for more than 70 per cent of the Indians. India ranks 1st in area (43.49 million hectares) and 2nd in production (106.54 million tonnes) after China (Anon, 2015). The average yield of rice in India is 2424 kg ha⁻¹. India exports 9.3 million tonnes of rice to the countries around the world (Anon, 2015).

Salinity is a serious problem affecting one third of all the irrigated land in the world (Mass and Hoffman, 1977) and is one of the major obstacles to increase production in rice growing areas worldwide. Area under salt stress is on the increase due to many factors including climate change, excessive irrigation without proper drainage in inlands, rise in sea levels *etc.*, vast areas of land are not utilized due to salinity and alkalinity problems. Rice is rated as an especially salt-sensitive crop (Shannon *et al.*, 1998). This problem needs to be tackled effectively which also includes the development of salt-tolerant varieties. Mutation is used as a prime strategy to improve the well-adapted plant varieties. In present study 57 M₆ mutants of two parent's viz., BPT-5204 and RP Bio-226 were evaluated at Agricultural Research Station, Gangavati during *kharif* 2016 with the following objectives

4. Evaluation of advanced M₆ mutants lines for salinity tolerance for yield and quality traits.
5. Association of traits in salt tolerant mutant lines.
6. Genotyping of salinity tolerant mutant through SSR markers.

The experimental results obtained in the present investigation are summarized below.

- In normal and saline conditions, the analysis of variance showed highly significant differences among the rice mutants for all the parameters studied in M₆ generation.

- The rice mutants exhibited high variability for the characters like number of grain per panicle (21.25%, 20.15%), panicle weight (25.54%,23.51%), panicle exertion (53.40%, 52.25%), panicle length, and test weight (21.26%, 20.60%), in normal soil condition (PCV, GCV), whereas, in the saline soil condition number of grains per panicle (20.85%, 19.59%), per cent chaffyness (47.83%, 46.24 %), grain yield per plant(22.36%,21.63%), panicle weight (26.76%, 25.92%) and panicle exertion (46.01%, 42.30%). PCV and GCV were found to be differing very narrowly indicating lesser influence of environment over these characters.
- These are traits which recorded higher heritability in the mutant genotype viz., number of productive tillers per plant (60.68%), number of grain per panicle (88.3%), per cent chaffyness (93.50%), panicle weight (93.8%), total number of tillers per plant(70.56%), length of flag leaf(76.2%), panicle exertion(84.6%), grain yield per hectare (80.1%), grain yield per plant(93.6%) and test weight (92.0%) in the saline soil. Number of grain per panicle(89.9%), per cent chaffyness (98.30%), panicle weight (84.80%), total number of tillers per plant (64.14%), length of flag leaf (73.9%), panicle exertion (95.7%), plant height (79.8%), yield(82.7%) grain yield per plant (91.8%) and test weight (93.9%) in normal soil condition exhibited high heritability coupled with high genetic advance over the mean indicating that simple selection scheme would be sufficient for these traits to bring genetic improvement in desired direction.
- In normal soil condition grain yield had positive and highly significant genotypic association with number of grains per panicle, total number of tillers and panicle exertion. In saline soil grain yield has strong association with panicle length, number of grains per panicle and panicle exertion, which revealed that selection based on these traits would ultimately improve grain yield.
- In normal soil condition grain yield had positive and highly significant phenotypic association with number of grains per panicle and panicle exertion. In saline soil grain yield has strong association with panicle length, number of grains per panicle and panicle exertion. Which revealed that selection based on these traits would ultimately improve grain yield

- Path coefficient analysis revealed that number of productive tillers, panicle length, panicle exertion and number of grains per panicle in normal and in saline soil condition number of productive tillers, panicle length, panicle exertion and test weight exhibited direct positive effect on grain yield. Hence, it would be rewarding to lay stress on these characters in selection programme for increasing yield.

Based on SSI, SES, Na^+/K^+ and per se performance of the genotypes In RP Bio-226 mutant lines, RP Bio-226-20, RP Bio-226-23, RP Bio-226-29, RP Bio-226-37, RP Bio-226-41, RP Bio-226-109, RP Bio-226-153, RP Bio-226-172 and RP Bio-226-199. Similarly in BPT-5204 mutant lines, BPT-5204-69, BPT-5204-94, BPT-5204-134 and BPT-5204-166 has recorded higher per cent gain in the yield with respect to per se performance with national check, Pokkali. These genotypes has recorded lesser SSI values for plant height, number of grains per panicle, panicle length, number of productive tillers per plant and grain yield per plant. These genotype has scored one in the standard Evaluation System, as they observed phenotypically high tolerance, The sodium potassium ratio also explains these genotype are highly tolerant to salinity, lesser the value of Na^+/K^+ in shoot higher the tolerance. The variety showed very low Na^+/K^+ which may be an indication that this variety shows saline tolerance when compared with all other. Low Na^+/K^+ of ion uptake is positively correlated with a high level of salt tolerance and can be taken into consideration as a desired characteristic while screening rice lines.

SSR markers profile resulted in 2 clusters are Cluster I consists four genotypes which are mainly susceptible checks, Cluster II consists 25 genotypes with included tolerant checks and mutant lines. Clusters through SSR data revealed that presence of genetic similarity at molecular level with genotypes. The polymorphism observed in SSR markers among rice mutants showed that effectiveness of this method in determining genetic variations between lines.

Conclusion

- The characters with high heritability such as panicle exertion, per cent chaffyness, grain yield per panicle, tiller number per plant, panicle weight, flag leaf length, panicle exertion in yield and yield attributed characters, grain length, grain breadth, grain shape (L/B ratio), and amylose content in quality parameters characters should be given top priority during selection of the tolerant genotypes and for further utilization as parents in breeding programme.
- These are the genotypes selected for M₆ program are RP Bio-226 mutant lines, RP Bio-226-20, RP Bio-226-23, RP Bio-226-29, RP Bio-226-37, RP Bio-226-41, RP Bio-226-109, RP Bio-226-153, RP Bio-226-172 and RP Bio-226-199. Similarly in BPT-5204 mutant lines, BPT-5204-69, BPT-5204-94, BPT-5204-134 and BPT-5204-166 these may be used in future breeding programme to achieve desired saline tolerant varieties with higher yield.
- As SSR or microsatellite markers are well known for constructing genetic maps, aiding in selection and studying genetic diversity in germplasms, they play a vital role in detecting salt tolerant gene to assist the plant breeder in developing new cultivars. Accordingly, these markers used in this study showed polymorphism for the rice genotypes RP Bio-226 -120, RP Bio-226 -37, RP Bio-226 -23 , RP Bio-226 -29, RP Bio-226 -153, RP Bio-226 -199, RP Bio-226 -41, RP Bio-226 -63, RP Bio-226 -172, RP Bio-226 -109, RP Bio-226 -191, RP Bio-226 -131, RP Bio-226 -151, RP Bio-226 -130, RP Bio-226 -63. BPT-5204-69, BPT-5204-94, BPT-5204-134, BPT-5204-38, BPT-5204-77, BPT-5204-10 and BPT-5204-166 which can be used further in breeding program.

Future line of work

- ❖ The desired mutant line for salinity tolerant selected in M₆ generation from BPT-5204 and RP-Bio 226 viz., RP Bio-226-20, RP Bio-226-23, RP Bio-226-29, RP Bio-226-37, RP Bio-226-41, RP Bio-226-109, RP Bio-226-153, RP Bio-226-172 and RP Bio-226-199, BPT-5204-69, BPT-5204-94, BPT-5204-134 and BPT-5204-166 will be advanced to next generation for further evaluation and to be used in further breeding programme.

- ❖ The selected saline tolerant M₆ mutant lines also confirmed by SSR markers, indicating phenotypic and genotypic correlation, these lines would be further evaluated in multi-location trials to assess the consistency in yield.

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VII. REFERENCES

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APPENDICES

APPENDIX – I

Mean performance of 64 mutant rice genotypes for yield and yield attributed traits in normal soil

Line Name	DFF	PH	PL	NGP	PW	NPT	TNT	LF	%CH	GYP	TW	PE	YLD
BPT-5204-10	101	97.50	23.10	211.00	14.40	17.00	21.55	28.74	3.72	31.20	12.80	2.45	7030
BPT-5204-15	95	99.00	20.85	196.45	13.47	10.50	13.18	27.50	4.57	28.70	12.73	4.20	6838
BPT-5204-16	101	94.00	22.28	181.30	18.12	15.00	17.31	28.25	9.77	35.04	12.55	3.00	6507
BPT-5204-22	103	96.50	23.50	180.40	11.17	11.00	13.27	26.90	3.38	28.60	12.55	1.80	6421
BPT-5204-29	103	96.00	20.15	268.60	9.53	11.50	14.83	25.00	2.36	26.80	13.35	2.45	7564
BPT-5204-37	103	101.00	22.30	231.80	13.96	14.75	17.07	24.50	12.84	29.50	13.15	2.35	7329
BPT-5204-38	101	93.50	22.70	149.20	8.56	14.53	18.71	28.43	3.32	34.60	12.25	4.90	5737
BPT-5204-42	102	100.50	22.90	176.80	15.96	14.50	17.35	29.40	2.88	28.00	12.49	3.15	6015
BPT-5204-46	101	94.50	22.35	180.20	11.62	13.75	16.90	29.75	3.39	27.40	12.53	3.10	6410
BPT-5204-57	101	100.00	23.30	208.60	16.16	19.00	22.30	30.50	23.80	33.60	12.78	3.90	6987
BPT-5204-60	102	100.00	24.00	205.00	13.25	14.60	17.57	26.23	3.43	28.40	12.75	3.00	6870
BPT-5204-67	105	96.50	23.00	169.60	14.28	10.00	12.00	32.70	3.09	31.80	12.35	2.90	5738

BPT-5204-69	100	93.00	23.15	149.40	14.70	13.50	17.40	25.00	7.06	33.00	12.25	1.75	5694
BPT-5204-77	101	97.50	23.45	212.20	13.76	12.50	15.60	28.65	5.12	44.60	12.60	3.55	6667
BPT-5204-88	101	95.50	22.18	179.20	14.07	15.00	17.81	29.50	21.59	31.50	12.51	3.80	6207
BPT-5204-94	101	89.00	22.50	212.80	16.72	13.50	17.30	27.58	4.35	37.60	12.60	1.60	6667
BPT-5204-96	102	100.00	23.00	178.00	10.65	14.65	17.77	29.00	3.20	29.60	12.50	2.45	6069
BPT-5204-98	101	98.00	23.50	196.20	13.42	12.95	15.78	28.55	5.70	29.20	12.66	2.35	6806
BPT-5204-103	102	103.00	23.10	206.60	11.25	13.70	16.72	27.73	5.53	30.60	12.75	0.50	6966
BPT-5204-115	103	93.00	23.28	171.20	9.52	14.61	16.25	28.01	3.42	32.60	12.37	4.90	5780
BPT-5204-128	101	92.50	21.62	205.00	14.25	9.88	11.82	28.40	6.45	28.40	12.75	1.70	6912
BPT-5204-130	101	96.50	22.25	196.54	10.15	13.85	16.26	27.73	4.06	31.40	12.85	3.75	7094
BPT-5204-134	101	98.50	21.30	299.40	15.81	19.00	24.20	28.09	7.25	30.80	13.75	3.45	9715
BPT-5204-139	101	112.50	25.80	196.30	19.38	8.50	11.50	26.50	1.93	27.20	12.70	1.00	6816
BPT-5204-149	103	99.00	23.50	215.20	7.50	11.52	13.30	30.85	1.62	36.60	13.05	3.75	7318
BPT-5204-158	101	92.00	22.05	181.40	17.33	11.00	15.20	27.00	14.61	18.80	12.75	2.55	6870
BPT-5204-165	101	93.50	23.18	238.20	10.31	11.00	13.62	29.50	4.36	30.20	13.20	5.00	7493
BPT-5204-166	101	87.50	24.59	294.60	16.98	20.50	23.80	25.75	3.62	39.80	13.55	3.75	7816

BPT-5204-183	104	120.50	21.25	143.20	14.90	12.00	13.50	28.90	31.51	28.52	12.40	3.00	5256
Rp Bio-226-18	99	93.00	22.60	209.80	11.25	10.50	15.20	22.50	11.75	24.80	12.80	2.90	6998
Rp Bio-226-23	92.25	90.70	22.30	213.10	12.81	15.05	17.84	27.00	3.50	32.15	13.05	4.35	7180
Rp Bio-226-29	93	92.00	21.60	207.20	15.17	13.50	17.58	25.50	3.01	36.20	12.75	1.80	6978
Rp Bio-226-37	92	87.10	25.70	213.00	14.26	12.50	15.80	23.50	1.67	23.20	12.65	1.95	6678
Rp Bio-226-41	94	94.50	22.50	235.40	14.10	16.45	19.46	24.50	3.47	28.40	13.15	5.70	7393
Rp Bio-226-45	97	101.00	23.40	197.20	15.13	16.25	19.10	24.68	11.25	29.00	12.99	5.75	7158
Rp Bio-226-57	98	96.50	22.23	264.00	17.38	13.50	16.90	22.00	7.77	30.40	13.35	2.80	7554
Rp Bio-226-63	97	95.50	23.82	283.40	11.64	13.50	16.92	25.00	2.69	34.40	13.35	1.90	7568
Rp Bio-226-65	96	94.50	23.15	214.00	21.36	13.50	17.22	23.08	13.21	31.40	13.05	1.80	7274
Rp Bio-226-78	99	91.50	23.78	179.00	13.27	12.50	15.73	24.58	1.51	34.80	12.50	1.90	6111
Rp Bio-226-83	98	95.00	23.55	233.60	16.02	13.98	17.66	26.75	6.66	31.60	13.15	1.00	7329
Rp Bio-226-90	99	94.50	25.32	175.20	21.12	11.12	14.50	26.08	7.12	29.55	12.45	3.45	5898
Rp Bio-226-103	99	93.00	22.83	277.00	24.73	12.50	16.75	26.58	5.27	29.60	12.25	2.65	4872
Rp Bio-226-109	97	98.50	23.00	237.60	15.30	12.50	15.80	22.50	2.60	31.30	13.15	3.35	7489
Rp Bio-226-115	97	92.50	23.83	214.40	13.96	15.87	19.05	23.00	6.38	32.60	13.05	1.60	7276

Rp Bio-226-120	91	86.90	23.10	193.60	14.40	14.02	16.70	25.05	4.94	26.80	12.65	3.90	6706
Rp Bio-226-130	97	99.00	22.10	260.00	14.59	14.00	17.10	23.58	4.73	37.20	13.35	3.55	7511
Rp Bio-226-131	97	79.70	22.50	196.87	17.36	12.75	15.18	21.06	10.56	33.10	12.95	1.60	7132
Rp Bio-226-147	98	96.00	22.78	213.20	11.57	13.38	16.25	22.75	6.79	41.80	13.05	5.80	7265
Rp Bio-226-151	97	99.50	22.60	291.00	16.01	11.15	15.63	27.25	3.73	30.40	13.35	1.60	7607
Rp Bio-226-152	98	93.50	22.55	149.60	15.04	14.00	17.08	24.25	8.25	35.32	12.25	4.00	5673
Rp Bio-226-153	93	95.00	22.78	195.00	13.91	14.50	17.07	26.50	7.47	28.20	12.65	1.70	6774
Rp Bio-226-159	99	95.50	23.25	205.60	16.30	11.00	14.60	23.95	11.78	31.40	12.75	3.00	6934
Rp Bio-226-168	100	93.00	23.06	175.40	17.39	14.55	18.77	29.66	8.71	45.80	12.48	1.90	5919
Rp Bio-226-172	97	95.00	23.65	297.60	14.53	13.38	17.12	25.78	4.73	34.20	13.71	2.00	7901
Rp Bio-226-190	99.5	94.50	22.89	193.60	10.68	12.50	16.70	22.50	5.46	39.63	12.65	2.55	6710
Rp Bio-226-191	97	96.50	23.60	293.20	16.05	11.88	15.98	25.00	2.89	26.60	13.37	3.35	7767
Rp Bio-226-199	94	93.00	22.62	196.48	10.89	13.00	17.25	23.50	6.91	30.00	12.85	1.80	7073
BPT 5204	108	72.50	17.00	204.00	10.44	16.00	18.85	24.60	3.15	27.20	13.15	0.00	3654
Rp -BIO 226	114	91.50	23.25	215.00	10.99	16.00	19.05	25.00	2.45	18.06	13.65	0.00	6881
POKKALI	105	159.00	28.00	135.60	25.16	10.50	12.50	40.50	2.42	23.80	30.80	0.00	4872

CSR 22	105	95.00	24.50	152.00	14.02	14.50	16.50	26.50	6.16	23.40	20.25	2.20	5566
FL 478	115	80.00	19.00	360.00	9.21	15.15	21.50	21.50	3.89	32.40	19.55	0.00	5160
Swarna Sub 1	113.5	78.00	20.00	250.00	16.16	14.81	16.13	26.50	15.43	31.00	23.20	1.00	7435
IRRI 154	125	71.50	19.50	220.00	9.19	16.25	19.76	22.80	6.80	35.20	13.95	0.50	5108

DFF : Days to 50 per cent flowering, NPT : Number of productive tillers per plant, TW : Test weight (g), PE : Panicle exertion (cm), YLD : Yield per hectare,
 TNT : Total number of tillers, LF : Length of flag leaf (cm), %CH : Per cent chaffyness (%), GYP : Grain yield per plant, PH : Plant height (cm), PL : Panicle
 length (cm), NGP: Number of grains per panicle, PW : Panicle weight (g)

APPENDIX - II

Mean performance of 64 mutant rice genotypes for yield and yield attributed traits in saline soil

line name	DFF	PH	PL	NGP	PW	NPT	TNT	LF	%CH	GYP	TW	PE	YLD
BPT-5204-10	108	84.50	23.60	199.00	7.84	13.00	16.95	26.50	30.25	24.60	12.40	5.30	4,113
BPT-5204-15	116	77.50	22.00	184.45	16.76	12.00	15.00	27.25	18.07	30.60	12.80	3.30	3,411
BPT-5204-16	110	80.00	23.90	169.30	6.25	16.05	19.96	28.88	12.31	24.20	12.78	4.45	4,060
BPT-5204-22	107	77.00	23.60	168.40	14.20	15.50	18.75	26.56	7.27	25.43	12.49	4.10	3,483
BPT-5204-29	113	78.50	21.00	256.60	9.62	13.50	16.88	25.95	14.76	25.20	13.50	3.80	3,451
BPT-5204-37	110	79.50	22.60	219.80	10.47	14.05	16.62	30.50	16.51	32.30	12.65	0.50	3,490
BPT-5204-38	110	85.00	22.60	137.20	8.77	15.40	18.77	27.50	27.76	24.14	12.65	2.60	4,081
BPT-5204-42	106	86.40	23.20	164.80	12.30	13.68	16.21	27.50	24.77	20.00	12.43	6.85	3,697
BPT-5204-46	110	76.50	22.40	168.20	8.33	13.65	16.05	26.11	26.18	26.00	12.35	4.37	4,049
BPT-5204-57	106	78.50	23.60	196.60	12.05	13.00	15.55	29.51	21.56	18.19	12.60	4.75	3,739
BPT-5204-60	105	82.60	20.90	193.00	7.86	13.13	15.12	27.00	21.74	31.20	13.40	5.49	3,622
BPT-5204-67	109	86.10	22.80	157.60	8.60	13.00	16.65	32.00	18.01	32.40	12.55	4.75	3,280
BPT-5204-69	101	81.00	23.50	137.40	10.75	15.55	18.62	26.25	50.14	21.40	12.20	4.45	4,252
BPT-5204-77	107	77.50	23.40	200.20	11.81	9.00	10.80	27.50	28.27	21.54	12.35	5.25	4,178

BPT-5204-88	109	77.00	22.00	167.20	9.00	13.40	16.10	29.53	27.29	24.40	12.19	4.94	3,793
BPT-5204-94	100	75.00	21.20	200.80	13.33	18.55	22.63	27.90	32.57	31.60	12.23	5.15	4,231
BPT-5204-96	109	78.50	21.70	166.00	15.74	14.00	17.11	28.90	29.54	26.20	12.65	4.47	3,611
BPT-5204-98	109	75.50	23.40	184.20	9.28	11.75	15.10	26.24	31.12	16.80	12.28	4.60	3,793
BPT-5204-103	110	77.50	23.00	194.60	11.66	13.60	16.68	27.30	18.79	23.00	12.99	0.00	3,590
BPT-5204-115	105	82.00	22.80	159.20	8.08	15.90	19.50	28.13	12.18	24.40	12.33	4.25	3,483
BPT-5204-128	110	78.00	22.70	193.00	10.81	10.00	13.65	27.06	41.33	21.80	12.60	4.40	3,862
BPT-5204-130	107	73.50	23.40	184.54	10.23	10.50	12.95	29.15	16.97	21.00	12.15	4.44	3,846
BPT-5204-134	106	77.00	21.40	287.40	10.57	13.50	16.05	28.50	29.03	22.40	12.23	5.15	4,135
BPT-5204-139	109	97.50	25.80	184.30	18.77	12.75	15.92	31.00	9.40	23.00	12.53	0.00	4,081
BPT-5204-149	113	77.00	23.20	203.20	10.10	11.06	14.27	26.78	19.99	28.60	12.99	4.10	3,475
BPT-5204-158	103	83.00	21.60	169.40	11.11	17.65	22.90	27.75	45.13	30.60	12.10	4.55	4,220
BPT-5204-165	110	73.50	22.10	226.20	8.23	12.66	15.67	28.00	12.88	25.60	12.50	5.30	4,008
BPT-5204-166	101	83.00	24.20	282.60	13.19	16.00	19.60	29.85	25.62	32.40	12.75	3.60	4,209
BPT-5204-183	125	112.40	21.80	131.20	12.01	15.00	18.65	28.95	28.70	29.40	12.45	4.00	3,312
Rp Bio-226-18	109	84.60	22.00	197.80	9.06	15.00	17.85	22.55	23.65	8.80	12.43	3.95	4,444
Rp Bio-226-23	107	86.90	22.75	201.10	10.63	12.95	16.00	27.20	10.15	30.80	13.40	4.35	5,427

Rp Bio-226-29	104	84.00	21.59	195.20	9.04	17.00	20.50	26.96	15.56	24.40	12.66	4.70	5,395
Rp Bio-226-37	104	87.35	26.00	201.00	11.08	16.50	18.50	23.65	14.63	26.40	13.25	3.25	5,725
Rp Bio-226-41	109	79.00	22.19	223.40	6.89	16.50	18.90	28.00	29.24	18.20	13.05	3.45	4,947
Rp Bio-226-45	105	89.50	23.50	185.20	6.00	14.90	17.38	25.27	3.74	23.00	12.73	4.19	4,519
Rp Bio-226-57	109	85.00	22.40	252.00	9.36	17.00	20.00	25.50	26.53	38.20	12.45	2.40	4,509
Rp Bio-226-63	109	80.50	23.60	271.40	8.85	16.60	21.15	28.50	26.59	28.90	12.55	3.85	4,530
Rp Bio-226-65	105	79.00	23.15	202.00	13.72	16.00	18.95	26.90	19.71	26.40	12.75	3.50	4,926
Rp Bio-226-78	109	85.70	23.30	167.00	17.48	15.00	17.73	23.70	17.87	24.60	11.85	4.05	4,413
Rp Bio-226-83	108	87.00	22.20	221.60	12.12	13.30	17.50	26.05	45.72	28.20	12.20	2.65	4,487
Rp Bio-226-90	110	80.50	22.80	163.20	10.37	11.60	14.88	26.60	45.97	26.20	12.00	4.50	4,412
Rp Bio-226-103	108	75.50	22.60	265.00	14.89	19.00	22.15	26.45	9.93	31.60	12.20	4.55	4,402
Rp Bio-226-109	109	80.00	23.00	225.60	9.45	14.50	16.50	29.50	29.13	23.90	12.85	2.55	4,755
Rp Bio-226-115	105	86.20	23.60	202.40	12.15	14.40	16.70	28.50	31.13	24.80	12.51	2.55	4,519
Rp Bio-226-120	107	85.45	23.00	181.60	13.60	14.30	16.75	25.45	13.94	23.40	13.55	3.60	6,166
Rp Bio-226-130	105	81.00	22.70	248.00	11.05	16.05	20.00	25.75	27.35	24.60	12.95	3.61	4,605
Rp Bio-226-131	107	84.40	22.40	184.87	12.69	12.50	15.50	23.00	17.70	28.20	12.25	2.40	4,701
Rp Bio-226-147	105	88.00	22.00	201.20	7.61	16.00	19.50	29.00	41.35	10.80	13.20	3.55	4,509

Rp Bio-226-151	106	74.50	21.80	279.00	10.61	11.20	14.55	27.45	13.04	28.76	12.80	3.70	4,605
Rp Bio-226-152	108	85.30	22.60	137.60	6.71	12.50	16.50	24.00	32.48	28.20	12.45	2.95	4,477
Rp Bio-226-153	108	84.00	22.69	183.00	12.04	18.00	20.50	17.00	30.12	29.00	13.05	3.95	5,203
Rp Bio-226-159	109	81.50	23.40	193.60	11.61	11.70	13.88	24.25	23.43	23.80	12.28	4.50	4,428
Rp Bio-226-168	100.5	86.70	22.70	163.40	13.66	12.55	15.72	28.00	36.61	33.65	12.40	5.20	4,263
Rp Bio-226-172	106	83.50	22.89	285.60	10.09	11.80	14.80	25.75	17.17	23.00	13.00	3.85	4,872
Rp Bio-226-190	99.5	84.30	22.70	181.60	9.60	12.90	15.71	22.70	37.06	23.40	12.48	4.00	4,263
Rp Bio-226-191	107	77.00	23.20	281.20	15.84	11.20	14.00	29.50	22.41	29.60	12.70	3.35	4,733
Rp Bio-226-199	107	87.00	22.75	184.48	10.27	17.55	20.05	27.00	18.60	30.80	13.75	3.90	5,128
BPT 5204	123	66.50	19.75	192.00	7.08	12.75	16.60	21.00	28.42	18.60	12.90	0.00	3,045
Rp -BIO 226	111	67.00	21.25	203.00	7.15	19.00	23.00	21.00	18.04	21.20	12.99	1.00	3,002
POKKALI	110	136.95	22.75	123.60	8.91	10.00	12.70	38.50	12.96	10.80	26.70	0.00	3,248
CSR 22	104	83.50	21.50	140.00	7.03	11.75	19.50	31.50	2.50	24.80	20.45	1.80	3,130
FL 478	128	83.58	16.55	167.50	6.81	15.50	19.50	20.55	5.50	24.40	16.45	0.00	2,970
Swarna Sub 1	117	65.00	22.50	172.00	9.24	13.50	16.55	26.73	5.03	31.20	23.00	2.00	2,895
IRRI 154	125	56.50	17.61	197.50	9.83	17.00	20.00	21.00	22.23	15.60	9.60	0.00	1,763

DFF : Days to 50 per cent flowering, NPT : Number of productive tillers per plant, TW : Test weight (g), PE : Panicle exertion (cm), YLD : Yield per hectare, TNT : Total number of tillers, LF : Length of flag leaf (cm), %CH : Per cent chaffyness (%), GYP : Grain yield per plant, PH : Plant height (cm), PL : Panicle length (cm), NGP: Number of grains per panicle, PW : Panicle weight (g)

Genotypes	SES	SSI								LEAF Na ⁺ /K ⁺			Per se performance of yield			
	score	PH	PL	NGP	NPT	%CH	GYP	TW	YLD	% Na ⁺	% K ⁺	Na ⁺ / K ⁺	N	% R or G	S	% R or G
BPT-5204-10	1	0.95	-1.74	-5.93	-3.11	2.89	1.09	1.04	10.79	0.613	2.484	0.247	7030	21.58	4,113	8.66
BPT-5204-15	1	1.54	-4.46	3.60	1.89	1.18	-0.34	-0.26	13.03	0.23	2.21	0.104	6838	19.66	3,411	1.64
BPT-5204-16	1	1.06	-5.80	1.77	0.93	0.10	1.59	-0.48	9.78	0.364	2.143	0.17	6507	16.35	4,060	8.12
BPT-5204-22	1	1.43	-0.33	10.32	5.41	0.46	0.57	0.29	11.90	0.258	2.277	0.113	6421	15.49	3,483	2.35
BPT-5204-29	1	1.29	-3.40	4.39	2.30	2.08	0.31	-0.25	14.14	0.256	2.31	0.111	7564	26.92	3,451	2.03
BPT-5204-37	1	1.51	-1.09	-1.20	-0.63	0.12	-0.49	1.39	13.62	0.654	1.97	0.332	7329	24.57	3,490	2.43
BPT-5204-38	1	0.64	0.38	1.51	0.77	2.99	1.55	-0.95	7.50	0.614	2.298	0.267	5737	8.65	4,081	8.34
BPT-5204-42	1	0.99	-1.05	-1.44	-0.75	3.04	1.47	0.19	10.02	0.256	2.456	0.104	6015	11.43	3,697	4.49
BPT-5204-46	1	1.35	-0.16	-0.18	-0.10	2.70	0.26	0.40	9.57	0.309	2.089	0.148	6410	15.38	4,049	8.02
BPT-5204-57	1	1.52	-1.03	-7.96	-4.18	-0.04	2.36	0.52	12.08	0.317	2.593	0.122	6987	21.15	3,739	4.92
BPT-5204-60	1	1.23	10.48	-2.54	-1.33	2.17	-0.51	-1.56	12.29	0.253	2.155	0.117	6870	19.98	3,622	3.75
BPT-5204-67	1	0.76	0.72	7.57	3.97	1.94	-0.10	-0.40	11.13	0.245	1.761	0.139	5738	8.66	3,280	0.32
BPT-5204-69	1	0.91	-1.21	3.83	2.01	2.44	1.81	0.27	6.58	0.688	2.526	0.272	5694	8.22	4,252	10.05
BPT-5204-77	1	1.45	0.19	-7.06	-3.70	1.83	2.66	0.66	9.71	0.299	2.21	0.135	6667	17.95	4,178	9.30
BPT-5204-88	1	1.37	0.75	-2.69	-1.41	0.11	1.16	0.83	10.11	0.293	2.841	0.103	6207	13.35	3,793	5.45
BPT-5204-94	1	1.12	4.71	9.43	5.88	2.58	0.82	0.98	9.50	0.479	2.592	0.185	6667	17.95	4,231	9.83
BPT-5204-96	1	1.52	4.59	-1.12	-0.59	3.32	0.59	-0.40	10.53	0.289	2.34	0.124	6069	11.97	3,611	3.64

BPT-5204-98	1	1.63	0.36	-2.34	-1.23	1.80	2.18	1.10	11.51	0.273	2.358	0.116	6806	19.34	3,793	5.45
BPT-5204-103	1	1.75	0.37	-0.18	-0.10	0.97	1.28	-0.50	12.60	0.296	2.31	0.128	6966	20.94	3,590	3.42
BPT-5204-115	1	0.84	1.76	2.24	1.18	1.04	1.29	0.19	10.33	0.122	1.041	0.118	5780	9.08	3,483	2.35
BPT-5204-128	1	1.11	-4.11	0.31	0.13	2.16	1.19	0.52	11.47	0.392	2.326	0.169	6912	20.40	3,862	6.15
BPT-5204-130	1	1.69	-4.18	-6.10	-3.20	1.27	1.70	1.94	11.90	0.312	2.5	0.125	7094	22.22	3,846	5.99
BPT-5204-134	1	1.55	-0.36	-7.30	-3.83	1.22	1.40	3.79	14.93	0.557	2.229	0.25	9715	48.43	4,135	8.87
BPT-5204-139	1	0.95	0.02	12.61	6.61	1.59	0.79	0.45	10.43	0.32	2.3	0.139	6816	19.44	4,081	8.34
BPT-5204-149	1	1.58	1.05	-1.01	-0.51	4.63	1.12	0.28	13.65	0.213	2.01	0.106	7318	24.46	3,475	2.28
BPT-5204-158	5	0.69	1.67	15.24	10.22	0.84	-3.23	1.82	10.03	0.798	1.59	0.502	6870	19.98	4,220	9.73
BPT-5204-165	1	1.52	3.85	3.81	2.00	0.78	0.78	1.77	12.09	0.302	2.479	0.122	7493	26.21	4,008	7.60
BPT-5204-166	1	0.36	1.34	-5.54	-2.90	2.47	0.96	2.08	11.99	0.617	2.629	0.235	7816	29.44	4,209	9.62
BPT-5204-183	1	0.48	-2.08	6.30	3.31	-0.04	-0.16	-0.13	9.62	0.237	2.259	0.105	5256	3.84	3,312	0.64
Rp Bio-226-18	5	0.64	2.17	10.81	5.67	0.41	3.32	0.96	9.49	0.644	1.933	0.333	6998	21.26	4,444	11.97
Rp Bio-226-23	1	0.30	-1.64	-3.52	-1.85	0.77	0.21	-0.76	6.34	0.441	2.519	0.175	7180	23.08	5,427	21.80
Rp Bio-226-29	1	0.62	0.02	6.54	3.43	1.69	1.68	0.36	5.90	0.583	2.723	0.214	6978	21.06	5,395	21.48
Rp Bio-226-37	1	-0.02	-0.95	8.07	4.23	3.07	-0.71	-1.44	3.71	0.578	2.421	0.239	6678	18.06	5,725	24.77

Rp Bio-226-41	1	1.16	1.10	0.08	0.04	2.96	1.85	0.38	8.60	0.535	2.62	0.204	7393	25.21	4,947	16.99
Rp Bio-226-45	1	0.81	-0.33	-2.10	-1.10	-0.27	1.06	0.69	9.58	0.474	2.3	0.206	7158	22.86	4,519	12.72
Rp Bio-226-57	1	0.85	-0.53	6.54	3.43	0.97	-1.32	2.36	10.48	0.766	2.383	0.322	7554	26.82	4,509	12.61
Rp Bio-226-63	1	1.11	0.70	5.79	4.90	3.57	0.82	2.11	10.44	0.608	2.852	0.213	7568	26.96	4,530	12.82
Rp Bio-226-65	1	1.16	0.00	4.67	2.45	0.20	0.82	0.89	8.39	0.234	1.7	0.138	7274	24.02	4,926	16.78
Rp Bio-226-78	1	0.45	1.72	5.04	2.65	4.40	1.51	1.73	7.23	0.853	3.535	0.241	6111	12.39	4,413	11.65
Rp Bio-226-83	5	0.60	4.67	-1.22	-0.66	2.35	0.55	2.52	10.08	0.75	2.479	0.303	7329	24.57	4,487	12.40
Rp Bio-226-90	5	1.05	8.02	1.09	0.60	2.21	0.58	1.33	6.55	1.203	2.409	0.499	5898	10.26	4,412	11.65
Rp Bio-226-103	5	1.33	0.91	13.11	6.88	0.35	-0.35	0.27	2.51	1.359	2.617	0.519	4872	0.00	4,402	11.55
Rp Bio-226-109	1	1.33	0.02	4.03	2.12	4.11	1.22	0.88	9.49	1.018	2.617	0.389	7489	26.17	4,755	15.07
Rp Bio-226-115	1	0.48	0.87	-2.33	-1.21	1.56	1.23	1.50	9.85	0.835	2.533	0.33	7276	24.04	4,519	12.72
Rp Bio-226-120	1	0.12	0.35	0.51	0.28	0.74	0.65	-2.23	2.09	0.236	2.31	0.102	6706	18.34	6,166	29.18
Rp Bio-226-130	1	1.29	-2.18	3.69	1.94	1.94	1.74	1.12	10.06	0.596	2.31	0.258	7511	26.39	4,605	13.57
Rp Bio-226-131	1	-0.42	0.38	-0.49	-0.26	0.27	0.76	1.92	8.86	0.801	2.877	0.278	7132	22.60	4,701	14.53
Rp Bio-226-147	1	0.59	2.86	4.95	2.57	2.05	3.81	-0.25	9.86	0.663	2.662	0.249	7265	23.93	4,509	12.61
Rp Bio-226-151	1	1.78	2.89	0.11	0.06	1.02	0.28	1.49	10.26	0.431	2.845	0.152	7607	27.35	4,605	13.57

Rp Bio-226-152	1	0.62	-0.16	-2.70	-1.42	1.17	1.03	-0.41	5.48	0.732	2.91	0.252	5673	8.01	4,477	12.29
Rp Bio-226-153	1	0.82	0.37	6.09	7.30	1.22	-0.15	-0.92	6.03	0.889	2.455	0.362	6774	19.02	5,203	19.56
Rp Bio-226-159	1	1.04	-0.51	1.61	0.84	0.40	1.24	1.35	9.40	0.772	2.646	0.292	6934	20.62	4,428	11.81
Rp Bio-226-168	1	0.48	1.25	-3.47	-1.82	1.29	1.36	0.27	7.27	0.779	3.511	0.222	5919	10.47	4,263	10.15
Rp Bio-226-172	1	0.86	2.59	-2.98	-1.58	1.07	1.68	1.70	9.97	0.792	2.118	0.374	7901	30.29	4,872	16.24
Rp Bio-226-190	1	0.77	0.73	0.81	0.42	2.31	2.10	0.58	9.48	0.576	2.91	0.198	6710	18.38	4,263	10.15
Rp Bio-226-191	1	1.43	1.39	-1.44	-0.78	2.71	-0.58	1.74	10.16	0.804	2.482	0.324	7767	28.95	4,733	14.85
Rp Bio-226-199	1	0.46	-0.54	8.83	8.65	0.68	-0.14	-2.20	7.15	0.519	2.797	0.185	7073	22.01	5,128	18.81
BPT 5204	7	0.59	-13.12	-5.12	0.83	3.29	1.63	0.76	4.33	0.745	1.251	0.596	3654	-12.18	3,045	-2.03
Rp -BIO 226	7	1.90	6.98	4.73	5.79	2.51	-0.88	1.73	14.65	0.654	1.2	0.545	6881	20.09	3,002	-2.45
Pokkali	3	0.98	15.21	-1.21	-0.64	1.77	2.81	4.44	8.67	0.641	1.798	0.356	4872	0.00	3,248	0.00
CSR 22	3	0.86	9.93	-4.78	8.21	-0.24	-0.31	-0.25	11.38	0.179	1.738	0.103	5566	6.94	3,130	-1.17
FL 478	3	-0.32	10.46	0.58	1.56	0.17	1.27	5.36	11.03	0.379	1.77	0.214	5160	2.88	2,970	-2.77
Swarna Sub 1	7	1.18	-10.14	-2.23	-1.16	-0.27	-0.03	0.29	15.87	0.589	1.035	0.569	7435	25.63	2,895	-3.53
IRRI 154	7	1.49	7.88	1.16	-1.84	0.91	2.86	10.47	17.02	0.654	1.045	0.626	5108	2.36	1,763	-14.85

APPENDIX- III

Grain shape, kernel length and amylose content of mutants in normal soil

Genotype	Grain shape	KL	L/B	AC	Designation
BPT-5204-10	MS	5.31	2.89	24.65	Intermediate
BPT-5204-15	MS	5.23	2.99	22.80	Intermediate
BPT-5204-16	MS	5.21	2.80	23.36	Intermediate
BPT-5204-22	MS	5.23	2.99	25.25	High
BPT-5204-29	MS	5.33	2.96	21.92	Intermediate
BPT-5204-37	MS	5.41	2.93	25.25	High
BPT-5204-38	MS	5.31	2.88	22.35	Intermediate
BPT-5204-42	MS	5.26	2.72	22.25	Intermediate
BPT-5204-46	MS	5.11	2.73	21.75	Intermediate
BPT-5204-57	MS	5.21	2.70	23.65	Intermediate
BPT-5204-60	MS	5.31	2.73	23.15	Intermediate
BPT-5204-67	MS	5.43	2.94	21.92	Intermediate
BPT-5204-69	MS	5.41	3.00	21.92	Intermediate
BPT-5204-77	MS	5.41	2.99	23.75	Intermediate
BPT-5204-88	MS	5.41	2.82	23.15	Intermediate
BPT-5204-94	MS	5.21	2.89	22.27	Intermediate
BPT-5204-96	MS	5.41	3.00	23.01	Intermediate
BPT-5204-98	MS	5.21	2.73	23.00	Intermediate
BPT-5204-103	MS	5.41	3.00	26.05	High
BPT-5204-115	MS	5.43	3.00	26.35	High
BPT-5204-128	MS	5.41	2.86	24.80	Intermediate
BPT-5204-130	MS	5.31	2.80	22.40	Intermediate

BPT-5204-134	MS	5.31	2.91	24.53	Intermediate
BPT-5204-139	MS	5.41	2.92	23.45	Intermediate
BPT-5204-149	MS	5.43	2.86	24.05	Intermediate
BPT-5204-158	MS	5.16	2.95	22.80	Intermediate
BPT-5204-165	MS	5.36	2.90	24.48	Intermediate
BPT-5204-166	MS	5.43	3.02	22.80	Intermediate
BPT-5204-183	MS	5.21	2.89	22.14	Intermediate
Rp Bio-226-18	MS	5.21	2.82	24.73	Intermediate
Rp Bio-226-23	MS	5.16	3.00	23.39	Intermediate
Rp Bio-226-29	MS	5.21	2.82	22.75	Intermediate
Rp Bio-226-37	MS	5.31	3.00	24.23	Intermediate
Rp Bio-226-41	MS	5.16	2.95	24.30	Intermediate
Rp Bio-226-45	MS	5.21	2.89	24.95	Intermediate
Rp Bio-226-57	MS	5.21	2.98	22.03	Intermediate
Rp Bio-226-63	MS	5.31	2.95	23.00	Intermediate
Rp Bio-226-65	MS	5.16	2.79	24.14	Intermediate
Rp Bio-226-78	MS	5.21	2.90	22.54	Intermediate
Rp Bio-226-83	MS	5.31	2.95	24.52	Intermediate
Rp Bio-226-90	MS	5.41	2.94	24.70	Intermediate
Rp Bio-226-103	MS	5.41	2.99	24.80	Intermediate
Rp Bio-226-109	MS	5.31	2.87	21.63	Intermediate
Rp Bio-226-115	MS	5.36	2.99	24.48	Intermediate
Rp Bio-226-120	SS	5.41	3.09	24.63	Intermediate
Rp Bio-226-130	SS	5.21	3.16	21.99	Intermediate
Rp Bio-226-131	MS	5.41	2.92	22.58	Intermediate

Rp Bio-226-147	MS	5.21	2.82	22.95	Intermediate
Rp Bio-226-151	MS	5.31	2.87	22.04	Intermediate
Rp Bio-226-152	MS	5.36	2.90	23.73	Intermediate
Rp Bio-226-153	MS	5.28	3.00	23.64	Intermediate
Rp Bio-226-159	MS	5.26	2.92	22.80	Intermediate
Rp Bio-226-168	MS	5.21	2.89	24.85	Intermediate
Rp Bio-226-172	MS	5.11	2.69	21.38	Intermediate
Rp Bio-226-190	SS	5.11	3.10	24.99	Intermediate
Rp Bio-226-191	MS	5.16	2.65	22.50	Intermediate
Rp Bio-226-199	MS	5.05	2.75	24.10	Intermediate
BPT 5204	MS	5.05	2.80	23.80	Intermediate
Rp -BIO 226	SB	5.20	2.31	27.00	Intermediate
Pokkali	LS	6.60	3.64	23.10	Intermediate
CSR 22	SS	5.10	3.12	25.23	High
FL 478	LS	6.60	3.84	25.23	High
Swarna Sub 1	MS	5.03	3.20	22.50	Intermediate

Grain shape, kernel length and amylose content of mutants in saline soil

Genotype	Grain shape	KL	L/B	AC	Designation
BPT-5204-10	MS	5.25	2.86	24.40	Intermediate
BPT-5204-15	MS	5.15	2.94	22.30	Intermediate
BPT-5204-16	MS	5.15	2.77	22.90	Intermediate
BPT-5204-22	MS	5.15	2.95	24.80	Intermediate
BPT-5204-29	MS	5.25	2.92	21.40	Intermediate
BPT-5204-37	MS	5.35	2.89	24.80	Intermediate
BPT-5204-38	MS	5.25	2.85	22.10	Intermediate
BPT-5204-42	MS	5.20	2.69	21.80	Intermediate
BPT-5204-46	MS	5.05	2.70	21.30	Intermediate
BPT-5204-57	MS	5.15	2.68	23.20	Intermediate
BPT-5204-60	MS	5.25	2.70	22.70	Intermediate
BPT-5204-67	MS	5.35	2.89	21.40	Intermediate
BPT-5204-69	MS	5.35	3.00	21.60	Intermediate
BPT-5204-77	MS	5.35	2.96	23.50	Intermediate
BPT-5204-88	MS	5.35	2.79	22.70	Intermediate
BPT-5204-94	MS	5.15	2.86	22.00	Intermediate
BPT-5204-96	MS	5.35	2.97	22.50	Intermediate
BPT-5204-98	MS	5.15	2.70	22.50	Intermediate
BPT-5204-103	MS	5.35	3.00	25.60	High
BPT-5204-115	MS	5.35	2.97	25.90	High
BPT-5204-128	MS	5.35	2.83	24.30	Intermediate
BPT-5204-130	MS	5.25	2.77	21.90	Intermediate
BPT-5204-134	MS	5.25	2.88	24.20	Intermediate

BPT-5204-139	MS	5.35	2.89	23.00	Intermediate
BPT-5204-149	MS	5.35	2.82	23.60	Intermediate
BPT-5204-158	MS	5.10	2.92	22.50	Intermediate
BPT-5204-165	MS	5.20	2.77	25.00	Intermediate
BPT-5204-166	MS	5.30	2.87	24.20	Intermediate
BPT-5204-183	MS	5.35	2.97	22.30	Intermediate
Rp Bio-226-18	MS	5.15	2.86	21.70	Intermediate
Rp Bio-226-23	MS	5.20	2.81	24.20	Intermediate
Rp Bio-226-29	MS	5.15	3.00	22.90	Intermediate
Rp Bio-226-37	MS	5.20	2.81	22.30	Intermediate
Rp Bio-226-41	MS	5.25	3.00	23.70	Intermediate
Rp Bio-226-45	MS	5.10	2.92	23.80	Intermediate
Rp Bio-226-57	MS	5.15	2.86	24.60	Intermediate
Rp Bio-226-63	MS	5.15	2.95	21.50	Intermediate
Rp Bio-226-65	MS	5.25	2.92	22.50	Intermediate
Rp Bio-226-78	MS	5.10	2.76	23.70	Intermediate
Rp Bio-226-83	MS	5.15	2.87	22.10	Intermediate
Rp Bio-226-90	MS	5.25	2.92	24.10	Intermediate
Rp Bio-226-103	MS	5.35	3.00	24.30	Intermediate
Rp Bio-226-109	MS	5.35	3.00	24.30	Intermediate
Rp Bio-226-115	MS	5.25	2.84	21.10	Intermediate
Rp Bio-226-120	MS	5.35	2.99	24.00	Intermediate
Rp Bio-226-130	SS	5.35	3.06	24.10	Intermediate
Rp Bio-226-131	SS	5.15	3.12	21.50	Intermediate
Rp Bio-226-147	MS	5.35	2.89	22.20	Intermediate

Rp Bio-226-151	MS	5.15	2.79	22.50	Intermediate
Rp Bio-226-152	MS	5.25	2.84	21.60	Intermediate
Rp Bio-226-153	MS	5.35	2.89	23.20	Intermediate
Rp Bio-226-159	MS	5.25	2.98	23.20	Intermediate
Rp Bio-226-168	MS	5.20	2.89	22.40	Intermediate
Rp Bio-226-172	MS	5.15	2.86	24.40	Intermediate
Rp Bio-226-190	MS	5.05	2.66	21.00	Intermediate
Rp Bio-226-191	SS	5.05	3.06	24.50	Intermediate
Rp Bio-226-199	MS	5.15	2.64	22.00	Intermediate
BPT 5204	MS	5.09	2.76	24.10	Intermediate
Rp -BIO 226	MS	5.07	2.83	22.80	Intermediate
Pokkali	SB	5.22	2.32	25.90	High
CSR 22	LS	6.40	3.29	21.90	Intermediate
FL 478	SS	5.00	3.10	25.23	High
Swarna Sub 1	LS	6.50	3.98	23.66	High
BPT-5204-10	MS	5.03	3.25	22.30	Intermediate

APPENDIX – IV

Weather data of Agricultural Research Station, Gangavathi during January 2016 to April 2017

Standard week	Months	Maximum temperature (°C)	Minimum temperature (°C)	Rainfall (mm)	Rainy day
1	Jan 01-07	31.6	16.8	0	0
2	Jan 08-14	30.9	15.3	0	0
3	Jan 15-21	29.6	18.6	1.4	0
4	Jan 22-28	31.5	20.0	0	0
5	Jan 29-Feb	35.1	18.1	0	0
6	Feb 05-11	34.2	21.0	0	0
7	Feb 12-18	34.8	21.8	0	0
8	Feb 19-25	36.9	22.3	0	0
9	Feb 26-Mar	34.9	24.2	0	0
10	Mar 05-11	36.6	22.9	0	0
11	Mar 12-18	38.5	23.9	0	0
12	Mar 19-25	40.9	25.3	0	0
13	Mar 26-Apr	39.7	26.4	0	0
14	Apr 02-08	40.5	26.6	0	0
15	Apr 09-15	41.3	28.2	0	0
16	Apr 16-22	42.2	29.5	0	0
17	Apr 23-29	43.2	28.7	0	0
18	Apr 30-May	41.7	27.6	14	1
19	May 07-13	38.5	25.3	16	1
20	May 14-20	39.8	27.6	5.2	1
21	May 21-27	39.0	26.2	37	1
22	May 28-Jun	39.8	26.4	27	2
23	Jun 04-10	33.6	24.3	45.6	1
24	Jun 11-17	35.3	24.8	0.5	0
25	Jun18-24	32.8	23.6	111.8	4
26	Jun 25-Jul	31.8	23.7	24.2	1
27	July 02-08	33.0	24.3	5.4	1
28	July 09-15	32.3	23.8	8.4	1
29	July 16-22	33.3	23.4	32.4	3
30	July 23-29	30.3	23.0	26.8	4
31	July 30-Aug	28.6	22.7	84.6	4
32	Aug 06-12	32.3	22.8	2.4	0

Contd..

Standard week	Months	Maximum temperature (°C)	Minimum temperature (°C)	Rainfall (mm)	Rainy day
33	Aug 13-19	33.4	22.9	2	0
34	Aug 20-26	34.9	22.8	12	1
35	Aug 27-Sep	31.2	23.8	47.2	2
36	Sep 03-09	30.9	22.3	16.5	2
37	Sep 10-16	28.6	22.8	136.2	5
38	Sep 17-23	28.5	22.2	79	4
39	Sep 24-Oct	28.9	22.8	60.8	4
40	Oct 01-07	30.4	22.4	5.2	1
41	Oct 08-14	31.2	22.2	34	1
42	Oct 15-21	31.6	18.1	0	0
43	Oct 22-28	31.4	16.6	0	0
44	Oct 29-Nov	31.6	20.2	0	0
45	Nov 05-11	31.2	15.6	0	0
46	Nov 12-18	30.9	18.1	0	0
47	Nov 19-25	30.4	14.8	0	0
48	Nov 26-Dec	31.4	13.5	0	0
49	Dec 03-09	31.2	16.7	0	0
50	Dec 10-16	29.7	16.7	8.2	0
51	Dec 17-23	30.5	13.4	0	0
52	Dec 24-31	30.1	13.8	0	0
1	Jan 01-07	30.4	14.6	0	0
2	Jan 08-14	30.4	14.7	0	0
3	Jan 15-21	29.9	16.4	0	0
4	Jan 22-28	31.0	17.9	0	0
5	Jan 29-Feb	32.6	18.7	0	0
6	Feb 05-11	33.1	19.7	0	0
7	Feb 12-18	31.9	19.0	0	0
8	Feb 19-25	36.5	20.0	0	0
9	Feb 26-Mar	35.7	19.1	0	0
10	Mar 05-11	37.1	21.9	0	0
11	Mar 12-18	34.9	22.5	30	1
12	Mar 19-25	37.4	23.2	0	0
13	Mar 26-Apr	39.5	24.9	0	0
14	Apr 02-08	40.4	26.1	0	0

GENETIC AND MOLECULAR ASSESSMENT OF SALINE TOLERANT RICE MUTANT FOR YIELD AND QUALITY ATTRIBUTES

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Major advisor

ABSTRACT

The present study was undertaken to evaluate 57 mutant lines of M₆ generation comprising of 29 mutants from BPT-5204 and 28 mutants of RP Bio-226, during *Kharif* 2016. The experiment was laid out in randomized block design with two replications in both normal and saline stress soil. Salinity screening and molecular characterization under saline soil was done. Genotypes were also evaluated for variability, correlation and path analysis, based on both phenotypic and genotypic level. ANOVA revealed high significant difference among the genotypes for all traits. High PCV and GCV were recorded for number of grain per panicle, panicle weight and panicle exertion under normal soil, whereas, under the saline stress soil, number of grains per panicle, per cent chaffyness and grain yield per plant. High heritability coupled with high genetic advance over the mean was recorded in per cent chaffyness, grain yield per plant and panicle exertion in both saline and normal soil. Number of grains per panicle and panicle exertion exhibited highly significant phenotypic and genotypic association with grain yield. Phenotypic path coefficient revealed that panicle exertion and number of grains per panicle had the high positive direct effect on grain yield under normal soil, whereas, under the saline stress soil, number of productive tillers per plant and test weight. 15 Salinity tolerant genotypes selected based on Stress Susceptibility Index, Standard Evaluation System and Na⁺ K⁺ ratio. Based on SSR analysis, dendrogram revealed that two different cluster, cluster I consist of sensitive checks, cluster II includes tolerant checks and mutant lines, and this shows the mutants share similar genetic back ground and tolerant to saline condition. In conclusion, the selected saline tolerant BPT-5204 rice mutants would be used in further breeding program and used as variety after conforming yield consistency trail in multi-location under saline situation over two or three years.