**Original Research Article**

**Selection Criteria and Genetic Variability Studies in Salinity Tolerant Rice Genotypes**

**ABSTRACT:** **The field experiment was carried out using 72 rice genotypes at Agricultural Research Station, Kampasagar, Nalgonda district which is located at geographical co-ordinates of 16.8536 N latitude and 79.4569 longitudes.**

Analysis of variance revealed significant genotypic difference for all the traits studied indicating that a large amount of variability present in germplasm and there is a scope for selecting promising genotypes to develop salinity tolerant rice varieties. The values of genotypic and phenotypic coefficients of variation (GCV and PCV) were moderate for Total no. of tillers/plant (16.72 and 17.70), No. of effective tillers/plant (15.82 and 17.90) and spikelet fertility (%)(19.14 and 20.38), grain length (mm)(12.83 and 13.62) and grain breadth(15.54 and 16.01); low for days to 50% flowering(6.72 and 696). Selection for these traits would offer better scope for genotypes A close difference between phenotypic and genotypic coefficient of variation revealed that there was a little influence of environment on the expression of the character studied. Selection for these traits would offer better scope for development of these traits. High heritability coupled with high genetic advance as percent of mean was observed for all the traits except for plant height and reproductive stage salinity stage scoring indicating the preponderance of additive type of gene action for the expression of this characters and selection may be effective for improving this character. The study of simple correlation in the present investigation suggested that positive and significant assosiation of yield with number of filled grains per panicle (0.8477\*\* ), spikelet fertility (0.6621\*\*), productive tillers (0.4107\*\* ) test weight (0.4105\*\*) panicle length (0.2864\*\* ), plant height (0.2815\*\*). However, it exhibited significant and negative correlation with seedling mortality (-0.9124\*\*Present study revealed that there was good amount of genetic variability in the traits number of effective tillers per plant, panicle length, grains/panicle and test weight, selection would be more effective for developing these traits.

**Keywords:** Rice, GCV, PCV, Heritability, Genetic advance as percent of mean

**INTRODUCTION**

Abiotic stressors that impact plant metabolism and lower plant development and output include drought, floods, heat, oxidative stress, low temperatures, water scarcity, excessive salinity, and metal toxicity (Razzaque *et al*., 2017). Salinity is the second most destructive abiotic danger to rice production, behind drought, which affects around 1 billion hectares of land worldwide (Kakar *et al*., 2019). Worldwide, 50% of irrigated land and 20% of Earth's surface area are salinized (Malumpong *et al*., 2019). Over 90% of the world's rice is produced in Asia, specifically in South and Southeast Asia, which contains 21.5 million hectares of salt-affected land, of which 9.5 million are alkaline/sodic and 12 million are saline (Mohammadi *et al*., 2013). Sodic and saline soils are the two categories of salt-affected soils. High concentrations of carbonate and bicarbonate anions, as well as an excess of sodium ions on swap sites, are characteristics of sodic soils. High pH (8.2 to 10.8) is typically linked to these. Conversely, saline 1 soils have increased electrical conductivity (>4 dS/m) due to their dominant chloride and sulphate anions and abundant sodium (Ali *et al*., 2013). Coastal salinity and inland salinity, primarily sodicity, are concerning on the rise in irrigation commands among the many salinity situations. These factors include poor irrigation water with high salt levels, water table depletion, flooding from seawater, excessive use of chemical fertilizers, and inadequate drainage (Kakar *et al*., 2019).

Among cereal crops, rice is the most susceptible to salt, exhibiting a variety of responses at different phases of development. The reproductive stage is critical because it ultimately decides grain yield, yet numerous studies have shown that rice is resistant to salinity during the germination, tillering, and maturity stages but becomes extremely vulnerable during the seedling and reproductive stages (Zhang *et al*., 2020). However, because it affects crop establishment, the significance of the seedling stage cannot be overlooked (Mondal *et al*., 2019). Unfortunately, rice plants are susceptible to salt stress while they are seedlings, and high salt levels typically cause osmotic stress and ion toxicity in rice plants.

Particularly during the pollination and fertilization phases, the reproductive stage is extremely susceptible to salinity. Salinization during the blooming stage has an impact on pollen germination and spikelet development, which eventually lowers the number of filled grains or panicles and raises the number of unfilled grains, which lowers spikelet fertility. Additionally, salinity decreases 1000 grain weight and panicle length, which lowers productivity (Sen *et al*., 2017). Grain yield is significantly reduced by salinity during the reproductive stage compared to the vegetative stage (Mondal *et al*., 2019).

**MATERIALS AND METHOD**

Reproductive stage salinity screening was conducted at Agricultural Research Station, Kampasagar. The 72 genotypes were screened for salinity tolerance as per protocol of Pani *et al.*(2013) with certain modifications. The scoring was given below as per SES of IRRI (1997).The experimental design adopted was Alpha lattice design. The crop was raised under irrigated conditions during *kharif* 2023-2024. Nursery was raised in normal condition and all recommended package of practices were adopted to raise a healthy nursery. The twenty five days old seedlings were transplanted in the main field with spacing of 20×15 cm and soil salinity recorded at 30 DAS was 4.3 dSm-1,. Peizometer was installed in field to measure soil salinity at different growth stages. A total of 72 germplasm including 4 checks were transplanted in continuous three rows of 4 m row length at spacing of 20 cm between rows and 15 cm between plants within the row. Cultural practices like weeding, irrigation and necessary crop protection practices were followed to maintain good crop.

Data on days to 50% flowering, plant height (cm), total number of tillers plant-1, number of effective tillers plant-1,panicle length (cm),number of filled grains panicle-1, grain yield plant-1 (g), spikelet fertility (%),test weight, grain length(mm),grain breadth(mm), grain L/B ratio (mm) and reproductive stage salinity scoring were recorded based on 5 plants per genotype. The details of the observations recorded and methodology followed is presented here under character wise.

Estimates of phenotypic and genotypic coefficients of variation according to Burton & De Vane (1952), heritability estimates in broad sense according to Lush (1940) and genetic advance as per suggested by Johanson *et al.* (1955) and correlation coefficient according to Robinson *et al.* (1951) were calculated following standard statistical procedures.

**RESULTS AND DISCUSSION**

Analysis of variance was carried out as per standard procedure by Patterson and Williams, 1956. The range, mean, variability estimates *i.e.* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as percentage of mean were estimated for yield, its components presented in table 1. The analysis of variance revealed significant genotypic difference for all the traits studied indicating that a large amount of variability was present in the material under salinity condition.

Variability of a character is measured by its coefficient of variation. The genotypic and phenotypic coefficients of variation are classified (low: less than 10%, moderate: 10-20% and high: more than 20%) as suggested by Sivasubramanian and Madhava Menon (1973). Heritability estimates are categorized (low: less than 30%, moderate: 30-60% and high: more than 60%) as recommended by Johnson *et al*. (1955). The range of genetic advance as percent of mean is classified (low: less than 10%, moderate: 10-20% and high: more than 20%) as suggested by Johnson *et al.* (1955).

**Table 1: Estimates of variability and genetic parameters of fourteen yield traits in rice genotypes under salinity condition.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Character** | **Range** | **Mean** + **SE** | **Mean sum of squares** | **GCV (%)** | **PCV (%)** | **Heritability (bs) (%)** | **Genetic advance** | **Genetic advance as % of mean** |
| |  | | --- | | Days to 50% flowering | | 85 - 124 | 103.42 + 1.3 | 100.26 | 6.72 | 6.96 | 93.43 | 13.85 | 8.39 |
| |  | | --- | | Plant height (cm) | | 53.3 - 125 | 77.16+ 1.59 | 528.2 | 20.95 | 21.26 | 98.10 | 32.99 | 42.76 |
| Total no. of tillers/plant | 4 - 17.67 | 12.20 + 0.58 | 8.83 | 16.72 | 17.70 | 89.18 | 3.96 | 32.53 |
| |  | | --- | | No. of effective tillers/plant | | 5 - 14 | 9.63 + 0.57 | 5.29 | 15.82 | 17.90 | 78.05 | 2.77 | 28.79 |
| |  | | --- | | Panicle length (cm) | | 14 - 26.4 | 20.29+ 0.44 | 14.33 | 13.01 | 13.36 | 94.83 | 5.29 | 26.11 |
| |  | | --- | | No. of filled grains/panicle | | 10 - 191 | 108.43 + 5.75 | 2126.07 | 29.59 | 30.53 | 93.96 | 64.08 | 59.10 |
| Spikelet fertility (%) | 20.6 - 91.93 | 64.98 + 3.21 | 330.26 | 19.14 | 20.38 | 88.22 | 24.07 | 37.04 |
| |  | | --- | | Test weight (g) | | 9.12 - 26.98 | 17.15+ 0.68 | 33.26 | 23.49 | 24.10 | 94.58 | 8.05 | 46.97 |
| |  | | --- | | Single plant yield (g/plant) | | 5.5 - 29.23 | 17.59 + 0.84 | 56.21 | 29.76 | 30.52 | 95.03 | 10.51 | 59.76 |
| Reproductive stage salinity scoring | 3-9 | 5.6 + 0.78 | 2.45 | 13.97 | 24.28 | 23.11 | 0.92 | 9.56 |
| Grain length (mm) | 4.2 - 9.7 | 5.86 + 0.18 | 1.204 | 12.83 | 13.62 | 88.78 | 1.46 | 24.9 |
| Grain breadth(mm) | 1.01 - 2.23 | 1.62 + 0.04 | 0.129 | 15.54 | 16.01 | 94.20 | 0.5 | 31.06 |
| Grain L/B ratio(mm) | 2.29 - 6.51 | 3.84 + 0.126 | 1.699 | 23.75 | 24..20 | 96.28 | 1.84 | 48.01 |
| Seedling mortality (%) | 20.51-95 | 36.7 + 3.06 | 536.02 | 39.93 | 42.22 | 89.43 | 30.99 | 77.8 |

The results on genetic variability revealed that phenotypic coefficient of variation were higher than genotypic coefficient of variation. The difference between PCV and GCV was minimum for all the characters studied. The apparent variation is not only due to influence of genotype but also due to environment. A close difference between phenotypic and genotypic coefficient of variation revealed that there was a little influence of environment on the expression of the character studied. The values of genotypic and phenotypic coefficients of variation (GCV and PCV) were moderate for Total no. of tillers/plant, No. of effective tillers/plant and spikelet fertility (%),Grain length (mm) and grain breadth; low for days to 50% flowering. Selection for these traits would offer better scope for genotypes under study and there is a need for creation of variability either by hybridization or mutation followed by selection. Spikelet fertility ranged from 20.6% to 91.93%, with a mean of 64.98%. The moderate GCV (19.14%) and PCV (20.38%) suggest some environmental influence, but the high heritability (88%) indicates that most variation is genetic. The genetic advance of 24.07% (37.04% of the mean) means breeders can significantly improve fertility through selection.

Single plant yield varied from 5.5 g to 29.23 g, with a mean of 17.59 g. The high GCV (29.76%) and PCV (30.52%) indicate significant variability, but the very high heritability (95%) confirms that yield is strongly influenced by genetics. The genetic advance of 10.51 g (59.76% of the mean) suggests excellent potential for yield improvement through breeding. Salinity tolerance at the reproductive stage was scored from 3 to 9, with a mean of 5.6. The moderate GCV (13.97%) and high PCV (24.28%) indicate that environmental factors play a major role. The low heritability (33.11%) suggests limited genetic control, making this trait harder to improve through breeding alone. Seedling mortality under stress conditions ranged from 20.51% to 95%, with a mean of 36.7%. The very high GCV (39.93%) and PCV (42.22%) indicate extreme variability, but the high heritability (89.43%) suggests that genetics play a major role. The large genetic advance (30.99%, 77.8% of the mean) indicates strong potential for breeding stress-tolerant varieties.

Most traits, especially yield-related ones (plant height, panicle length, grains per panicle, test weight, and single plant yield), exhibit high heritability and genetic advance, indicating that they can be efficiently increased by breeding. Traits like reproductive stage salinity tolerance have low heritability, indicating that improving them may require additional strategies beyond pure genetic selection. Overall, this data helps breeders prioritize traits for crop improvement programs. The trait Days to 50% flowering has high heritability (93.43) c with low genetic advance (8.39) indicates non additive gene action and selection for this trait may not be rewarding.

High heritability (broad sense) estimates (>60%) were observed for all the traits except reproductive stage salinity screening *viz*., days to 50% flowering (93.43%), plant height (98.10),total number of tillers per plant(89.18), number of effective tillers per plant (78.05), panicle length (94.83), number of filled grains per panicle (93.96), single plant yield(95.03), test weight (94.58),spikelet fertility percentage(88.22),),grain length(88.78),grain breadth(94.20),grain L/B ratio(96.28) and seedling mortality percentage(89.43) except reproductive stage salinity score (23.11). Since the estimates of heritability alone sometimes misleads interpretation hence estimates of genetic advance as percent of mean is used for better prediction of characters under study. The values of genetic advance as percent of mean were high for the traits under studied except for plant height and reproductive stage salinity scoring. Reproductive stage salinity score has low heritability (23.11) coupled with low genetic advance (9.56) indicating that this trait is highly influenced by environmental effects and selection would be ineffective.

Heritability alone fails to indicate the response to selection and a character having high heritability may not necessary give high genetic advance. Therefore heritability should be always considered along with genetic advance as percent of mean to arrive at a more reliable conclusion. High heritability coupled with high genetic advance as percent of mean was observed for all the traits except for plant height and reproductive stage salinity stage scoring indicating the preponderance of additive type of gene action for the expression of this characters and selection may be effective for improving this character.

The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. Character association provides information on the nature and extent of association between pairs of metric traits and helps in selection for the improvement of the character. The knowledge regarding relative contribution of individual traits to yield may be accomplished by correlation studies. Further, the component characters of yield exhibit different associations among themselves and also with yield. Unfavorable associations between the desired attributes under selection may limit genetic advance. Therefore, knowledge on the magnitude of association between the yield and its attributing characters is essential for planning sound breeding program.

In the present investigation, simple correlation studies were estimated for yield and its components. Estimates of simple correlation coefficients for yield traits under salinity condition are presented in (table 2).

**Table 2: Estimates of simple correlation coefficients for yield traits under salinity condition.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait** | **DFF** | **PH** | **TL** | **PT** | **PL** | **FG** | **SFP** | **TW** | **SPY** | **GL** | **GB** | **L/B ratio** | **SES** | **SM%** |
| **DFF** | **1** | -0.209 | -0.111 | -0.233 \* | 0.034 | 0.012 | -0.0227 | -0.0614 | 0.03 | 0.1263 | -0.0063 | 0.0385 | 0.1374 | -0.102 |
| **PH** |  | **1** | 0.215 | 0.1537 | 0.67 \*\* | 0.39 \*\* | 0.2385 \* | 0.0119 | 0.293 \* | -0.1053 | 0.21 | -0.236 \* | -0.1985 | -0.243 \* |
| **TL** |  |  | **1** | 0.94 \*\* | 0.2005 | 0.55 \*\* | 0.41 \*\* | 0.049 | 0.484 \*\* | 0.1663 | 0.105 | -0.107 | -0.482 \*\* | -0.481 \*\* |
| **PT** |  |  |  | **1** | 0.114 | 0.4272 \*\* | 0.379 \*\* | 0.192 | 0.459 \*\* | 0.1187 | -0.031 | -0.027 | -0.3762 \*\* | -0.444 \*\* |
| **PL** |  |  |  |  | **1** | 0.3544 \*\* | 0.306 \*\* | -0.071 | 0.303 \*\* | 0.1295 | 0.172 | -0.036 | -0.1079 | -0.251 \* |
| **FG** |  |  |  |  |  | **1** | 0.792 \*\* | 0.199 | 0.89 \*\* | 0.0694 | 0.190 | -0.165 | -0.4233 \*\* | -0.849 \*\* |
| **SFP** |  |  |  |  |  |  | **1** | 0.072 | 0.72 \*\* | 0.2135 | 0.061 | 0.002 | -0.4234 \*\* | -0.72 \*\* |
| **TW** |  |  |  |  |  |  |  | **1** | 0.431 \*\* | -0.071 | 0.027 | -0.087 | -0.0124 NS | -0.435 \*\* |
| **SPY** |  |  |  |  |  |  |  |  | **1** | 0.056 | 0.196 | -0.136 | -0.2632 \* | -0.930 \*\* |
| **GL** |  |  |  |  |  |  |  |  |  | **1** | -0.2614 \* | 0.757 \*\* | -0.1455 | -0.083 |
| **GB** |  |  |  |  |  |  |  |  |  |  | **1** | -0.769 \*\* | 0.0821 | -0.084 |
| **L/B ratio** |  |  |  |  |  |  |  |  |  |  |  | **1** | -0.0015 | 0.063 |
| **SES** |  |  |  |  |  |  |  |  |  |  |  |  | **1** | 0.257 \* |
| **SM%** |  |  |  |  |  |  |  |  |  |  |  |  |  | **1** |

\* Significant at p< 0.05; \*\*Significant at p<0.01 (DFF-Days to 50% flowering; PH-Plant height; TL- Total tillers per plant; PT-Productive tillers per plant; Pl-Panicle length; FG- No. of filled grains per panicle; SFP-Spikelet fertility percentage; TW-Test weight; SPY-Single plant yield per plant; GL-Grain length; GB- grain breadth; SES-Reproductive stage salinity score; SM- Seedling mortality (%).

The genotypic correlation of days to 50% flowering was positive but non-significant with RES (0.1374 NS), GL (0.1263 NS), L/B Ratio (0.0385 NS), PL (0.0346 NS), SPY (0.03 NS), and FG (0.0124 NS). Plant height was positive and significant correlated with panicle length and grain yield. Similar results were observed for panicle length (Ramesh *et al.,* (2018) and grain yield per plant by Tiwari *et al.* (2016), Sanju *et al.,* (2019), Ramesh et al.(2018), Reddy *et al.,* (2018). A significant negative correlation was observed with PT (-0.233 \*). Productive tillers per plant was significantly and positively correlated with TL (0.9455 \*\*), SPY (0.4593 \*\*), FG (0.4272 \*\*), and SFP (0.3799 \*\*). Kumar *et al.,* (2017) also noted that higher tillering potential positively affects yield under abiotic stress. Similar findings were reported by Hakim *et al.,* (2013) and Hossen *et al.,* (2017)., who observed strong positive associations between productive tillers and other yield components while screening rice varieties under saline conditions at multiple electrical conductivity levels (4, 8, and 12 dSm⁻¹). It also had positive, though non-significant, correlations with TW, PH, GL, and PL. Filled grains per panicle was significantly and positively associated with SPY (0.8907 \*\*), SFP (0.7923 \*\*), TL (0.5571 \*\*), PT (0.4272 \*\*), PH (0.3995 \*\*), and PL (0.3544\*\*). It also had non-significant positive correlations with TW, GB, GL, and DFF. On the other hand, FG had significant negative correlations with SM% (-0.8496 \*\*) and RES (-0.4233 \*\*), and a non-significant negative correlation with L/B Ratio. SFP displayed significant positive correlations with FG (0.7923 \*\*), SPY (0.7223 \*\*), TL (0.4114 \*\*), PT (0.3799 \*\*), PL (0.3064 \*\*), and PH (0.2385 \*) (Mahalakshmi et al. (2024)

Reproductive stage salinity score (RES) was significantly and positively correlated with SM% (0.2571\*), and had non-significant positive correlations with DFF and GB(Ibrahim *et al*. (2016). Significant negative associations were found with TL (-0.482 \*\*), SFP (-0.4234 \*\*), FG (-0.4233 \*\*), PT (-0.3762 \*\*), and SPY (-0.2632 \*), while PH, GL, PL, TW, and L/B Ratio had non-significant negative correlations. The present investigation revealed that SM% (Seedling Mortality Percentage) had a positive and significant correlation with RES (0.2571 \*), indicating that genotypes with higher resistance scores tend to exhibit increased seedling mortality. Additionally, a positive but non-significant correlation was observed with L/B Ratio (0.0635 NS). In contrast, SM% showed strong and significant negative correlations with several important agronomic traits, including SPY (-0.9304 \*\*), FG (-0.8496 \*\*), SFP (-0.722 \*\*), TL (-0.4818 \*\*), PT (-0.4446 \*\*), TW (-0.4359 \*\*), PL (-0.2511 \*), and PH (-0.2435 \*), suggesting that increased seedling mortality adversely affects yield components and plant growth traits. Furthermore, negative but non-significant associations were found with DFF (-0.1022 NS), GB (-0.0849 NS), and GL (-0.0835 NS), indicating weak or inconsistent relationships with these traits.

The study of simple correlation in the present investigation suggested that selection of plants with more number of productive tillers per plant, panicle length, number of grains per panicle and test weight which had significant positive association with yield may be taken in to account in rice breeding program for yield improvement to develop salinity tolerant rice varieties.

**Conclusion**

**The analysis of genetic variability across these fourteen traits show that most yield traits in rice exhibit high heritability and substantial genetic advance, signifying a prevalence of additive gene action. Particularly, single plant yield ranged from 5.5 to 29.23 g, with a mean of 17.59 g. It exhibited very high GCV (29.76%) and PCV (30.52%), with a heritability of 95.03(%) and an outstanding GAM of 59.76%. These results show that yield is strongly heritable and responsive to selection, making it a primary target for improving productivity in rice genotypes, test weight, filled grains per panicle, and grain L/B ratio are key selection targets due to their high heritability. The character association analysis under salinity condition revealed that single plant yield is significantly and positively influenced by key yield-contributing traits such as number of filled grains per panicle, spikelet fertility, productive tillers, test weight, panicle length, and plant height, highlighting their importance in selecting high-yielding genotypes for salinity tolerance.**

**REFERENCES**

Ali, S., Gautama, R. K., Mahajanb, R., Krishnamurthy, S. L., Sharma, S. K., Singh, R. K and Ismail, A. M. (2013). Stress indices and selectable traits in Saltol QTL introgressed rice genotypes for reproductive stage tolerance to sodicity and salinity stresses. *Field Crops Research,*154. 65-73.

Burton GW, De Vane EH. Quantitative inheritance in grasses. Proc 6th Int Grassland Congr.

1952;11:277-83.

Hakim, M. A., Juraimi, A. S., Hanafi, M. M., Ali, E., Ismail, M. R., Selamat, A and Karim, S.

M. R. (2013). Effect of salt stress on morpho-physiology, vegetative growth and yield of rice. *Journal of Environmental Biology*,35: 317-326.

Hossen, B., Haque, M. S., Miah, K and Tareq, M. Z.( 2017). Phenotypic and genotypic screening of rice genotypes at reproductive stage for salt tolerance. *SAARC journal of Agriculture*,15 (2): 69-70.

Ibrahim, M. A. A., Rani, M. H., Begum, S., Akter, M. B and Islam, M. M. 2016. Performance of Rice Landraces under Salt Stress at the Reproductive Stage Using SSR Markers. *International Journal of Plant & Soil Science*. 13(2): 1-11.

Johnson, H. E., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. Agronomy Journal, 47: 314-318.

Kakar, N., Jumaa, S. H., Redoña, E. D., Warburton, M. L and Reddy, K. R. (2019). Evaluating rice for salinity using pot-culture provides a systematic tolerance assessment at the seedling stage. *Rice*,12 (57): 1-14.

Kakar, N., Jumaa, S. H., Redoña, E. D., Warburton, M. L and Reddy, K. R. (2019). Evaluating rice for salinity using pot-culture provides a systematic tolerance assessment at the seedling stage. Rice. 12 (57): 1-14.

Kumar, A., Mandal, A and Sarangi, S. (2018). Genetic divergence and PCA for salinity tolerance in rice at reproductive stage. *ORYZA*. 55 (2): 2018 342-348.

Lush, J.L., (1940). Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *Journal of animal science*, *1940*(1),293-301.

Mahalakshmi, P.J., Satish, Y., Ramana, J.V. and Raju, M.R.B.2024.Correlation and Path Coefficient Analysis for Yield and Its Component Traits in Advanced Breeding Lines of Rice (*Oryza sativa* L.). *Journal of Advances in Biology & Biotechnology*. 27(9): 769–777.

Malumpong, C., Youngkom, P., Vanavichit, A and Liw, S. M. (2019). Variation in tolerance to salinity stress at the reproductive stage in a large fast neutron mutant rice (*Oryza sativa* L.) population. *International Journal of Agricultural Technology*, 15(3): 445-464.

Mohammadi, R., Mendioro, M. S., Genaleen, Q., Diaz, Gregorio, G. B and Singh, R. K. (2013). Mapping quantitative trait loci associated with yield and yield components under reproductive stage salinity stress in rice (*Oryza sativa* L.). *Journal of genetics*, 92:433-443.

Mondal, S., Borromeo, T. H. M., Genaleen, Q., Diaz, Amas, J., Rahman, M. A., Thomson, M. J and Gregorio, G. B. (2019). Dissecting QTLs for Reproductive Stage Salinity Tolerance in Rice from BRRI dhan 47. *Plant Breeding Biotechnology*, 7(4): 302-312.

Pani, D. R., Sarangi, S. K., Misra, R. C., Pradhan, S. K., Subudhi, H. N and Mandal, T. K. 2013. Performance of rice germplasm (*Oryza sativa* L.) under coastal saline conditions. *Journal of the Indian Society of Coastal agricultural Research*. 31 (1): 11-20.

Patterson HD and ER Williams, (1976). A new class of resolvable incomplete block designs.Biometrika,63:83-92.

Ramesh, Ch., Raju, Ch.D., Raju, S and Varma, N.R.G. (2018). Character association and path coefficient analysis for grain yield and yield components of parents and hybrids in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*,7 (4): 2692-2699

Razzaque, S., Haque, T., Elias, S. M., Rahman, M. S., Biswas, S., Schwartz, S., Ismail, A. M., Walia, H., Juenger, T. E and Seraj, Z. (2017). Reproductive stage physiological and transcriptional responses to salinity stress in reciprocal populations derived from tolerant (Horkuch) and susceptible (IR29) Rice*. Nature*,1-16.

Reddy, O.R., Lal, G.M and Lal, S.S. (2018b). Genetic variability and correlation studies for yield and quality traits of elite medium duration rice (*Oryza sativa* L.) hybrids. *International Journal of Advanced Biological Research*, 8 (2): 165-173

Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1951). Genotypic and phenotypic correlations in corn and their implications in selection. *Agronomy Journal*, 43: 282-287.

Sanju, K., S., Pawan, K., Bisen, P., Loitongbam, B., Rai, V and Sinha, B. (2019). Genetic diversity analysis of rice germplasm through morphological markers,953-957.

Sen, T. T. H., Nhi, P. T. P and Sen, T. T. (2017). Salinity Effect at Seedling and Flowering Stages of Some Rice Lines and Varieties (*Oryza sativa* L.). *Journal of Agricultural Science and Technology,* 7: 32-39.

Sivasubramanian, S., & Madhava Menon, P. (1973). Genotypic and phenotypiv variability in rice*. Madras Agriculture Journal*, 60(9-12): 1093-1096.

Sivasubramanian, S., & Madhava Menon, P. (1973). Genotypic and phenotypiv variability in rice*. Madras Agriculture Journal*, 60(9-12): 1093-1096.

Tiwari, S., Krishnamurthy, S. L., Kumar, V., Singh, B., Rao, A. R., Mithra, A. S. V., Rai, V., Singh, A. K and Singh, N. K. (2016). Mapping QTLs for salt tolerant in rice (Oryza sativa L.) by bulked segregant analysis of recombinant inbred lines using 50K SNP chip. Plus one, 11 (4): 1-19

Zhang, K. Y., Ponce, S., Meng, L., Chakraborty, P., Zhao, Q., Guo, L., Gao, Z., Leng, Y and Ye, G. (2020). QTL identification for salt tolerance related traits at the seedling stage in indica rice using a multi-parent advanced generation intercross (MAGIC) population. *Plant Growth Regulation*, 1-9.