

Genetic variability Studies in Rice (*Oryza sativa* L.) varieties for Three Seasons under Saline conditions of Annamalai Nagar, an East Coast Region of Tamil Nadu

S.R. Sruthi¹, Laleeth Kumar N.¹, Y. Anbuselvam^{2*}, J.L. Joshi³ and Johnny Subakar Ivin⁴

¹Ph.D. Scholar, Department of Genetics and Plant Breeding,
Faculty of Agriculture, Annamalai University, Annamalai Nagar (Tamil Nadu), India.

²Professor, Department of Genetics and Plant Breeding,
Faculty of Agriculture, Annamalai University, Annamalai Nagar (Tamil Nadu), India.

³Assistant Professor, Department of Genetics and Plant Breeding,
Faculty of Agriculture, Annamalai University, Annamalai Nagar (Tamil Nadu), India.

⁴Assistant Professor, Mother Teresa College of Agriculture,
Mettusalai, Illuppur, Pudukkottai (Tamil Nadu), India.

(Corresponding author: Y. Anbuselvam*)

(Received: 23 June 2023; Revised: 27 July 2023; Accepted: 29 August 2023; Published: 15 September 2023)
(Published by Research Trend)

ABSTRACT: The current study was conducted on 50 rice genotypes to evaluate the mean performance and genetic variability of various biometrical traits viz., fifty percent flowering, plant height, panicle length, number of tillers per panicle, number of productive tillers per plant, number of grains per panicle, 100 grain weight with grain yield per plant for three seasons under saline environment. Vandana disclosed significant mean values for productive tillers, grains per panicle and grain yield per plant while CTH-1 exhibited high per se performance for number of tillers per plant, number of productive tillers per plant, number of grains per panicle and grain yield per plant in pooled over environment. The consistent performance of CTH-1 makes it suitable for breeding programs to improve grain yield under saline conditions. Understanding the roles of genetic variability and heritable components are critical for progressive breeding program. The trait days to fifty percent flowering exhibited low PCV and GCV disclosing the presence of low level of variability while the traits viz., total number of tillers per plant, number of grains per panicle and grain yield per plant laid out moderate PCV and GCV revealing the existence of moderate level of variability in all the three seasons. The traits such as total number of tillers per plant, number of productive tillers per plant and panicle length demonstrated high heritability and genetic advance in all the three seasons which proved that selection of such traits is effective as heritability was due to additive gene effects.

Keywords: Variability, Rice, Heritability, Genetic advance, Phenotypic coefficient of variation, Genotypic coefficient of variation.

INTRODUCTION

Rice, a staple monocarpic cereal, is pivotal for food security and poverty alleviation worldwide (Elert, 2014). With a production of 519.5 million tonnes in 2022, rice ranks third among all crops grown worldwide. Despite being able to thrive in a variety of ecosystems, rice is vulnerable to drought, frequent floods, seawater inundations, etc. that are brought on by changing climatic conditions, which minimize the yield potential of present-day rice varieties (Rasheed *et al.*, 2020). Abiotic stresses have a detrimental effect on agricultural productivity and have the potential to substantially decrease yields of important food crops by up to 70% (Waqas *et al.*, 2019).

One of the main abiotic stresses, salt stress, affects roughly 6% of the world's agricultural land, or nearly one billion ha (Kakar *et al.*, 2019). The east coast regions of Tamil Nadu, India have fields lined with salt

slush and salt cakes as a direct consequence of the devastation caused by the tsunami in 2004. The current limitations, which include erratic weather patterns, rising temperatures, decreasing water availability, and the encroachment of coastal salinity, built an important constraint for plant breeders in complying with demands for rice production in Tamil Nadu. It is therefore essential to focus upon the development of saline-tolerant and high-yielding rice cultivars because managing salinity is an energy-intensive agricultural practice. The genetic gain is very important when using plant breeding techniques to develop cultivars that could withstand salinity.

Genetic variability is crucial for selection in plant breeding, but selection is challenging due to non-heritable variation masking. Therefore, understanding the roles of heritable components is critical for progressive breeding programs. In light of this context, the current study was carried out on rice to evaluate the

mean performance and variability of various biometrical traits with yield over the course of three seasons in saline environments.

MATERIALS AND METHODS

The experiment was conducted at the experimental farm of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu located at latitude 11°24'N, longitude 79°44'E and height + 5.79 m for all three seasons during January 2022 - June 2023. The pH of the soil was 7.70, 7.50 and 7.60 respectively for seasons 1, 2 and 3 which was measured during the beginning of every season by using the Systronics pH meter. The electrical conductivity (EC) of soil and irrigation water determined at the beginning of the experiment using the Systronics conductivity meter were 5.0, 4.8 and 5.0 dsm^{-1} respectively for season 1, 2 and 3. The experimental sample consisted of 50 genotypes, including checks from the University of Agricultural Sciences, Bangalore. The genotypes TRY3 and CSR27 were deployed as tolerant checks, whereas IR36 and ADT46 were taken as susceptible checks. Twenty-five-day-old seedlings were transplanted in the main field adapting a Randomized Block Design (RBD) with three replications. For parameters such as days to fifty percent flowering, plant height, panicle length, number of tillers per panicle, number of productive tillers per plant, number of grains per panicle, hundred grain weight and grain yield per plant, the observations were recorded on five randomly selected plants of each genotype in every replication. Recommended agronomic practices and need-based plant production measures were carried out. The observations recorded for the quantitative traits were analyzed for mean and variability by following standard statistical techniques and using TNAU STAT software. The genotypic and phenotypic coefficients of variation were calculated as per the formula suggested by Burton (1952). GCV and PCV values were categorized as low (0-10%), moderate (11-20%) and high (> 20%) as indicated by Sivasubramanian and Menon (1973). Heritability (broad sense) was calculated as per Hanson *et al.* (1956). The heritability percentage was categorized as low (0-30%), moderate (30 -60 %) and high (>60%) as given by Lush (1940). Genetic advance as per cent of the mean was categorized as low (0-10%), moderate (11 - 20%) and high (>20%) as suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The mean performance of 50 genotypes in the three seasons for the eight yield attributing characters are presented in the figures (Fig. 1-8).

For the trait days to fifty per cent flowering, the genotype AC32525 in season 2 (66 days) followed by the same genotype in season 1 (68.67 days) recorded the least days to first flowering. The other genotypes *viz.*, PS36, JBT37/85, JBT37/154, PS367, PS91, Vandana, CTH-1 in season 1 and the genotypes such as AC39010, Vandana, CTH-1 PS376, AC35066, JBT36/169, JBT36/119 in season 2 while the genotypes JBT37/154, AC35361, AC39010, AC35170, PS325,

Vandana, CTH-1, AC35066, JBT73/164, AC35298, AC39020, KRH2, AC35341 in season 3 recorded significantly lower values than their corresponding general mean. The genotypes Vandana and CTH-1 recorded significantly took lesser days to flowering in all three seasons (Fig. 1).

Among the fifty genotypes PS366 in season 3 (71.07 cm) followed by AC35341 in season 3 (72.07 cm) registered the lowest plant height while PS91 (120.03 cm) in season 2 recorded the highest mean value for this trait. The other genotypes *viz.*, AC35548, JBT37/85, AC35361, AC39010, AC35170, Vandana, CTH-1, BPT5204, AC35187, Dottabatta, KRH2 and JBT37/29 in season 1 and the genotypes such as PS267, AC35548, P36, JBT37/85, AC35361, AC39010, AC35170, Vandana, CTH-1, JBT73/164, AC35298, KRH2, AC35406, B62655, PS307, PS242, JBT36/114 in season 2 while the genotypes PS267, AC35548, AC36110, AC32525, JBT37/85, JBT37/89, PS259, AC39010, PS325, Vandana, CTH-1, PS376, JBT73/164, AC39020, KRH2, JBT36/169, JBT36/79, AC35406, PS329, AC35341, B62655, PS307 and JBT38/116 in season 3 showed significantly desirable mean for the character plant height. The genotypes AC35548, JBT37/85, AC39010, Vandana and CTH-1 exhibited significantly lesser plant height in all three seasons (Fig. 2).

For the trait total number of tillers per plant AC35135 in season 2 (33.33) followed by S-9 (32.67) in season 3 recorded the highest mean value. PS267 and AC35361 (17.33) recorded the lowest number of tillers per plant in the second season. The other genotypes such as JBT37/154, AC35135, Vandana, CTH-1 and JBT37/29 in season 1 while genotypes AC32525, PS91, AC35135, Vandana, CTH-1, AC35066 and JBT36/119 in season 2 and the genotypes *viz.*, PS267, JBT37/154, JBT38/96, PS325, Vandana, CTH-1, S-9 and AC39020 in season 3 described significantly higher mean value. The genotypes AC3554, Vandana and CTH-1 unveiled a significantly higher total number of tillers per plant in all three seasons (Fig. 3).

The mean performance for the trait number of productive tillers per plant revealed that the genotype CTH-1 in season 3 (29.08) followed by PS267 in season 3 (28.00) recorded higher mean value. The other genotypes such as JBT37/85, JBT37/85, Vandana and CTH-1 in season 1 while genotypes AC32525, JBT37/154, AC35135, Vandana and CTH-1 in season 2 and the genotypes *viz.*, JBT37/85, JBT37/154, JBT38/96, Vandana, CTH-1, AC35187, Dottabatta, JBT37/29 and AC35406 in season 3 disclosed significantly higher mean value. The genotypes JBT37/154, Vandana and CTH-1 unveiled significantly higher number of productive tillers per plant in all the three seasons (Fig. 4).

Among the fifty genotypes JBT37/85 in season 3 (141.00) followed by G9 in season 1 (140.93) recorded higher mean value for number of grains per panicle. The genotype JBT73/164 in season 3 (55.67) recorded the least mean value. The genotypes *viz.*, JBT37/85, JBT37/154, Vandana and CTH-1 in season 1, while the genotypes AC35450, PS366, JBT37/85, JBT37/154,

PS259, PS91, JBT38/96, PS325, Vandana and CTH-1 in season 2 and PS360, PS366, JBT37/85, JBT37/154, PS259, AC35170, Vandana, CTH-1, PS376, JBT36/169, JBT37/29 and PS242 in season 3 reported significantly high mean value. The genotypes JBT37/85, JBT37/154, Vandana and CTH-1 recorded significantly more number of grains per panicle in all the three seasons (Fig. 5).

The genotype JBT37/29 in season 3 (2.25) followed by season 1 (2.21) showed significantly higher mean than the grand mean for the trait 100 grain weight. The genotype S-9 in season 2 (1.13) registered least mean value. The genotype JBT37/29 in season 1, while AC35361 and JBT37/29 in season 2 and season 3 recorded high mean than the general mean. The genotype JBT37/29 recorded significantly higher 100 grain weight in all the three seasons (Fig. 6).

The mean performance of panicle length of the genotype ADT46 in season 3 (27.28 cm) followed by JBT38/96 and JBT36/114 in season 3 (26.00 cm) recorded significantly higher mean. Among the genotypes evaluated AC35450, JBT37/85, Vandana and B62655 in season 1, JBT37/85, JBT38/96, Vandana, CTH-1 and B62655 in season 2 and AC35450, JBT37/85, JBT38/96, Vandana, CTH-1, B62655 and JBT36/114 in season 3 recorded significantly higher mean value. The genotypes JBT37/85, Vandana and B62655 revealed significantly lengthier panicle length of rice in all the three seasons (Fig. 7).

The mean values of grain yield per plant of the genotype CTH-1 in season 2 (41.84) followed by the genotype Vandana in season 3 (40.81) recorded a significantly higher mean and the genotype AC35170 (17.95) recorded low mean than the general mean respectively. The genotypes *viz.*, JBT37/85, JBT37/154, Vandana, CTH-1 in season 1 while Vandana and CTH-1 in season 2 and PS360, AC35450, JBT37/85, JBT37/154, PS259, Vandana, CTH-1 and PS242 in season 3 exhibited higher mean value. The genotypes Vandana and CTH-1 recorded significantly higher grain yield per plant in all the three seasons (Fig. 8).

The study found that among the 50 genotypes, Vandana and CTH-1 genotypes recorded significantly higher mean values for seven traits in the first, second, and third seasons. The genotype CTH-1 expressed the highest grain yield in all the seasons and over the pooled seasons. The *per se* expression of the characters by the genotypes for different traits were used to evaluate the genotypes. Vandana disclosed significant mean values for the traits such as productive tillers, grains per panicle, and grain yield per plant while CTH-1 exhibited high *per se* performance for number of tillers per plant, number of productive tillers per plant, number of grains per panicle and grain yield per plant in pooled over environment. The consistent performance of CTH-1 makes it suitable for breeding programs to improve grain yield under saline conditions.

Variability refers to the presence of differences among the individuals of a population which results due to the differences either in the genetic constitution of the individuals of a population or in the environment in

which they are grown. The development of an effective plant breeding program is dependent on the existence of genetic variability. The efficiency of selection largely depends upon the magnitude of variability present in the breeding population. Thus, the success of genetic improvement in any character depends on the nature of the variability present in the gene pool for that character. Hence, assessment of existing variability for any character present in the gene pool of a crop species is of utmost importance to a plant breeder for starting a judicious plant breeding programme.

Analysis of variance revealed significant differences for all the characters studied, indicating the presence of significant variability among the genotypes *viz.*, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability, and genetic advance as per cent of mean for eight characters for three seasons (Fig 9 to 11). PCV was higher than GCV for all the traits under investigation, indicating the role of environmental variance in the total variance which was in accordance with the results obtained by Aravind *et al.* (2021); Sruthi *et al.* (2023). Low PCV and GCV was observed for the traits *viz.*, days to fifty percent flowering (8.10 and 8.09) (Mahantashivayogayya *et al.*, 2016) and plant height (7.658 cm and 7.655 cm) (Swapnil *et al.*, 2020) indicating the low level of variability while moderate PCV and GCV was recorded for the traits such as total number of tillers per plant (12.255 and 12.223) (Kahani and Hittalmani 2015), number of productive tillers per plant (16.29 and 16.25) (Lingaiah *et al.*, 2018), panicle length (14.08 cm and 14.07 cm) (Sheshaiah *et al.*, 2018), number of grains per panicle (14.141 and 8.929) (Ramanjaneyulu *et al.*, 2014), 100 seed weight (10.237 and 10.194) (Abhilash *et al.*, 2018) and grain yield per plant (15.92 and 15.91) (Sala *et al.*, 2015) manifesting moderate level of variability in season 1 (Fig. 9).

Low PCV and GCV was observed for the traits *viz.*, days to fifty percent flowering (7.378 and 7.374) (Sandeep *et al.*, 2018) and 100 seed weight (8.822 and 8.773) (Khandappagol *et al.*, 2020) representing the low level of variability while moderate PCV and GCV was recorded for the traits such as plant height (11.325 cm and 11.323 cm) (Bhargava *et al.*, 2021), total number of tillers per plant (15.575 and 15.554), number of productive tillers per plant (19.636 and 19.611) (Lingaiah *et al.*, 2018), panicle length (14.402 cm and 14.400 cm) (Kalaiselvan *et al.*, 2019), number of grains per panicle (16.025 and 11.271) and grain yield per plant (13.126 and 13.109) demonstrating the moderate level of variability in season 2 (Fig. 10).

In season 3, high PCV and GCV was observed for number of productive tillers per plant (26.12 and 26.09) (Lakshmi *et al.*, 2022) and panicle length (21.169 cm and 21.168 cm) (Shinde *et al.*, 2015) revealing the high level of variability of such trait. Low PCV and GCV was observed for the trait days to fifty percent flowering (8.667 and 8.663) (Gautam *et al.*, 2016) indicating the low level of variability of while moderate PCV and GCV was recorded for the traits such as plant height (12.222 cm and 12.220 cm), total number of tillers per plant (18.247 and 18.228)

(Mahantashivayogayya *et al.*, 2016), number of grains per panicle (16.164 and 11.838) , 100 grain weight (16.106 and 16.080) (Fathima *et al.*, 2021) and grain yield per plant (15.844 and 15.829) unveiling the moderate level of variability (Fig. 11).

The trait days to fifty percent flowering exhibited low PCV and GCV disclosing the presence of low level of variability while the traits *viz.*, total number of tillers per plant, number of grains per panicle and grain yield per plant laid out moderate PCV and GCV revealing the existence of moderate level of variability in all the three seasons.

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. In season 1, high heritability percentage was observed in the traits *viz.*, days to fifty percent flowering (99.90), plant height (99.92), total number of tillers per plant (99.47), number of productive tillers per plant (99.56), panicle length (99.98), 100 grain weight (99.17) and grain yield per plant (99.81) (Kahani and Hittalmani 2015) while a low heritability per cent was recorded for number of grains per panicle (39.87) (Mohan *et al.*, 2015). High genetic advance as mean percent was observed for traits *viz.*, total number of tillers per plant (25.11) (Swapnil *et al.*, 2020), number of productive tillers per plant (33.41), panicle length (29.00) (Ali *et al.*, 2018), 100 grain weight (20.915) (Seneega *et al.*, 2019) and grain yield per plant (32.749) (Sala *et al.*, 2015) while moderate genetic advance as mean percent was recorded for traits such as days to fifty percent flowering (16.67), plant height (15.76) (Thippeswamy *et al.*, 2016) and number of grains per panicle (11.61). High heritability and genetic advance as mean percent was observed for traits *viz.*, total number of tillers per plant, number of productive tillers per plant, panicle length, 100 grain weight and grain yield per plant (Fig. 9).

In season 2, high heritability per cent was observed in the traits *viz.*, days to fifty percent flowering (99.87), plant height (99.96), total number of tillers per plant (99.72), number of productive tillers per plant (99.74), panicle length (99.98), 100 grain weight (98.89) and

grain yield per (99.744) plant, while a moderate heritability was recorded for number of grains per panicle (49.46) (Rao *et al.*, 2014). High genetic advance as mean percent was observed for traits *viz.*, plant height (22.32), total number of tillers per plant (31.99), number of productive tillers per plant (40.34), panicle length (29.66), and grain yield per plant (26.97), while moderate genetic advance as mean percent was recorded for traits such as days to fifty percent flowering (15.18) (Lingaiah *et al.*, 2018), number of grains per panicle (16.33) and 100 grain weight (17.97) (Venkatesan *et al.*, 2017). High heritability and genetic advance as mean percent was observed for traits *viz.*, plant height, total number of tillers per plant, number of productive tillers per plant, panicle length and grain yield per plant (Fig. 10).

In season 3, high heritability per cent was observed in the traits *viz.*, days to fifty percent flowering (99.92), plant height (99.96), total number of tillers per plant (99.79), number of productive tillers per plant (99.83), panicle length (99.99), 100 grain weight (99.67) and grain yield per plant (99.81) while a moderate heritability was recorded for number of grains per panicle (53.63) (Sowjanya *et al.*, 2021). High genetic advance as mean percent was observed for traits *viz.*, plant height (25.16), total number of tillers per plant (37.51), number of productive tillers per plant (53.72), panicle length (43.60) (Sujitha *et al.*, 2020) while moderate genetic advance as mean percent was recorded for traits such as days to fifty percent flowering (17.84) (Mohan *et al.*, 2015), number of grains per panicle (17.85), 100 grain weight (33.07) (Kumar *et al.*, 2015) and grain yield per plant (32.57) (Chandramohan *et al.*, 2016). High heritability and genetic advance as mean percent was observed for traits *viz.*, plant height, total number of tillers per plant, number of productive tillers per plant and panicle length (Fig. 11).

High heritability and genetic advance as mean percent were observed in total number of tillers per plant, number of productive tillers per plant and panicle length in all the three seasons indicating that most likely the heritability was due to additive gene effects and selection of such traits would be effective.

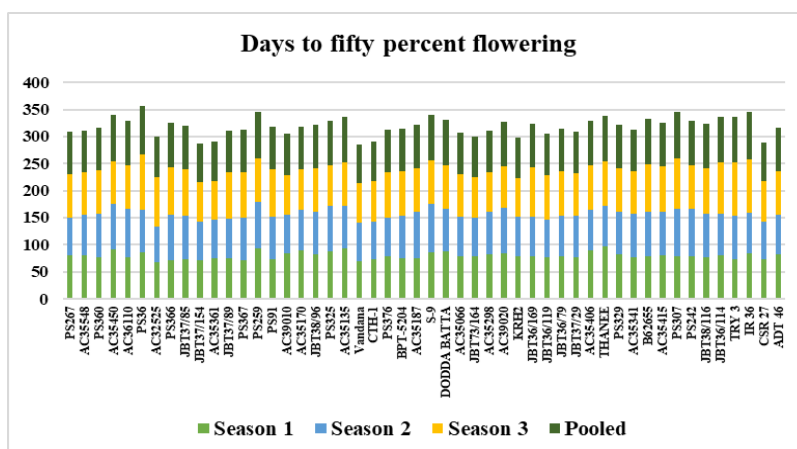


Fig. 1. Mean Performance of Days to Fifty Percent Flowering of Fifty Rice Genotypes for Three Seasons.

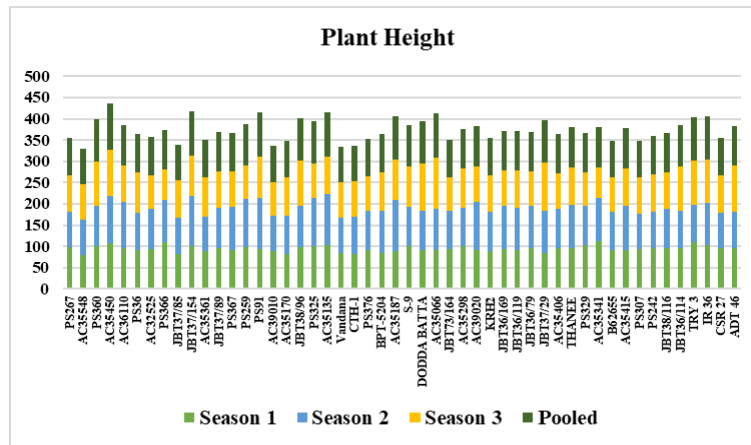


Fig. 2. Mean Performance of Plant Height of Fifty Rice Genotypes for Three Seasons.

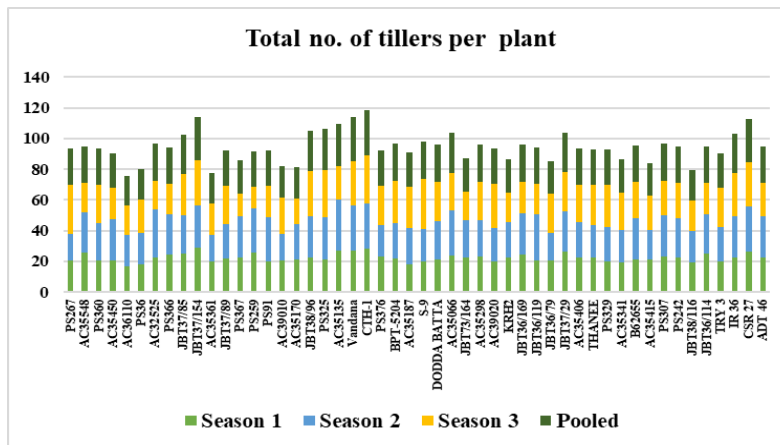


Fig. 3. Mean Performance of Total No. of Tillers Per Plant of Fifty Rice Genotypes for Three Seasons.

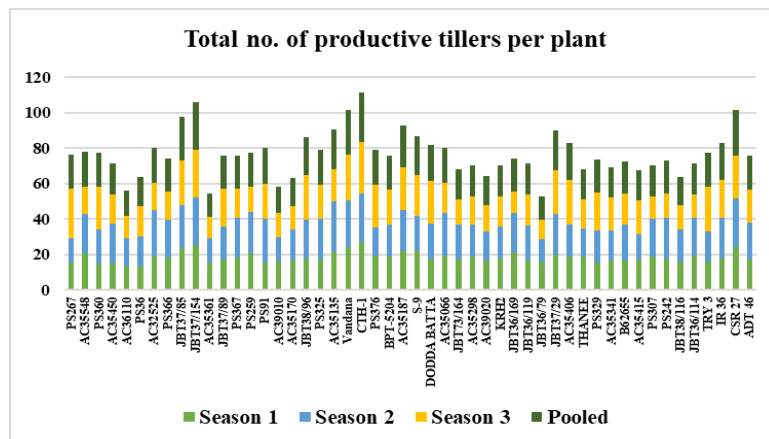


Fig. 4. Mean Performance of Total No. of Productive Tillers Per Plant of Fifty Rice Genotypes for Three Seasons.

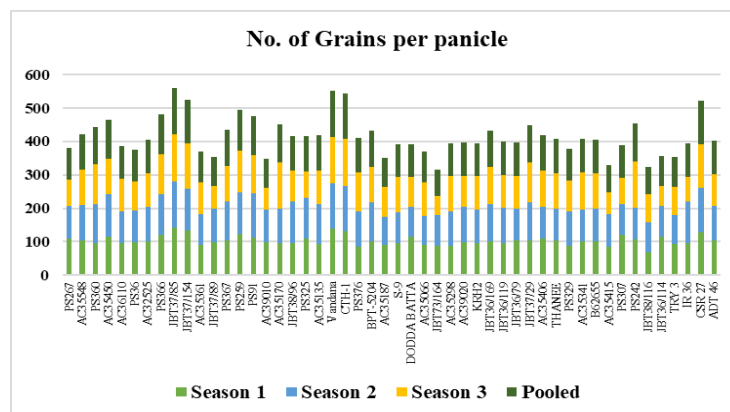


Fig. 5. Mean Performance of Grains per panicle of Fifty Rice Genotypes for Three Seasons.

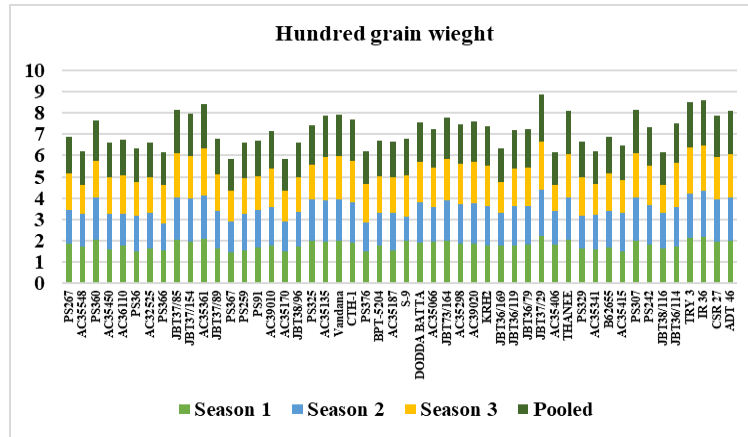


Fig. 6. Mean Performance of Hundred seed weight of Fifty Rice Genotypes for Three Seasons.

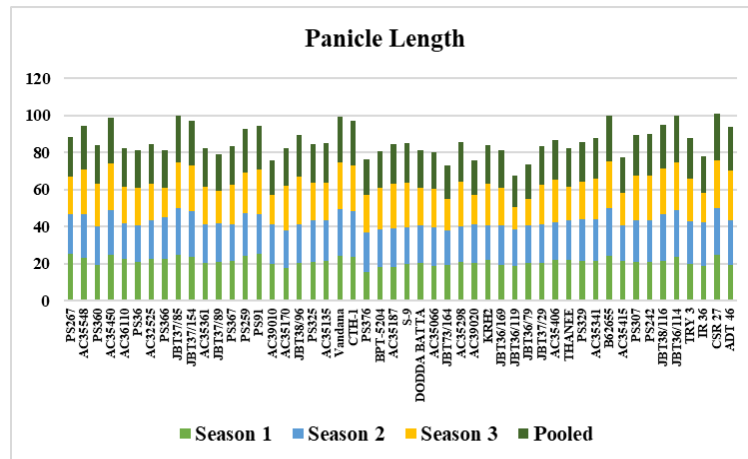


Fig. 7. Mean Performance of Panicle Length of Fifty Rice Genotypes for Three Seasons.

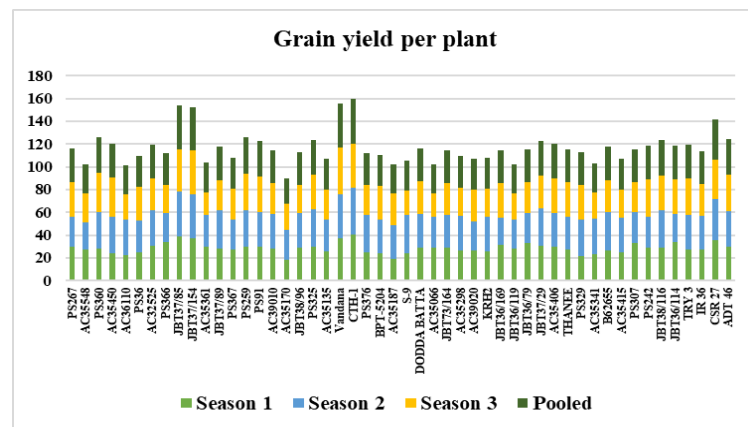
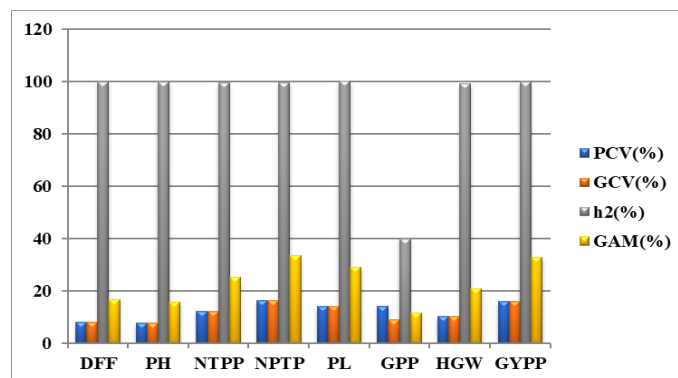
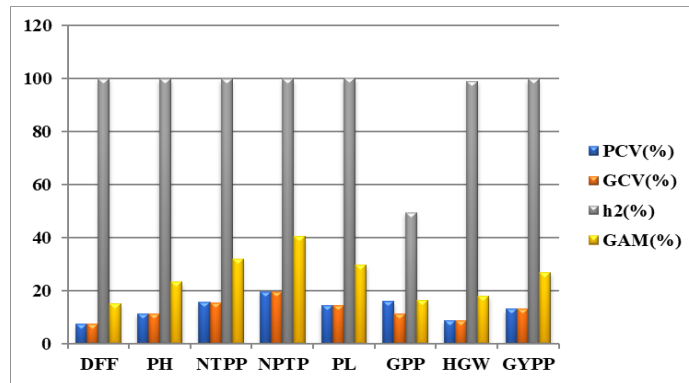


Fig. 8. Mean Performance of Grain Yield Per Plant of Fifty Rice Genotypes for Three Seasons.



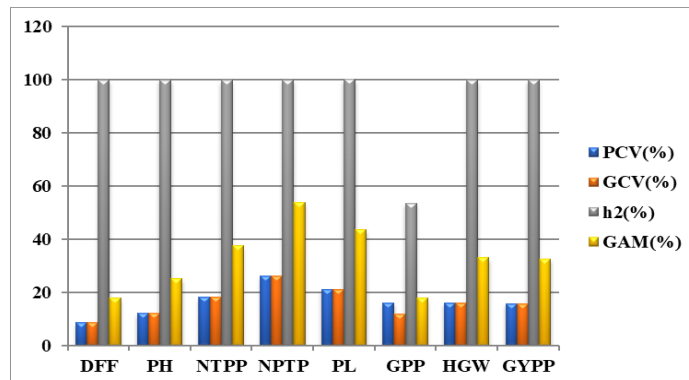
DFF- Days to fifty percent flowering, PH- Plant height (cm), NTPP- No. of tillers per plant, NPTP- No. of productive tillers per plant, PL- Panicle length (cm), GPP- grains per panicle, HGW- Hundred grain weight, GYPP- grain yield per plant.

Fig. 9. Genetic Variability Parameters for Fifty Rice Genotypes in Season 1.



DDF- Days to fifty percent flowering, PH- Plant height (cm), NTPP- No. of tillers per plant, NPTP- No. of productive tillers per plant, PL- Panicle length (cm), GPP- grains per panicle, HGW- Hundred grain weight, GYPP- grain yield per plant.

Fig. 10. Genetic Variability Parameters for Fifty Rice Genotypes in Season 2.



DDF- Days to fifty percent flowering, PH- Plant height (cm), NTPP- No. of tillers per plant, NPTP- No. of productive tillers per plant, PL- Panicle length (cm), GPP- grains per panicle, HGW- Hundred grain weight, GYPP- grain yield per plant.

Fig. 11. Genetic Variability Parameters for Fifty Rice Genotypes in Season 3.

CONCLUSIONS

Due to the consistent *per se* performance of CTH-1 for number of tillers per plant, number of productive tillers per plant, number of grains per panicle and grain yield per plant in pooled over environment, it could be concluded that CTH-1 is suitable for breeding programs to improve grain yield under saline conditions. The traits *viz.*, total number of tillers per plant, number of grains per panicle and grain yield per plant laid out moderate PCV and GCV revealing the existence of moderate level of variability in all the three seasons. The traits such as total number of tillers per plant, number of productive tillers per plant and panicle length demonstrated high heritability and genetic advance in all the three seasons which proved that selection of such traits would be effective as heritability was due to additive gene effects.

FUTURE SCOPE

Selection of genotypes with significant saline tolerant performance for use as donor parents in salinity stress breeding program would render new course of action in conserving prospects for ensuring food security in the midst of climate change and potentially pave way to expand crop yields for farmers in saline stress-vulnerable areas.

REFERENCES

Abhilash, R., Thirumurugan, T., Sassikumar, D. and Chitra, S. (2018). Genetic studies in F2 for biometrical traits in

Rice (*Oryza sativa*. L). *Electronic Journal of Plant Breeding*, 9(3), 1067-1076.

Ali, E. N., Rajeswari, S., Saraswathi, R. and Jeyaprakash, P. (2018). Genetic variability and character association for earliness, yield and its contributing traits in F2 population of rice (*Oryza sativa* L.). *Electronic Journal Plant Breeding*, 9(3), 1163-1169.

Aravind Balaji, A., Arumugam Pillai, M., Shoba, D., Aiyathan, E. A., Sathwik, B., Rapaka Percy, V. S., Madhuri, M., Bharath Kumar, M., Dileep Kumar, G. D., Chaithanya, K. and Fiyaz, R. A. (2022). Genetic variability studies in traditional rice landraces of India.

Bhargava, K., Shivani, D., Pushpavalli, S. N. C. V. L., Sundaram, R. M., Beulah, P. and Senguttuvel, P. (2021). Genetic variability, correlation and path coefficient analysis in segregating population of rice. *Electronic Journal of Plant Breeding*, 12(2), 549-555.

Burton, G. W. (1952). Quantitative inheritance in grasses. In: *Proc. 6th Inter Grassland Congr.*, 1, 356-363.

Chandramohan, Y., Srinivas, B., Thippeswamy, S. and Padmaja, D. (2016). Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Indian Journal of Agricultural Research*, 50(6), 609-613.

Elert, E. (2014). Rice by the numbers: a good grain. *Nature*, 514, S50-S51.

Fathima, M. A., Geetha, S., Amudha, K. and Uma, D. (2021). Genetic variability, frequency distribution and association analysis in ADT (R) 48 × Kavuni derived F2 population of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 12(3), 659-666.

Gautam, A., Suresh, J. and Madhav, M. S. (2016). Study of genetic variability in genotypes of rice (*Oryza sativa*

- L.). *Research Journal of Agricultural Sciences*, 7(1), 235-236.
- Hanson, C. H., Robinson, H. F. and Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza 1. *Agronomy journal*, 48(6), 268-272.
- Hosagoudar, G. N. and Shashidhar, H. E. (2018). Studies on variability and frequency distribution of yield and yield related traits in F₂ population of rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci*, 7(9), 2048-2052.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Genotypic and phenotypic correlations in Soybean and their application in selection. *Agronomy Journal*, 47:477-483.
- Kahani, F. and Hittalmani, S. (2015). Genetic analysis and traits association in F₂ intervarietal populations in rice under aerobic condition. *J Rice Res*, 3(152), 2.
- 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(1), 1-14.
- Kalaiselvan, S., Subramanian, A., Thirumurugan, T. and Rajanbabu, V. (2019). Genetic variability and association studies in F₂ population of rice under sodicity. *Electronic Journal of Plant Breeding*, 10(2), 601-613.
- Khandappagol, M., Rajanna, M. P. and Savita, S. K. (2019). Variability and frequency distribution studies in F₂ population of two crosses involving traditional varieties of rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, 8(1), 1630-1634.
- Kumar, V. (2015). Genetic diversity and character association studies for some economic traits in rice (*Oryza sativa* L.). *The Bioscan*, 10(2), 899-904.
- Lakshmi, M., Shanmuganathan, M., Jeyaprakash, P. and Ramesh, T. (2022). Genetic variability and diversity analysis in selected rice (*Oryza sativa* L.) varieties. *Electronic Journal of Plant Breeding*, 13(3), 959-966.
- Lingaiah, N. (2018). Variability studies in F₂ population of Rice (*Oryza sativa* L.). *International Journal of Agriculture Sciences*, 10(9).
- 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.
- Mahantashivayogayya, K., Lakkundi, B. S., Kuchunur, P. H. and Vishwanath, J. (2016). Genetic variability studies on rice (*Oryza sativa* L.) mutants for yield and yield components in normal and saline stress soil. *Electronic Journal of Plant Breeding*, 7(4), 1162-1168.
- Mohan, Y. C., Thippeswamy, S., Bhoomeshwar, K. and Madhavilatha, B. (2015). Diversity analysis for yield and gall midge resistance in rice (*Oryza sativa* L.) in northern Telangana zone, India. *SABRAO Journal of Breeding and Genetics*, 47(2), 160-171.
- Ramanjaneyulu, A. V., Shankar, V. G., Neelima, T. L. and Shashibhusahn, D. (2014). Genetic analysis of rice (*Oryza sativa* L.) genotypes under aerobic conditions on Alfisols. *SABRAO Journal of Breeding & Genetics*, 46(1).
- Rao, V. T., Mohan, Y. C., Bhadru, D., Bharathi, D. and Venkanna, V. (2014). Genetic Variability and Association Analysis in Rice.
- Rasheed, F., Anjum, N. A., Masood, A., Sofo, A. and Khan, N. A. (2020). The key roles of salicylic acid and sulfur in plant salinity stress tolerance. *Journal of Plant Growth Regulation*, 1-14.
- Sala, M. and Geetha, S. (2015). Variability studies for quality traits in rice with high iron and zinc content in segregating population. *Journal of Cereals and Oilseeds*, 6(7), 39-42.
- Sandeep, S., Sujatha, M., Subbarao, L. V. and Neeraja, C. N. (2018). Genetic variability, heritability and genetic advance studies in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Science*, 7(12), 3719-3727.
- Seneega, T. V., Gnanamalar, R.P., Parameswari, C., Vellaikumar, S. and Priyanka, A. R., (2019). Genetic variability and association studies in F₂ generation of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 10(2), 512-517.
- Shinde, S. R., Kamlesh, K. and Pawar, R. M. (2015). Genetic studies in upland rice (*Oryza sativa* L.). *International Journal of Plant Sciences (Muzaffarnagar)*, 10(1), 33-37.
- Sivasubramanian, J. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, 12, 15-16.
- Sruthi, S. R., Ivin, J. J. S., Williams, G. and Anbuselvam, Y. (2023). Genetic Variability and Diversity Analysis in Traditional Rice (*Oryza sativa* L.) Varieties of Tamil Nadu. *Environment and Ecology*, 41(2), 746-753.
- Sujitha, R., Pillai, M.A., Kannan, R. and Shoba, D. (2020). Genetic diversity and association studies in Rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, 9(6), 487-492.
- Swapnil, K. P., Chakraborty, M., Singh, D. N., Kumari, P. and Ekka, J. P. (2020). Genetic variability, correlation and path coefficient studies in F₂ generation of rice (*Oryza sativa* L.). *International Journal of Chemical Studies*, 8(4), 3116-3120.
- Thippeswamy, S., Chandramohan, Y., Srinivas, B. and Padmaja, D. (2016). Selection of diverse parental lines for heterotic hybrid development in rice (*Oryza sativa* L.). *Sabrao J. Breed. Genet*, 48(3), 285-294.
- Venkatesan, M., Sowmiya, C. A. and Anbarasi, B. (2017). Studies on variability, heritability and genetic advance analysis in rice (*Oryza sativa* L.) under submergence. *International Journal of Agricultural Sciences*, 13(1), 49-52.
- Waqas, M. A., Kaya, C., Riaz, A., Farooq, M., Nawaz, I., Wilkes, A. and Li, Y. (2019). Potential mechanisms of abiotic stress tolerance in crop plants induced by thiourea. *Frontiers in Plant Science*, 10, 1336.

How to cite this article: S.R. Sruthi, Laleeth Kumar N., Y. Anbuselvam, J.L. Joshi and Johnny Subakar Ivin (2023). Genetic variability Studies in Rice (*Oryza sativa* L.) varieties for Three Seasons under Saline conditions of Annamalai Nagar, an East Coast Region of Tamil Nadu. *Biological Forum – An International Journal*, 15(9): 528-535.