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Assessment of Genetic variability in Segregating Generations of Rice (*Oryza sativa* L.) under Saline Soil conditions

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ABSTRACT: Rice holds a crucial position in Indian agriculture and is cultivated in a wide range of environments and affected by various abiotic stresses such as salinity, alkalinity, drought, and cold. This research aims to explore the genetic diversity and potential adaptations of rice varieties to saline soil, which is critical for developing improved cultivars with enhanced salt tolerance. Two F_2 populations *i.e.*, KPS-10642 × RNR-11718 (cross 1) and KPS-10642 × CSR-27(cross 2) were evaluated at ARS, Kampasagar during *rabi* 2021-22 to assess the extent and nature of variability, heritability, and genetic advancement in rice for grain yield and its components under saline soil conditions. Sufficient amount of variation was observed in the two F_2 segregating populations for yield and its components. Number of tillers per plant, number of productive tillers per plant in cross 1, and number of filled grains per panicle and sterility percentage in both the crosses expressed high GCV and PCV indicating high level of variability. Furthermore, traits *viz.*, number of filled grains per panicle and sterility percentage in both the crosses and grain yield per plant in cross 1 exhibited high values of heritability and genetic advance as a per cent of mean indicating the role of additive gene action in governing these traits and effectiveness of simple selection. Consequently, these specific traits that contribute to grain yield under saline soil conditions hold promise for future utilization in rice breeding programs.

Keywords: Rice, genetic variability, heritability, genetic advance, salinity.

INTRODUCTION

Rice (*Oryza sativa* L.), being the predominant cereal crop, acts as the primary source of sustenance for over 3.5 billion global population. Enhanced rice productivity is crucial to meet the nutritional needs of the growing population and counterbalance the diminishing availability of arable land. However, the production and productivity of rice are significantly affected by various environmental stresses, including salinity. Salinity stress, caused by high levels of salt in the soil or water, poses a substantial threat to rice cultivation, leading to reduced growth, yield losses, and compromised food security. The area of salt-affected land in India amounts to around 6.727 million ha, which represents roughly 2.1% of the country's geographical area, out of which 2.956 million ha is saline affected and the rest 3.771 million ha is affected by sodicity (Kumar and Sharma 2020).

To alleviate soil salinity, understanding the genetic basis of salinity tolerance in rice is very important. It is widely accepted that studies on genetic variability and heritability plays a vital role in determining the adaptability and resilience of plants under saline conditions. These studies aim to identify genetic variations and their associations with salinity tolerance traits in rice populations. One effective approach for studying genetic variability is through the use of segregating generations. Segregating generations, such as F_2 and recombinant inbred lines (RILs), are derived from controlled crosses between two genetically diverse parental lines. These populations exhibit a wide range of genetic variations and by phenotyping segregating generations under salinity stress conditions, researchers can measure various salinity tolerance traits. These traits reflect the overall performance of rice plants under salinity stress and provide valuable information for understanding the genetic mechanisms underlying salinity tolerance.

By harnessing the inherent genetic variability in the F_2 segregating generation of rice, breeders have the potential to develop new varieties that possess enhanced yield and salinity tolerant traits. This progress ultimately contributes to global food security and the long-term sustainability of agriculture. Therefore, the present investigation was under taken with the view to find out genetic variability present in the segregating generations and the mode of inheritance.

MATERIAL AND METHODS

The experimental material comprised of six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of each of the two single crosses and were evaluated during *rabi* 2021-22 in Compact Family Block Design with two replications at ARS, Kampasagar. Six generations were then randomly allotted to each plot within a block. Each plot consisted of row length of 3m and two rows for each parent, F_1s and back cross generations and forty rows for F_2 generations. Inter and Intra row spacing was 20 cm and 15 cm, respectively. In this paper, studies on genetic variability and heritability were restricted to F_2 populations *i.e.*, KPS-10642 × RNR-11718 (cross 1) and KPS-10642 × CSR-27 (cross 2). Observations were taken on randomly selected 150 plants in each replication for days to 50% flowering, plant height, panicle length, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, sterility percentage, length-breadth ratio, 1000-grain weight and grain yield per plant. The phenotypic and genotypic coefficient of variation were computed by the method reported by Burton and De Vane (1953). Parents and F_1 were evaluated along with the F_2 population to calculate the environmental variance using the following formulae (Globerson *et al.*, 1987).

Environmental variance (Error variance) = $(V_{pP1} + V_{pP2} + V_{pF1})/3$

Genotypic variance of F_2 population = Phenotypic variance of F_2 population - Error variance

where;

V_{pP1} = Phenotypic variance in parent 1 of the cross

V_{pP2} = Phenotypic variance in parent 2 of the cross

V_{pF1} = Phenotypic variance in F_1

RESULT AND DISCUSSION

The F_2 population resulting from the cross between KPS-10642 and RNR-11718 indicated significant variation for all the studied traits (Table 1, Fig. 1). Days to flowering ranged from 75 to 103 days, with an average of 89 days. Plant height varied from 51 cm to 105 cm, with a mean of 87 cm. Panicle length ranged from 17 cm to 30 cm, averaging at 23 cm. The number of tillers per plant varied from 5 to 25, with an average of 11 tillers. Similarly, the number of productive tillers per plant ranged from 1 to 24, with a mean of 11 productive tillers. The number of filled grains per panicle was in the range of 31 to 230, with a mean of 115 filled grains. Sterility percentage ranged from 2.67% to 57.90%, averaging at 15%. The length-breadth ratio ranged from 2.48 to 5.03, with a mean value of 3.7. The 1000-grain weight ranged from 12 g to 24 g, with an average weight of 18 g. Grain yield per plant varied from 6 g to 28 g, with a mean yield of 17 g. Similarly, the F_2 population of the cross, KPS-10642 × CSR-27 had shown notable variation for all the traits analyzed (Table 2, Fig. 2). Days to flowering ranged from 78 to 98 days, with an average of 90 days. Plant height ranged from 26 cm to 106 cm, with a mean of 76 cm. Panicle length ranged from 12.5 cm to 28 cm, averaging at 21 cm. The number of tillers per plant varied from 7 to 22, with an average of 11 tillers. The number of productive tillers per plant ranged from 7 to 21, with a mean of 10 productive tillers. The number of filled grains per panicle spanned from 40 to 212, with a mean of 104 filled grains. Sterility percentage ranged from 1.87% to 54.40%, averaging at 14%. The length-breadth ratio ranged from 2.90 to 5.04, with a mean value of 4.04. The 1000-grain weight ranged from 12 g to 26 g, with an average weight of 19 g. Grain yield per plant ranged from 6 g to 27 g, with a mean yield of 15 g.

Genetic variability in any crop is a pre-requisite for selection of superior genotypes over the existing cultivars. In the present investigation, the Phenotypic Coefficient of Variation (PCV) was greater than the Genotypic Coefficient of Variation (GCV) for all traits studied in both F_2populations representing the magnitude of environmental influence on expression of the traits (Table 1 and 2). In the cross 1 (KPS-10642 × RNR-11718), number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle and sterility percentage exhibited high GCV and PCV which were in accordance with Rani *et al.* (2016). Low GCV and PCV were found for days to flowering and plant height. These results were in accordance with that of Sala *et al.* (2015); Rani *et al*. (2016). Asante *et al*. (2019), Kalaiselvan *et al*. (2019); Priyanka *et al*. (2019); Bhargava *et al*. (2021) reported low GCV and PCV for days to flowering. Savitha and Ushakumari (2015); Roy *et al.* (2015); Asante *et al*. (2019) also reported low GCV and PCV for plant height. Panicle length had moderate GCV and PCV while, 1000-grain weight and grain yield per plant had moderate GCV and high PCV. Dhanwani *et al.* (2013) found similar results. Length-breadth ratio had low GCV and moderate PCV.

In the cross 2 (KPS-10642 × CSR-27), number of filled grains per panicle, sterility percentage and grain yield per plant had high GCV and PCV. These results were similar to the results of Mamata *et al*. (2018). The traits *viz.*, plant height and 1000-grain weight exhibited moderate GCV and PCV. Dhanwani *et al.* (2013) reported similar findings. Kalaiselvan *et al*. (2019); Priyanka *et al*. (2019); Bhargava *et al*. (2021) reported similar results for days to flowering and plant height. Panicle length and length-breadth ratio had low GCV and moderate PCV, while number of tillers per plant and number of productive tillers per plant reported had moderate GCV and high PCV. Low PCV and GCV were reported for days to flowering which was in accordance with Sala *et al.* (2015); Rani *et al.* (2016).

High heritability was observed for days to flowering, plant height, number of filled grains per panicle and sterility percentage (Table 1, Fig. 3) and the remaining traits had moderate values of heritability. High genetic advance as per cent of mean (GAM) was observed for number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle and sterility percentage. Panicle length, length-breadth ratio, 1000-grain weight and grain yield per plant had moderate genetic advance as per cent of mean, whereas days to flowering and plant height had low GAM.

Similarly in cross 2, high heritability was observed for days to flowering, plant height, number of filled grains per panicle and sterility percentage. All the other remaining traits exhibited moderate values of heritability except number of productive trillers per plant and length-breadth ratio. High genetic advance as per cent of mean (GAM) was observed for number of filled grains per panicle, sterility percentage and grain yield per plant. Dhanwani *et al*. (2013) also found similar results for number of filled grains per panicle. Plant height, panicle length, number of tillers per plant, number of productive tillers per plant and 1000-grain weight had moderate genetic advance as per cent of mean, whereas days to flowering and length-breadth ratio had low GAM (Table 2; Fig. 4).

The segregants of both the F_2 populations expressed high genetic advance as a per cent of mean for the traits *viz.*, number of filled grains per panicle and sterility percentage and for grain yield per plant in F_2 of cross 1 suggesting that additive gene action played a major role in governing these traits hence, selection could be effective for desired genetic improvement. Similar findings were reported by Dutta *et al*. (2013); Tuhina *et al*. (2015); Lingaiah *et al*. (2020); Priyanka *et al*. (2019); Seneega *et al*. (2019); Shrivastav *et al*. (2020); Bhargava *et al*. (2021) for number of filled grains per panicle. High heritability coupled with moderate GAM was reported for plant height in cross 1 indicating the preponderance of additive and non-additive gene action. Moderate heritability coupled with high GAM was observed for panicle length and number of tillers per plant in cross 1. This clearly emphasized that there is an ample scope for improvement of traits *i.e.*, number of filled grains per panicle, sterility percentage and grain yield per plant through selection.

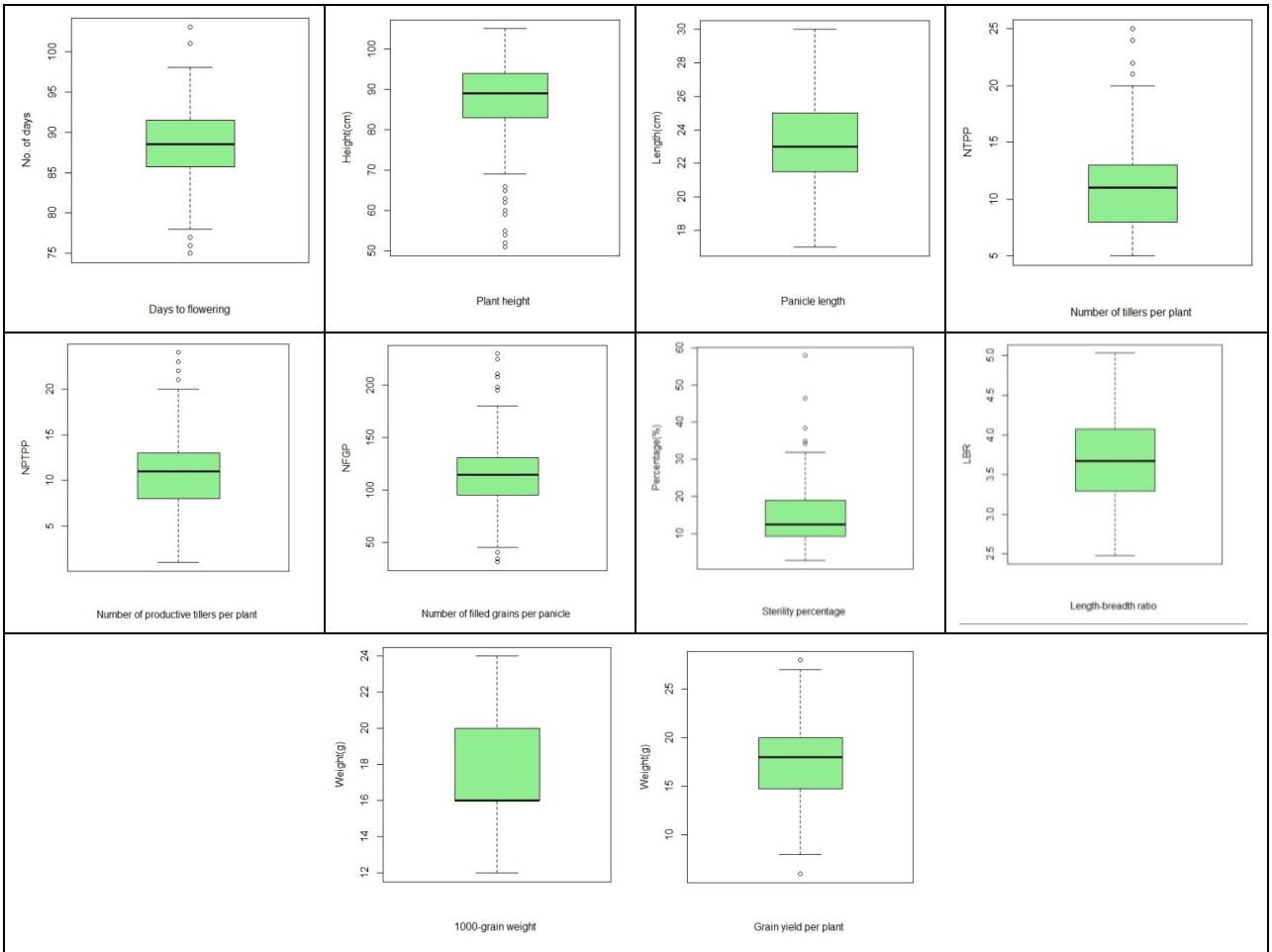

Fig. 1. Boxplots showing variation for yield and its components in F_2 population of KPS-10642 × RNR-11718 in rice under saline soil conditions.

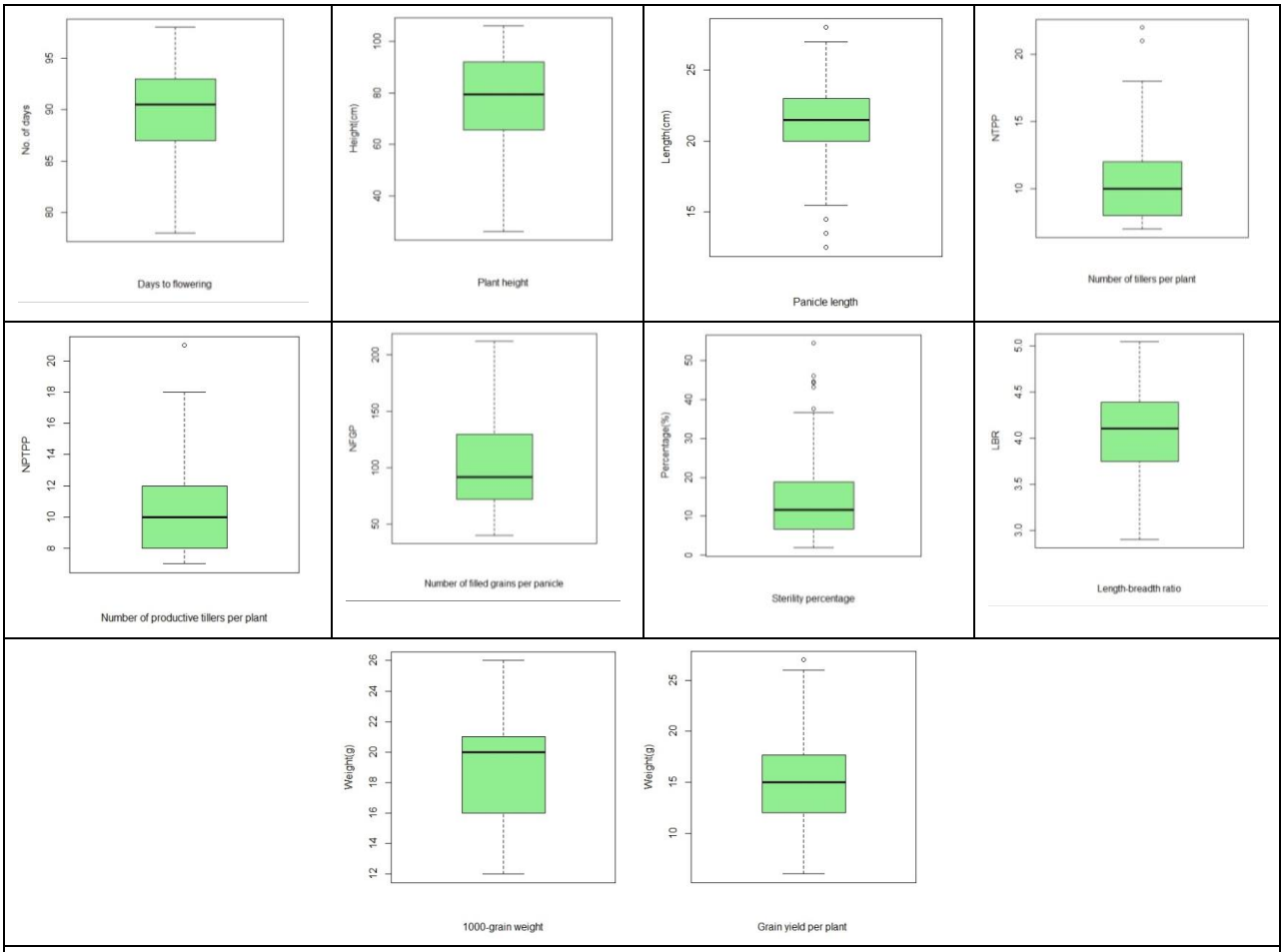

Fig. 2. Boxplots showing variation for yield and its components in F_2 population of KPS-10642 × CSR-27 in rice under saline soil conditions.

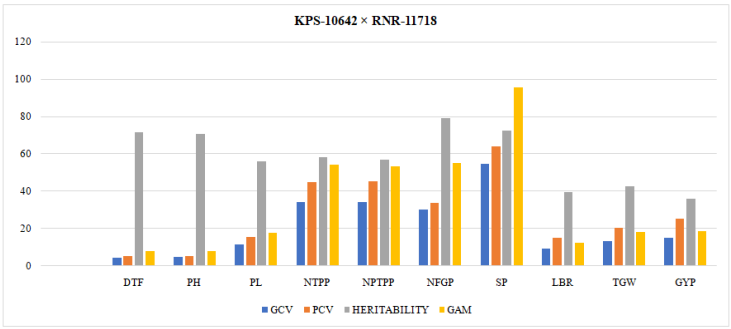

Fig. 3. GCV, PCV, h^2_{bs} and GAM for grain yield and its components in F_2 population of KPS-10642 × RNR-11718 in rice under saline soil conditions.

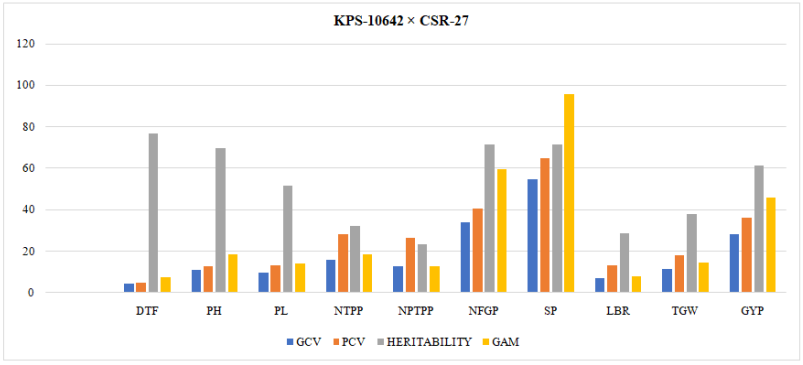

Fig. 4. GCV, PCV, h^2_{bs} and GAM for grain yield and its components in F_2 population of KPS-10642 × CSR-2 7 in rice under saline soil conditions.

Table 1: **Estimates of genetic variability parameters for grain yield and its components in F_2 population of KPS-10642 × RNR-11718 in rice under saline soil conditions.**

PARAMETERS	MEAN	RANGE		GCV (%)	PCV (%)	Heritability in broad-sense (h^2_{bs})	GAM (%)
		MIN	MAX				
Days to flowering	89	75	103	4.55	5.37	0.72	7.94
Plant height (cm)	87	51	105	4.69	5.56	0.71	8.14
Panicle length (cm)	23	17	30	11.62	15.52	0.56	17.94
Number of tillers per plant	11	5	25	34.52	45.14	0.58	54.37
Number of productive tillers per plant	11	1	24	34.51	45.71	0.57	53.66
Number of filled grains per panicle	115	31	230	30.26	33.99	0.79	55.49
Sterility percentage (%)	15	2.67	57.90	54.70	64.22	0.73	95.99
Length-breadth ratio	3.7	2.48	5.03	9.46	14.99	0.40	12.29
1000-grain weight (g)	18	12	24	13.44	20.50	0.43	18.16
Grain yield per plant (g)	17	6	28	15.29	25.47	0.36	18.91

Table 2: Estimates of genetic variability parameters for grain yield and its components in F_2 population of KPS-10642 × CSR-27 in rice under saline soil conditions.

Parameters	Mean	Range		GCV (%)	PCV (%)	Heritability in broad-sense (h^2_{bs})	GAM (%)
		Min	Max				
Days to flowering	90	78	98	4.25	4.85	0.77	7.68
Plant height (cm)	76	26	106	10.82	12.98	0.70	18.59
Panicle length (cm)	21	12.5	28	9.54	13.30	0.51	14.09
Number of tillers per plant	11	7	22	15.90	28.09	0.32	18.54
Number of productive tillers per plant	10	7	21	12.70	26.28	0.23	12.65
Number of filled grains per panicle	104	40	212	34.10	40.37	0.71	59.34
Sterility percentage (%)	14	1.87	54.4	54.90	64.91	0.72	95.66
Length-breadth ratio	4.04	2.90	5.04	7.12	13.32	0.29	7.85
1000-grain weight (g)	19	12	26	11.30	18.31	0.38	14.35
Grain yield per plant (g)	15	6	27	28.43	36.37	0.61	45.78

CONCLUSIONS

From the present study, it was revealed that there was an ample amount of genetic variability in the two F_2 populations for the traits *viz.,* number of filled grains per panicle, sterility percentage and grain yield per plant with high heritability coupled with genetic advance as per cent of mean and are the important yield influencing traits in specific crosses of rice under saline soil conditions. Hence, selection of these traits could enhance the grain yield in rice under such conditions. Therefore, it would be advantageous to prioritize these traits when designing crop improvement programs.

FUTURE SCOPE

The future direction of the study, focusing on the assessment of genetic variability in segregating generations of rice under saline soil conditions, involves advancing our understanding of the precise genes and molecular mechanisms responsible for salt tolerance. To accomplish this, cutting-edge genomic techniques like genome-wide association studies (GWAS) and transcriptomics analysis can be employed to identify pivotal genetic markers and pathways associated with salt tolerance. Furthermore, the investigation could extend into exploring the potential applications of gene editing technologies, such as CRISPR-Cas9, to precisely introduce or modify salt tolerance-related genes in rice varieties, thereby fostering the development of exceptionally salt-tolerant cultivars.

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Conflict of Interest. None.

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