

In vivo evaluation of genetic variability associated traits in advance hybrids of rice (*Oryza sativa*) for salt stress in different planting conditions

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ABSTRACT

The present investigation entitled "In vivo Evaluation of genetic variability associated traits in advance hybrids of rice for salt stress in different planting conditions" was conducted at Terrace of Phytotron lab of Genetics and Plant Breeding, SVPUIAT, Meerut Uttar Pradesh during *kharif* crop season 2024. The study aimed to evaluate the extent of genetic variation present among the hybrids and the parents of rice for yield and its contributing traits for salt Stress. The experiment followed a complete randomized design (CRD) with three replications. The experiment consisted of Controlled and saline (8EC) conditions. PCV was greater than GCV suggesting environmental influence additive gene action. The results underlined the potential of exploiting genetic variability for improving yield and accelerating genetic gains in mustard breeding programs. High heritability accompanied by high genetic advance as percent mean was recorded for traits including biological yield, grain yield per plant, spikelets per panicle and test weight across control, and treated environments. This combination of parameters points to the predominance of additive gene action in these traits, indicating that direct phenotypic selection would be efficient for genetic improvement. Traits with moderate to high heritability and genetic advance, such as tillers per plant, flag leaf area, and harvest index, further reinforce their suitability as selection criteria in breeding programs.

Key words: Rice, Salinity, variability, yield, F_1 , heritability, GCV (Genotypic coefficient of variation), PCV (Phenotypic coefficient of variation), GA (genetic advance), GAM (Genetic Advance % Mean), Hbs (broad-sense heritability).

Introduction

Rice (*Oryza sativa* and *Oryza glaberrima*) is a staple crop, providing over half the daily calories and 20% of global dietary energy to more than 3.5 billion people worldwide. In the 2024–25 agricultural cycle, global rice production hit a record high, with 168.8 million hectares harvested and 533.8 million tonnes

of milled rice produced. The USDA Rice Outlook (November 2024 edition), credited India as the top producer, cultivating 50.0 million hectares and producing 145.0 million tonnes, an increase of 3 million tonnes from the previous year driven by favorable growing conditions and strong yields.

Rice is diploid species with 12 chromosome pairs ($2n = 24$) and a genome size of about 430 Mb. Both

share the AA genome and wide genetic diversity, with wild relatives contributing drought and pest resistance (Sarla *et al.*, 2005). Rice's small, well-characterized chromosomes facilitate genetic mapping and marker-assisted selection for stress tolerance. Productivity is limited by abiotic stresses, with salinity second only to drought. Globally, 1.38 billion ha are salt-affected, including 6.73 million ha in India. Salinity hampers growth and yield by causing osmotic stress that reduces water uptake and ionic toxicity from excess Na and Cl⁻, disrupting nutrient balance, damaging membranes, and impairing photosynthesis.

Genetic variability for salt tolerance is pronounced in rice, varying considerably across genotypes, especially during sensitive growth stages such as seedling establishment and flowering. The ability to regulate ion homeostasis and maintain osmotic balance under saline conditions is key to varietal performance (Mohammadinezhad *et al.*, 2010). Pot screening offers a controlled environment to accurately evaluate this genetic diversity. Unlike field trials, pots allow uniform salinity treatment and minimize environmental variability due to uneven soils or changing weather (Kakar *et al.*, 2019).

This precision enables clearer differentiation of tolerant genotypes through traits like root/shoot growth and biomass under consistent conditions. Moreover, pot screening facilitates rapid, early-stage screening of large germplasm collections and complements molecular marker analyses targeting key salt tolerance genes (Aslam *et al.*, 1993).

This study focuses on evaluating genetic variability and morphological trait performance under salt stress in advanced rice hybrids across diverse planting conditions. Understanding the extent of genetic variability among rice genotypes under both normal and salt stress conditions is crucial for effective selection of promising lines. Parameters such as the genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) provide valuable estimates of the variability present for important traits. When heritability is high alongside high genetic advance and genetic advance as percent of mean (GAM), it indicates that additive gene effects are predominant, suggesting that selection for these traits will be effective. Pot screening under controlled environments allows for precise management of salinity levels, minimizing environmental variability and enabling accurate measurement of these genetic parameters. This controlled approach

makes it possible to reliably assess variability and identify superior rice genotypes for salt tolerance, accelerating breeding programs targeted at improving yield stability and performance under saline and non-saline conditions.

Materials and Methods

The present experiment was conducted at Terrace of Phytotron lab of Genetics and Plant Breeding, SVPUAT, Meerut, Modipuram, Uttar Pradesh during *Kharif* crop season 2024-25. The experimental material comprised twelve rice genotypes, including four salt-tolerant testers and eight salt-tolerant lines selected based on previous screening for salinity tolerance. All genotypes were sourced from established breeding programs and confirmed for distinct phenotypic traits associated with salt tolerance. The study employed a line × tester mating design (Kempthorne, 1957). Each of the eight lines was crossed with each of the four testers, resulting in a total of 32 hybrids. Parental genotypes and F1 hybrids, were grown under controlled and saline conditions. Standard cultural practices were followed and experimental pots were arranged using a completely randomized design (CRD) with 3 replication for each environment. In the present study, each pot measured 30 cm in length and 30 cm in width, and contained 18 kg of air-dried soil. Three rice plants were accommodated per pot, and for each genotype, three replicate pots were maintained per experimental replication.

Crossing Procedure

Crosses were made between all possible combinations of testers and lines, with the lines as female parents and the testers as male parents. Each cross was performed manually following emasculation and controlled pollination protocols to ensure genetic purity. Seeds from each successful cross were sown in pots under both controlled (non-saline) and Treated (Saline) conditions for evaluation as per experimental requirements.

Salinity Induction Protocol for Pot Experiment

To induce salinity stress, an 8 dS/m (EC) salt solution was prepared and applied to saturate the soil in each pot, ensuring uniform distribution of saline conditions at the start of the experiment. The electrical conductivity (EC) of the soil in every pot was monitored weekly. After collecting soil samples

from each pot, EC was measured, and if a deficit from the target value (8 dS/m) was detected, additional salt solution was supplemented to the respective pots to restore and maintain the desired salinity level. This approach effectively ensured that salinity stress remained consistent throughout the crop growth period, enabling accurate evaluation of genotype responses under controlled stress conditions.

Evaluation Criteria

The evaluation criteria encompassed a comprehensive assessment of morphological, physiological, and yield-related traits in all rice genotypes under both normal and salt stress conditions. Observations were recorded for key agronomic parameters including days to 50% flowering, days to maturity, plant height, flag leaf area, tillers per plant, panicle length, spikelets per panicle, grains per panicle, spikelet fertility percentage, grain length, grain breadth, and L/B ratio. In addition, physiological traits such as chlorophyll content, canopy temperature, relative water content, membrane stability, and other key salt stress indicators were systematically measured. Yield and contributing traits 1000 grain weight, biological yield, harvest index, and economic yield were also evaluated for all genotypes in both the control and salinity treatments. This comprehensive set of measurements enabled detailed analyses of genetic variability of both parental lines, testers, and hybrids were evaluated for a range of Morphological physiological, and yield-related traits under control and stress conditions.

Data analysis

The recorded data were analysed using appropriate statistical methods to assess the extent of genetic variability. Analysis of variance was carried out following the procedure described by Panse and Sukhatme (1954). Estimates of PCV and GCV were computed as outlined by Burton (1952), while heritability and GA were calculated using the methods suggested by Singh and Choudhary (1977).

Days to 50% flowering

Under control conditions, the duration ranged from 79.33 to 121.00 days with a GCV of 9.28% and PCV of 9.72%. The trait demonstrated a high broad-sense heritability of 91.09%, genetic advance GA of 17.46, and genetic advance as percent of mean GAM of 18.24%. Under salt stress, the flowering duration

increased to a range of 82.43 to 128.33 days, with GCV and PCV values rising to 10.64% and 10.95%, respectively. Heritability also improved to 94.52%, alongside GA of 22.53 and GAM of 21.32%. highlighting consistent genetic control across conditions.

Days to Maturity

Maturity period under control varied between 108.00 and 147.33 days, with GCV of 6.77%, PCV 7.32%, heritability of 85.53%, GA 16.26, and GAM 12.90%. Following salt treatment, maturity was slightly prolonged (110.32 to 148.33 days), accompanied by marginal increases in GCV (6.87%) and PCV (7.42%), heritability 85.61%, GA 17.46, and GAM 13.09%. indicating stable genetic variability under both conditions.

Plant Height

Control plant height showed a broad range of 72.43 cm to 134.87 cm, with GCV 14.51%, PCV 15.12%, heritability 92.06%, GA 29.30, and GAM 28.68%. Salt treatment reduced the height range to 68.38–125.03 cm but increased GCV to 17.11%, PCV to 17.60%, heritability to 94.46%, GA to 31.95, and GAM to 34.25%, confirming substantial genetic control for this trait.

Flag Leaf Area

Flag leaf area under control ranged from 12.81 to 27.76 cm², with GCV 17.75%, PCV 18.25%, heritability 94.63%, GA 7.57, and GAM 35.57%. Treated plants showed a narrower range (11.13–23.82 cm²) but higher GCV (18.79%), PCV (19.26%), heritability (95.25%), GA (6.68), and GAM (37.78%).

Tillers per Plant

Tiller number showed variation from 8.87 to 18.33 in control, with GCV 13.84%, PCV 14.43%, heritability 91.97%, GA 3.88, and GAM 27.34%. Salt treatment narrowed the range (6.07 to 16.33) but raised GCV to 18.42%, PCV to 18.86%, heritability to 95.47%, GA to 4.28, and GAM to 37.08%.

Panicle Length

Under control, panicle length ranged from 18.08 to 25.90 cm, showing GCV of 8.16% and PCV of 9.13%. Heritability was moderate at 80.00%, with a GA of 3.38 and GAM of 15.04%. Salt treatment reduced the range to 14.75–23.52 cm, slightly increasing GCV (8.88%), PCV (9.70%), heritability (83.89%), while GA and GAM stood at 3.25 and 16.76%.

Spikelets per Panicle

Control conditions exhibited 71.32 to 153.80 spikelets per panicle with GCV 14.44%, PCV 14.99%, heritability 92.84%, GA 37.72, and GAM 28.67%. The treated range was 68.32 to 148.47 spikelets, with increased GCV (17.93%), PCV (18.38%), heritability (95.18%), GA (41.37), and GAM (36.04%).

Grains per Panicle

The number of grains per panicle varied from 49.00 to 133.20 in control, with high GCV (19.11%) and PCV (19.53%). Heritability was 95.77%, GA 40.92, and GAM 38.53%. Under salt stress, grain numbers ranged 39.37 to 121.83 with increased GCV (24.63%), PCV (24.94%), heritability (97.50%), GA (41.38), and GAM (50.10%).

Spikelet Fertility (%)

Spikelet fertility ranged from 50.20% to 94.34% in control, with GCV 11.35%, PCV 12.03%, heritability 88.90%, GA 17.70, and GAM 22.04%. Treated plants had a similar range of 49.20% to 87.61%, but higher variability (GCV 15.04%, PCV 15.56%), heritability of 93.46%, GA 20.66, and GAM 29.96%.

Grain Length

Control grain length varied between 7.84 and 13.88 mm, with GCV 13.06%, PCV 13.69%, heritability 91.08%, GA 2.68, and GAM 25.68%. Treatment reduced the range slightly to 7.54–12.76 mm, with GCV 12.55%, PCV 13.22%, heritability 90.11%, GA 2.46, and GAM 24.55%.

Grain Length

Grain length ranged from 7.84 mm to 13.88 mm in control, with a genotypic coefficient of variation (GCV) of 13.06% and phenotypic coefficient of variation (PCV) of 13.69%. The trait showed high broad-sense heritability of 91.08%, genetic advance (GA) of 2.68, and genetic advance as percent of mean (GAM) of 25.68%. Under salt stress, grain length slightly decreased, ranging from 7.54 mm to 12.76 mm, with GCV 12.55%, PCV 13.22%, heritability 90.11%, GA 2.46, and GAM 24.55%.

Grain Breadth

Control plants had grain breadth ranging from 2.10 mm to 3.53 mm, with GCV 16.18%, PCV 16.73%, heritability 93.57%, GA 0.92, and GAM 32.24%. Under salt treatment, the range reduced to 1.73 mm to

3.27 mm, but GCV and PCV slightly increased to 17.22% and 17.73%, heritability reached 94.29%, GA was 0.80, and GAM 34.44%.

Length/Breadth Ratio

This ratio showed significant variability across environments. Control values ranged from 2.50 to 5.71 with GCV 24.25%, PCV 24.62%, heritability 96.98%, GA 1.84, and GAM 49.19%. Salt-treated plants varied from 2.47 to 5.87, showing a decrease in GCV (19.87%) and PCV (20.30%) but high heritability (95.77%), GA 1.76, and GAM 40.05%.

1000 Grain Weight

Under control conditions, 1000-grain weight ranged from 18.96 to 24.80 g, with a GCV of 6.62% and PCV of 7.23%. Heritability was 83.81%, with GA 2.73 and GAM 12.49%. Salt stress reduced the weight range to 16.04–23.63 g but increased GCV and PCV to 9.58% and 9.96%, heritability to 92.47%, GA to 3.83, and GAM to 18.98%.

Biological Yield

Biological yield under control ranged from 39.32 to 87.32 g with GCV 18.25% and PCV 18.71%. Heritability was very high at 95.16%, with GA 22.67 and GAM 36.67%. Under salt treatment, yield ranged from 33.28 to 76.94 g, with increased variability (GCV 20.29%, PCV 20.76%), higher heritability (95.52%), GA 22.68, and GAM 40.85%.

Harvest Index

Harvest index in control conditions ranged from 31.22% to 66.15%, with GCV of 20.03% and PCV of 20.47%. The heritability was notably high at 95.73%, accompanied by GA of 18.07 and GAM of 40.37%. Under salt stress, the range narrowed to 19.54%–55.30%, but GCV increased to 24.09%, PCV rose to 24.47%, and heritability improved to 96.86%, with GA of 19.42 and GAM of 48.84% revealing strong genetic contribution under all conditions.

Chlorophyll Content

Chlorophyll content in control plants ranged from 33.28 to 48.34 SPAD units, with GCV of 9.69%, PCV of 10.60%, heritability of 83.61%, GA of 7.22, and GAM of 18.26%. Treated plants showed slightly reduced ranges of 30.00 to 45.26 SPAD units, but increased GCV (10.57%), PCV (11.39%), heritability (86.09%), GA (7.37), and GAM (20.20%).

Table 1.

Character	Range		Heritability		GCV %		PCV %		GA		GAM	
	Controlled	Treated	Controlled	Treated	Controlled	Treated	Controlled	Treated	Controlled	Treated	Controlled	Treated
Days to 50% flowering	79.33 – 121.00	82.43 – 128.33	91.09	94.52	9.28	10.64	9.72	10.95	16.26	17.46	18.24	21.32
Days to Maturity	108.00 – 147.33	110.32 – 148.33	85.53	85.61	6.77	6.87	7.32	7.42	29.30	31.95	12.90	13.09
Plant Height (cm)	72.43 – 134.87	68.38 – 125.03	92.06	94.46	14.51	17.11	15.12	17.60	7.57	6.68	28.68	34.25
Flag Leaf Area (cm ²)	12.81 – 27.76	11.13 – 23.82	94.63	95.25	17.75	18.79	18.25	19.26	3.88	4.28	35.57	37.78
Tillers per Plant	8.87 – 18.33	6.07 – 16.33	91.97	95.47	13.84	18.42	14.43	18.86	3.38	3.25	27.34	37.08
Panicle Length (cm)	18.08 – 25.90	14.75 – 23.52	80.00	83.89	8.16	8.88	9.13	9.70	37.72	41.37	15.04	16.76
Spikelets per Panicle	71.32 – 153.80	68.32 – 148.47	92.84	95.18	14.44	17.93	14.99	18.38	40.92	41.38	28.67	36.04
Grains per Panicle	49.00 – 133.20	39.37 – 121.83	95.77	97.50	19.11	24.63	19.53	24.94	17.70	20.66	38.53	50.10
Spikelet Fertility %	50.20 – 94.34	49.20 – 87.61	88.90	93.46	11.35	15.04	12.03	15.56	2.68	2.46	22.04	29.96
Grain Length (mm)	7.84 – 13.88	7.54–12.76	91.08	90.11	13.06	12.55	13.69	13.22	0.92	0.80	25.68	24.55
Grain Breadth (mm)	2.10 – 3.53	1.73 – 3.27	93.57	94.29	16.18	17.22	16.73	17.73	1.84	1.76	32.24	34.44
Length/Breadth Ratio	2.50 – 5.71	2.47 – 5.87	96.98	95.77	24.25	19.87	24.62	20.30	2.73	3.83	49.19	40.05
1000 Grain Weight(g)	18.96 – 24.80	16.04 – 23.63	83.81	92.47	6.62	9.58	7.23	9.96	22.67	22.68	12.49	18.98
Biological Yield(g)	39.32 – 87.32	33.28 – 76.94	95.16	95.52	18.25	20.29	18.71	20.76	18.07	19.42	36.67	40.85
Harvest Index (%)	31.22 – 66.15	19.54 – 55.30	95.73	96.86	20.03	24.09	20.47	24.47	7.22	7.37	40.37	48.84
Chlorophyll Content (SPAD)	33.28 – 48.34	30.00 – 45.26	83.61	86.09	9.69	10.57	10.60	11.39	0.33	0.26	18.26	20.20
Canopy Temperature (°C)	33.13 – 34.89	33.12 – 35.32	28.86	23.54	0.87	0.74	1.63	1.53	11.77	6.82	0.97	0.74
Relative Water Content(%)	67.43 – 91.30	62.37 – 76.47	86.10	78.95	7.83	5.55	8.44	6.25	10.36	10.68	14.97	10.16
Membrane Stability(%)	69.52 – 90.27	59.55 – 83.63	76.75	81.00	7.29	8.29	8.32	9.21	9.83	11.27	13.16	15.36
Grain Yield (g)	18.34 – 35.53	11.49 – 31.39	94.98	97.51	17.86	25.32	18.32	25.65	17.46	22.53	35.85	51.51

Canopy Temperature

Control canopy temperature averaged 33.85°C, ranging between 33.13 and 34.89°C, with low heritability of 28.86%, GA 0.33, GAM 0.97%, GCV 0.87%, and PCV 1.63%. Treated plants showed a slight increase with average 34.39°C, range 33.12–35.32°C, heritability 23.54%, GA 0.26, GAM 0.74%, GCV 0.74%, and PCV 1.53%. indicating minimal genetic control over this trait.

Relative Water Content

RWC ranged from 67.43% to 91.30% (mean 78.59%) in control with heritability 86.10%, GA 11.77, GAM 14.97%, and moderate variation (GCV 7.83%, PCV 8.44%). In salt-treated plants, the mean dropped to 67.14% with a narrower range of 62.37%–76.47%, heritability decreased to 78.95%, GA 6.82, GAM 10.16%, with GCV 5.55% and PCV 6.25%.

Membrane Stability

The membrane stability index ranged from 69.52% to 90.27% (mean 78.72%) in control with heritability 76.75%, GA 10.36, GAM 13.16%, and GCV 7.29%, PCV 8.32%. Salt treatment reduced the mean to 69.51% and range to 59.55%–83.63%, though heritability was higher at 81.00%, GA increased to 10.68, GAM to 15.36%, with GCV 8.29%, PCV 9.21%.

Grain Yield

Grain yield ranged between 18.34 g and 35.53 g (mean 27.42 g) in control with high heritability of 94.98%, genetic advance of 9.83, and genetic advance as percent of mean of 35.85%. Under salt stress, yield dropped (11.49–31.39 g) but with higher heritability (97.51%), genetic advance (11.27), and GAM (51.51%), as well as increased GCV (25.32%) and PCV (25.65%) underscoring significant genetic variation and potential for improvement under stress conditions.

In all the traits studied, PCV was slightly higher than GCV indicating influence of environmental factors. The results are in agreement with (Kumar *et al.* (2018) and

Barde *et al.* (2021). High heritability accompanied by high GAM was recorded for traits including biological yield, grain yield per plant, spikelets per panicle, and test weight across control, treated environments. This combination of parameters points to the predominance of additive gene action in these traits, indicating that direct phenotypic selection would be efficient for genetic improvement. Traits with moderate to high heritability and genetic advance, such as tillers per plant, flag leaf area, and harvest index, further reinforce their suitability as selection criteria in breeding programs. Similar findings were reported earlier in Rice by Sravan *et al.* (2012), Yadav *et al.* (2018) and Dheeraj *et al.* (2023).

Conclusion

The study of genetic variability in evaluated genotypes revealed significant variation across many traits. Traits such as biological yield, grain yield per plant, tillers per plant, flag leaf area, plant height, and spikelet/panicle showed considerable ranges indicating substantial genetic diversity. High heritability coupled with high genetic advance as percent of mean was observed for biological yield, grain yield per plant, spikelet/panicle, among other key traits, illustrating predominant additive gene action and low environmental influence. This suggests that selection for these traits would effectively improve yield under both control and salt-stressed environments. Overall, the presence of substantial genetic variability indicates promising potential for selection and breeding to develop salt-tolerant, high-yielding rice cultivars. The traits with both high heritability and genetic advance offer the best opportunity for targeted breeding and selection efforts for improving salinity tolerance and yield performance.

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Conflict of Interest

The authors declare that there is no conflict of inter-

est regarding publication of this research paper.

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