

Exploring the Spectrum of Saline Tolerance in Rice (*Oryza sativa* L.) Through a Comparative Multi-Trait Evaluation at the Seedling Stage

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Abstract

The present study was conducted to screen ten rice genotypes from 3000 rice genome project against salt stress under normal and saline conditions during early seedling stage using a hydroponic culture system with an objective of identifying traits and genotypes affiliated with the saline tolerance mechanism that would assist with the salt stress challenge. Salt stress significantly altered associations between rice seedling growth metrics. While balanced root-shoot growth was key in normal conditions, biomass accumulation and shoot growth became more critical under salt stress. The relationship between dry matter accumulation and water content gained importance and Na^+/K^+ ratio emerged as a crucial factor in salt sensitivity under saline conditions. The first three principal components explained the majority of genetic variation among rice genotypes under both normal and saline conditions. The analysis revealed complex relationships between growth, biomass accumulation, ion homeostasis and water relations. The genotype IRRI 146 emerged as a promising candidate for saline breeding programs, displaying high tolerance, enhanced performance under stress for key traits, and superior performance across multiple traits, outperforming the check variety in most aspects. The genotypes ARC 10905 and GITANO were observed to be saline susceptible.

Key words : Rice, saline, seedling, ions, tolerance.

The world's population growth is accelerating, causing an 87% increase in agricultural crops by 2050²⁴, with rice (*Oryza sativa* L.) playing a crucial role in addressing this challenge. Soil salinity, caused by excess sodium chloride from irrigation or natural deposition⁶, affects over 20% of cultivated lands globally, including half of irrigated areas,

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and is predicted to worsen¹⁹. Rice, a sensitive crop plant exhibiting a threshold of 3 dSm⁻¹ (Hoang *et al.*, 2017), faces significant challenges from salt stress, particularly during early seedling and reproductive phases³⁷. Rice genotypes respond differently to salt stress³³. Ionic toxicity disrupts ionic balance, leading to nutritional deficiencies in rice². Salt-sensitive rice accumulates sodium, affecting lipid metabolism, protein synthesis, and photosynthesis¹⁸ while salt-tolerant rice has greater Na⁺ exclusion capacity³⁷. Salt-affected regions in India are expanding due to limited precipitation, overuse, weathering, saline irrigation, and cultural practices²⁶. The 2004 tsunami disrupted east coast parts of Tamil Nadu, requiring the development of saline-tolerant genotypes to adapt to saline conditions above 2 dSm⁻¹ during seedling and reproductive stages²⁹. In this context, the objective of the current study was to screen ten rice genotypes from 3000 rice genomes project (3K RGP) against salt stress under normal and saline conditions during early seedling stage using a hydroponic culture system with an intent of identifying traits and genotypes affiliated with the saline tolerance mechanism that would assist with the salt stress challenge.

A total of 11 rice genotypes including the saline tolerant check were used to evaluate salinity tolerance and relevant characters at the seedling stage (Table-1). The rice variety CSR 37 was used as the saline tolerant check. The Seeds of G2, G3, G6, G7, G9 and G10 were provided by Indian Council of Agricultural Research - Indian Institute of Rice Research, Hyderabad, India while the seeds of G1, G4, G5 and G8 were received from International Rice Research Institute, Philippines and CSR

37 from Department of Genetics and Plant Breeding, Annamalai University. All other accessions were collected from the “3000 rice genomes project (3K RGP)” (3K RGP, 2014). Evaluation protocols were conducted under hydroponic conditions as described by (Glenn, 1997). The experiment was conducted in a glasshouse set-up for rice at the Department of Genetics and Plant Breeding, Annamalai University with 30/20 °C day/night temperatures with 70 % humidity and 16 h photoperiod. The seeds of the genotypes were surface sterilized by soaking in 0.8 % sodium hypochlorite (NaClO) for 20 minutes, washed and then germinated using roll towel method. The pre-germinated seeds (5 days old) were then transplanted to the plastic trays (41 x 28 x 14 cm) filled with 10L Yoshida nutrient solution³⁵ until the solution level was about 1 mm above the styrofoam mesh (34 x 24 cm). The experimental set up was laid at completely randomized design (CRD) with three replications and each genotype comprised of fifteen plants per replication. The radicle of the pre germinated seeds were inserted through the nylon mesh. After three days of transplanting, when seedlings were well established, the nutrient solution was salinized by adding NaCl at electrical conductivity (EC) of 6 dS m⁻¹ (60 milimolar (mM) \approx 25.6 g NaCl/ 10 L) initially. Three days later, the EC was increased to 12 dS m⁻¹ (120 milimolar (mM) \approx 59.2 g NaCl/ 10 L). The solution was renewed every seven days and the pH was maintained at 5.00 daily. Test entries were visually scored at 10 and 14 days after initial salinization based on the modified standard evaluation score (SES) given by¹⁰. For control set up, the same protocol was followed but the NaCl was not introduced and SES was not noted as they did not develop

any symptoms.

Ten plants per genotype were selected following final scoring, and ten traits were observed *viz.*, root length (cm), shoot length (cm), total seedling length (cm), total fresh weight (g) (root fresh weight + shoot fresh weight), root dry weight (g), shoot dry weight (g), total dry weight (g) (root dry weight + shoot dry weight), relative water content (per cent) (total fresh weight – total dry weight/ total fresh weight x 100), root Na⁺/K⁺ (root Na⁺(ppm/g)/ root K⁺(ppm/g)) and shoot Na⁺/K⁺ (shoot Na⁺(ppm/g)/shoot K⁺(ppm/g)). Root and shoot dry weights were measured using a high-precision digital balance after drying plants at 80°C for 72 hours. Na⁺ and K⁺ ion concentrations in dried shoot and root samples were determined. Powdered samples were digested in a 9:2 HNO₃:HClO₄ mixture, diluted to 25 mL with distilled water, and analyzed using a Systronics Type 128 Flame Photometer. Each measurement was performed in triplicate, and averages were calculated. TNAUSTAT

software¹⁷ was used to perform Duncan's Multiple Range test (DMRT) based on the standard error calculated in Microsoft Excel. Pearson correlation was calculated at 5% ($p < .05$), 1% level ($p < 0.01$) and 0.1% ($p < 0.001$) significance among the seedling parameters to estimate the association among different traits using Grapesagri1 software⁹. Principal components were computed using R package FactoMineR (version 2.11)¹⁵ and factoextra (version 1.0.7)¹⁴.

Mean performance :

The mean performance of the genotypes for various traits at normal (control) and saline condition (12 dSm⁻¹) was given in the **Table 2a and 2b**. The varied performance of rice genotypes under normal and saline conditions revealed insights into their salt tolerance mechanisms and breeding potential, highlighting distinct capabilities among different genotypes. While several genotypes, such as G1, G2, G8 and G11, had particular capabilities

Table-1. List of the genotypes taken for the study

Code	Name of the Genotype	Irgc Number	Iris No.
G1	IRRI 146	IRGC 122401	IRIS 313-15902
G2	ARC 14358	IRGC 41523-2	IRIS 313-11267
G3	CUN GU NUO	IRGC 63576-1	IRIS 313-11664
G4	IR 4500-5-1-1	IRGC 40552-1	IRIS 313-11251
G5	AUS 278	IRGC 29068-1	IRIS 313-11052
G6	JAO' HAWN MAE JAN	IRGC 44022-2	IRIS 313-11327
G7	DAA MANASA	IRGC 67559-1	IRIS 313-8514
G8	GUMPANGAR	IRGC 71524-1-1	IRIS 313-9409
G9	ARC 10905	IRGC 12669-1	IRIS 313-10675
G10	GITANO	IRGC 82424-1	IRIS 313-10119
G11	CSR 37 (Check)	-	-

Table-2a. Mean performance of the rice genotypes for growth and biomass traits under control (0 dsm⁻¹) and saline conditions (12 dsm⁻¹)

Genot ypes	RL		SL		TSL		TFW	
	0 dsm ⁻¹	12 dsm ⁻¹	0 dsm ⁻¹	12 dsm ⁻¹	0 dsm ⁻¹	12 dsm ⁻¹	0 dsm ⁻¹	12 dsm ⁻¹
G1	19.50 ^b	24.50 ^a	34.80 ^f	21.50 ^g	54.30 ^c	46.00 ^b	0.5560 ^d	0.2600 ^a
G2	8.95 ^k	7.45 ^j	32.15 ^h	23.35 ^e	41.10 ^h	30.80 ^h	0.3900 ^g	0.1350 ^f
G3	9.10 ^j	7.80 ⁱ	36.70 ^d	30.60 ^b	45.80 ^f	38.40 ^e	0.5000 ^e	0.1440 ^e
G4	11.00 ^h	10.90 ^g	27.00 ⁱ	21.40 ^h	38.00 ^j	32.30 ^g	0.3520 ⁱ	0.1870 ^c
G5	30.00 ^a	19.40 ^b	40.30 ^b	27.65 ^c	70.30 ^a	47.10 ^a	0.7090 ^b	0.2120 ^b
G6	13.00 ^e	11.00 ^f	38.50 ^c	33.00 ^a	51.50 ^e	44.00 ^c	0.5820 ^c	0.1810 ^d
G7	12.35 ^g	12.00 ^e	22.30 ^k	15.10 ^j	34.65 ^k	27.10 ^j	0.2680 ^j	0.1210 ^g
G8	12.50 ^f	15.15 ^c	43.00 ^a	27.00 ^d	55.50 ^b	42.20 ^d	0.9000 ^a	0.1130 ^h
G9	9.30 ⁱ	10.85 ^h	34.00 ^g	22.00 ^f	43.30 ^g	32.90 ^f	0.3900 ^g	0.1060 ⁱ
G10	18.00 ^c	13.90 ^d	36.25 ^e	16.60 ⁱ	54.25 ^d	30.50 ⁱ	0.3850 ^h	0.0940 ^j
G11	15.42 ^d	13.73	23.95 ^j	21.37	39.37 ⁱ	35.1	0.4130 ^f	0.3033
SE	1.8792	0.8460	2.0044	1.665	3.1215	2.306	0.0551	0.017

RL – Root length, SL – Shoot length, TSL – total seedling length, TFW- total fresh weight, RDW- root dry weight, SDW – shoot dry weight, TDW – total dry weight, RWC – Relative Water Content SE – standard error ; Data on the same row with different superscript (a,b,c,d,e,f,g,h,i,j,k) are significantly different at $p < .05$

RDW		SDW		TDW		RWC	
0 dsm ⁻¹	12 dsm ⁻¹	0 dsm ⁻¹	12 dsm ⁻¹	0 dsm ⁻¹	12 dsm ⁻¹	0 dsm ⁻¹	12 dsm ⁻¹
0.0198 ^c	0.0092 ^d	0.0108 ^j	0.0459 ^b	0.0306 ^h	0.0551 ^b	94.50 ^b	78.81 ^f
0.0207 ^a	0.0063 ^f	0.0869 ^a	0.0105 ^j	0.1076 ^a	0.0168 ⁱ	72.41 ^k	87.56 ^a
0.0032 ^j	0.0043 ^h	0.0111 ⁱ	0.0158 ^f	0.0143 ^j	0.0201 ^g	97.14 ^a	86.04 ^c
0.0199 ^b	0.0141 ^b	0.0746 ^d	0.0311 ^c	0.0945 ^d	0.0452 ^d	73.15 ^j	75.83 ^h
0.0207 ^a	0.0150 ^a	0.0869 ^a	0.0304 ^d	0.1076 ^a	0.0454 ^c	84.82 ^g	78.58 ^g
0.0162 ^f	0.0063 ^f	0.0731 ^e	0.0498 ^a	0.0893 ^e	0.0561 ^a	84.66 ^h	69.01 ^j
0.0085 ^h	0.0071 ^e	0.0212 ^h	0.0124 ^b	0.0297 ⁱ	0.0195 ^h	88.92 ^f	83.88 ^d
0.0183 ^e	0.0102 ^c	0.0782 ^c	0.0183 ^e	0.0965 ^c	0.0285 ^e	89.28 ^d	74.78 ⁱ
0.0079 ⁱ	0.0051 ^g	0.0295 ^g	0.0153 ^g	0.0374 ^g	0.0204 ^f	90.41 ^c	80.75 ^e
0.0108 ^g	0.0011 ⁱ	0.0307 ^f	0.0108 ⁱ	0.0415 ^f	0.0119 ^j	89.22 ^e	87.34 ^b
0.0197 ^d	0.0083	0.0859 ^b	0.0248	0.1056 ^b	0.0331	74.43 ⁱ	89.09
0.0019	0.001	0.0098	0.005	0.0112	0.005	2.5718	1.919

Table 2b. Mean performance of rice genotypes for ion homeostasis under control (0 dsm⁻¹) and saline conditions (12 dsm⁻¹)

Genotypes	Root Na ⁺ /K ⁺		Shoot Na ⁺ /K ⁺	
	0 dsm ⁻¹	12 dsm ⁻¹	0 dsm ⁻¹	12 dsm ⁻¹
G1	0.31700 ^g	3.26043 ^j	0.25012 ^b	0.44545 ⁱ
G2	0.68518 ^e	3.57939 ⁱ	0.12642 ^f	2.87797 ^f
G3	0.80989 ^e	4.53261 ^h	0.25050 ^a	3.06869 ^e
G4	0.28199 ^h	4.83033 ^g	0.11719 ^g	3.71875 ^c
G5	0.27029 ⁱ	5.44035 ^f	0.10711 ⁱ	0.31473 ^j
G6	0.53998 ^f	7.07509 ^e	0.11516 ^h	2.33764 ^g
G7	0.89937 ^b	8.69262 ^d	0.20384 ^c	2.16376 ^h
G8	0.23402 ^j	12.04000 ^c	0.00108 ^k	10.77359 ^a
G9	1.11330 ^a	13.06186 ^b	0.12960 ^e	5.61351 ^b
G10	0.80191 ^d	15.80702 ^a	0.14700 ^d	3.09333 ^d
G11	0.01891 ^k	5.43561	0.10296 ^j	0.97487
SE	0.1033	1.393	0.0217	0.947

Root Na⁺/K⁺ – root Sodium Potassium ratio, shoot Na⁺/K⁺ – shoot Sodium Potassium ratio
SE – standard error ; Data on the same row with different superscript (a,b,c,d,e,f,g,h,i,j,k) are significantly different at $p < .05$

Table-3. Modified Standard evaluation score (SES) of visual salt injury at seedling stage based on Gregorio *et al.*¹⁰

Score	Observation	Tolerance	Genotypes
1	Normal growth, no leaf symptoms	Highly tolerant	G1
3	Nearly normal growth, but leaf tips Tolerant or few leaves whitish and rolled	Tolerant	G2,G3,G11
5	Growth severely retarded; most leaves Moderately tolerant rolled; only a few are elongating	Moderately tolerant	G4,G5
7	Complete cessation of growth; most leaves dry; some plants dying	Susceptible	G6,G7,G8
9	Almost all plants dead or dying.	Highly susceptible	G9,G10

Table-4. Eigenvalues, Proportion of Variance Explained and Factor scores of the First Three Principal Components under normal and saline conditions

Traits	Normal condition (Control)			Saline condition (12 dSm ⁻¹)		
	PC1	PC2	PC3	PC1	PC2	PC3
RL	0.443	0.518	0.643	0.598	-0.156	0.713
SL	0.297	0.835	-0.378	0.504	0.519	-0.609
TSL	0.457	0.848	0.144	0.831	0.300	0.030
TFW	0.588	0.695	-0.254	0.734	-0.552	-0.012
RDW	0.867	-0.173	0.293	0.662	0.003	0.136
SDW	0.907	-0.319	-0.172	0.923	0.072	0.025
TDW	0.934	-0.306	-0.100	0.967	0.063	0.057
RWC	-0.579	0.782	-0.040	-0.617	-0.692	-0.087
Root Na ⁺ /K ⁺	-0.789	0.034	-0.358	-0.599	0.470	0.521
Shoot Na ⁺ /K ⁺	-0.766	0.089	0.521	-0.363	0.792	0.127
Eigen value	4.830	3.011	1.168	4.939	2.026	1.198
Proportion of Variance	48.319	30.114	11.680	49.387	20.261	11.976
Cumulative Proportion	48.320	78.433	90.113	49.387	69.648	81.624

RL – Root length, SL – Shoot length, TSL – total seedling length, TFW- total fresh weight, RDW- root dry weight, SDW – shoot dry weight, TDW – total dry weight, RWC – Relative Water Content, root Na⁺/K⁺– Sodium Potassium ratio, shoot Na⁺/K⁺– Sodium Potassium ratio

in various aspects like root development, water content, biomass accumulation and ion homeostasis, the genotype G5 distinguished out as an excellent performer across various traits such as root length, shoot length, total seedling length, total fresh weight, root dry weight, shoot dry weight and total dry weight indicating its ability to perform outstandingly for growth and biomass parameters. However, the performance of the above genotypes needs to be evaluated under saline stress conditions to test its ability and potential for saline tolerance. Under saline condition, the genotype G1 exhibited superior performance (rank a) for traits such as root length, total fresh weight,

root Na⁺/K⁺ homeostasis and remarkable performance (rank b) for the traits such as total seedling length, shoot dry weight, total dry weight and shoot Na⁺/K⁺ homeostasis. The genotype G5 demonstrated superior performance (rank a) for the traits total seedling length, root dry weight, shoot Na⁺/K⁺ and exceptional performance (rank b) for root length and total fresh weight. The study found that genotypes G1 and G5 exhibited exceptional performance for most of the root and shoot traits, indicating their ability to maintain balance between both root and shoot^{1,21}. The genotype G2 outperformed in relative water content (87.56 per cent),

indicating superior control of stomatal opening⁷, potentially reducing salt load, improving plant growth and survival.

The study found that most genotypes showed a decrease in performance under saline conditions compared to normal conditions^{13,30}. However interestingly, the genotypes such as G1 and G8 for root length³¹, G3 and G10 for root dry weight, G1 and G3 for shoot dry weight, G1, G2, G3, G5 and G7 for total dry weight, G4 for relative water content exhibited greater performance under saline conditions compared to normal conditions. Genotypes with longer roots under saline stress might exhibit minimal inhibition of cell division and elongation²⁸. Given the importance of biomass accumulation²⁵ and root attributes³² in salinity stress. The genotypes G1 and G3 demonstrate potential for salt tolerance breeding, exhibiting enhanced performance at 12 dSm⁻¹. Further research at higher salinity levels could uncover additional adaptive mechanisms and salt tolerance strategies. The study focuses on the mechanism of ion exclusion in rice, which prevents excess Na⁺ and Cl⁻ accumulation in leaves, mainly involving Na⁺ and Cl⁻ transport processes in roots, as Na⁺ concentrations reach critical levels before Cl⁻ levels²⁰. The genotypes G1 and G2 demonstrated superior performance for root Na⁺/K⁺ homeostasis, while G5 and G1 showed superior performance for shoot Na⁺/K⁺ homeostasis by maintain high K⁺ and low Na⁺ concentrations. Salt-tolerant rice plants maintain ion homeostasis by excluding, compartmentalizing and dividing Na⁺ in shoots or roots, resulting in low Na⁺/K⁺ or high Na⁺/K⁺ ratios²⁰. In contrast, genotypes G8, G9, and G10 exhibited higher Na⁺/K⁺ values (**Table**

2b). To minimize damage, excessive Na⁺ movement to shoots was minimized. The study outcomes disclosed that roots have a higher Na⁺/K⁺ ratio than shoots, reducing sodium ion transfer²³. The genotypes G1 and G5 highlighted longer overall seedling lengths, which implied quicker growth and lower shoot ions concentrations indicating saline tolerance²⁵. The genotype G1 exhibited a comprehensive salt tolerance, efficient ion exclusion, improved Na⁺/K⁺ homeostasis, excess Na⁺ compartmentalization and quick development strategy, generating promising breeding opportunities for salt-resistant rice varieties. The study found that genotypes showed significant variation under saline stress (**Table 3**) in the standard evaluation score with G1 scoring 1 (highly tolerant), check variety CSR 37, G2 and G3 scoring 3 (tolerant), G4 and G5 scoring 5 (moderately tolerant), G6, G7, and G8 scoring 7 (susceptible), G9 and G10 scoring 9 (highly susceptible) which were consistent with the findings of Chen *et al.*⁵. The genotype G1 demonstrated the highest tolerance (score 1) and superior performance under saline stress compared to normal conditions and outperformed the saline-tolerant check variety in multiple traits, including root length, total fresh weight, Na⁺/K⁺ homeostasis and biomass parameters making it a promising candidate for saline breeding programs. In contrast, genotypes G9 and G10 performed poorly under saline stress.

Correlation analysis :

The correlogram demonstrating the relationships among various traits in rice seedlings under normal conditions is given in Fig. 1. The rice seedlings showed significant positive correlations between total seedling

length and total fresh weight, root length, and shoot length. Root and shoot dry weights negatively correlated with relative water content and Na^+/K^+ ratios revealing that seedlings tend to have lower amounts of Na^+/K^+ as they accumulate more dry matter. The correlogram illustrating the relationships among various traits in rice seedlings under saline conditions is presented in Fig. 2. The SES positively correlated with root Na^+/K^+ ratios and negatively with total fresh weight suggesting that salt stress negatively impacted the biomass accumulation in rice seedlings. Total seedling length positively associated with shoot and total dry weights. Shoot dry weight exhibited a negative association with relative water content. Total dry weight negatively correlated with relative water content highlighting the impact of salt stress on the plant's water status. The results were in line with the findings of Le *et al.*¹⁵, Alshiekheid *et al.*⁴ and Yah *et al.*³⁴. The associations between the growth metrics in rice seedlings were substantially disrupted by salt stress. While balanced root and shoot growth was favored under normal conditions, biomass accumulation and shoot growth constitute more important measures of salt tolerance under salinized conditions. Under conditions of salt stress, the harmony between the buildup of dry matter and water content turned more pertinent and the Na^+/K^+ ratio, a significant aspect of ion homeostasis became apparent as an important variable in determining salt sensitivity. Therefore, breeding programs for salt-tolerant rice should be more concrete and geared towards an understanding of these representative correlations, with an emphasis on critical traits such as ion exclusion, biomass build-up and water uptake.

Principal Component Analysis (PCA) :

PCA, a multidimensional preference analysis, helps identify key variables influencing salinity tolerance by examining correlations between measured salinity stress components³² revealed three significant components (PC1, PC2, PC3) with Eigen values greater than one in both saline and control conditions explaining 90.113% and 81.624% of total genetic variation, respectively (**Table 4**). PC1 accounted for the majority of variability (48.319% in control, 49.387% in saline) (Hakim *et al.*,¹¹ and Akilan *et al.*,³). PCA revealed distinct patterns in control and saline conditions. In control, PC1 primarily represented overall biomass and ion balance, with an inverse relationship between these ion balances and overall biomass, while PC2 revealed an inverse relationship between biomass and growth parameters and water content. Under saline stress, PC1's positive correlation with growth and biomass traits, coupled with its negative correlation with water content and Na^+/K^+ ratios, suggested plants achieving better growth and biomass accumulation tend to have lower Na^+/K^+ ratios under saline condition. PC2 in saline condition demonstrated positive correlations with shoot length and ion homeostasis, but negative with fresh weight and water content. These shifts highlight complex adaptations to salt stress, emphasizing trade-offs between growth, biomass, ion homeostasis and water relations. Scree plot analysis (Fig. 3 and 4) confirmed the significance of the first three PCs, with PC1 accounting for most variability in both conditions. Genotypes excelling in traits with higher PC1 values could be valuable for breeding programs targeting improved crop yield under both control and saline conditions.

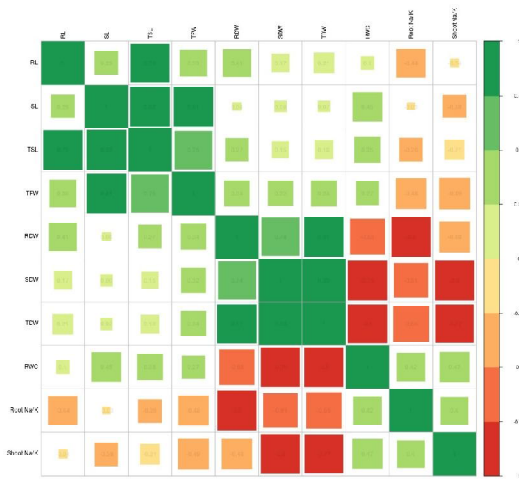


Fig. 1 Correlogram depicting correlation among the seedling traits in control treatment ($p < .05$)

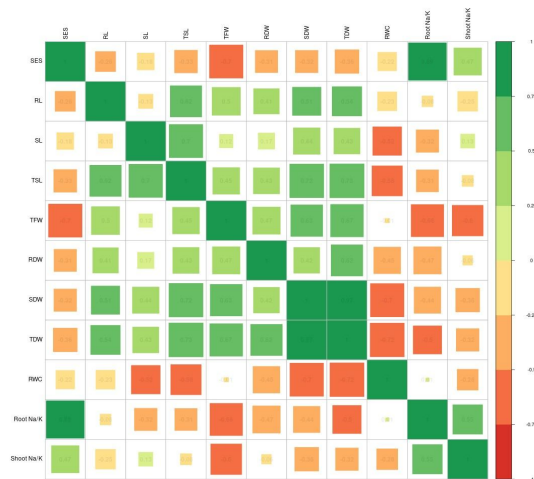


Fig. 2 Correlogram depicting correlation among the seedling traits in saline treatment ($p < .05$)

RL – Root length, SL – Shoot length, TSL – total seedling length, TFW- total fresh weight, RDW- root dry weight, SDW – shoot dry weight, TDW – total dry weight, RWC – Relative Water Content, root Na/K – Sodium Potassium ratio, shoot Na⁺/K⁺ – Sodium Potassium ratio

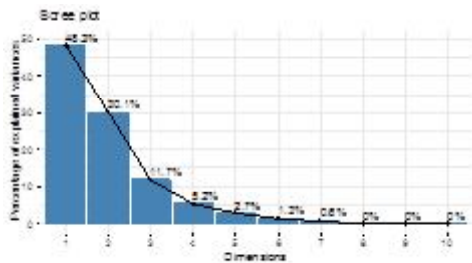


Fig. 3 Scree Plot Illustrating the Eigenvalues and Percentage of Variance Explained by Principal Components for control condition

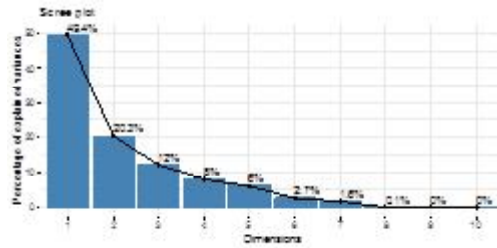


Fig. 4 Scree Plot Illustrating the Eigenvalues and Percentage of Variance Explained by Principal Components for saline condition

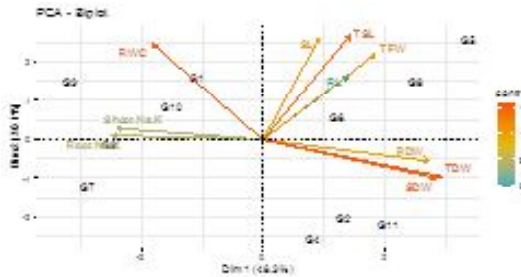


Fig. 5 PCA biplot for PCA 1 Vs PCA 2 for control condition

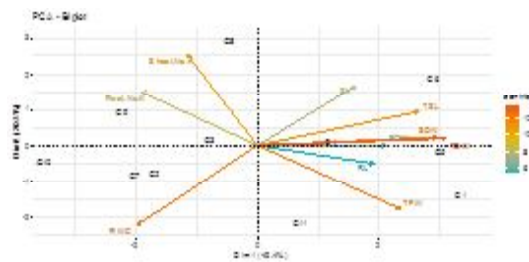


Fig. 6 PCA biplot for PCA 1 Vs PCA 2 for saline condition

PCA biplots (Fig. 5 and 6) revealed total dry weight and shoot dry weight as key drivers of genotypic variance in both normal and saline conditions. Growth and biomass traits showed positive correlations, while ion traits were negatively correlated with most other traits. Relative water content showed different correlations under normal and saline conditions. Under normal conditions, genotypes G5, G6, and G8 excelled in growth traits, while G2 and G4 performed well in biomass traits. In saline conditions, G1 and G5 showed better performance in root length and total fresh weight, with lower Na⁺/K⁺ levels. G6 and G4 exhibited higher biomass traits, while G2 and G10 maintained better relative water content under stress. These genotypes, demonstrating various physiological adaptations, could be valuable in breeding programs for salt-tolerant, high-yielding rice varieties.

In conclusion, this current study on rice genotypes under normal and saline conditions unmasked significant variations in their performance and salt tolerance mechanisms. Genotype IRRI 146 emerged as a promising candidate for salt tolerance breeding programs, showcasing superior performance across multiple traits and demonstrating effective ion homeostasis while the genotypes such as ARC 10905 and GITANO were observed to be poor performers under saline stress. Principal component and correlation analyses highlighted the complex interplay among growth parameters, biomass accumulation, ion homeostasis and water relations under salt stress. The findings emphasized the importance of traits such as total dry weight, shoot dry weight, and Na⁺/K⁺ ratios in determining salt tolerance. Therefore these findings would provide valuable channel for breeding programs aimed

at developing salt-tolerant rice varieties with improved yield potential under saline conditions. However, it is vital to remember that distinct gene sets influence salt tolerance at different stages of growth. Thus, even though these results offer insightful information about tolerance at the seedling stage, further examination of the detected genotypes at the reproductive and maturity stages must be conducted. A solid assessment across the growth stages would be necessary to conclusively identify truly salt-tolerant genotypes suitable for breeding programs aimed at developing rice varieties with improved yield potential under saline conditions throughout their life cycle.

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