International Journal of Plant & Soil Science

Volume 38, Issue 1, Page 50-59, 2026; Article no.IJPSS.150607
ISSN: 2320-7035

Standardization and Comparative Evaluation of Salinity Stress Levels for Rice Seed Germination Using the Paper Towel Method Under Laboratory Conditions

Patil Poonam Dilip [a++*], Vijay kumar kurnalliker [a†], N.M. Shakuntala [a#], Sangeeta I Macha [a†], Mukesh Kumar Meena [b†] and Kisan B [c†]

[a] Department of Seed Science and Technology, University of Agricultural Sciences, Raichur-Karnataka, India.
[b] Department of Crop Physiology, University of Agricultural Sciences, Raichur-Karnataka, India.
[c] Department of Biotechnology, University of Agricultural Sciences, Raichur-Karnataka, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.9734/ijpss/2026/v38i15925

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://pr.sdiarticle5.com/review-history/150607

Original Research Article

Received: 27/10/2025
Published: 09/01/2026

[++] Ph.D. Scholar; [#] Professor and Head; [†] Associate Professor;
**Corresponding author: E-mail: patilpoonam5269@gmail.com;*

Cite as: *Dilip, Patil Poonam, Vijay kumar kurnalliker, N.M. Shakuntala, Sangeeta I Macha, Mukesh Kumar Meena, and Kisan B. 2026. "Standardization and Comparative Evaluation of Salinity Stress Levels for Rice Seed Germination Using the Paper Towel Method Under Laboratory Conditions". International Journal of Plant & Soil Science 38 (1):50-59. https://doi.org/10.9734/ijpss/2026/v38i15925.*

Abstract

Salinity stress poses a serious constraint to rice production by impairing seed germination and early seedling growth. The present study was undertaken to evaluate the salinity tolerance of rice (*Oryza sativa* L.) genotypes under laboratory and hydroponic conditions, with particular emphasis on seed quality traits. The experiment was conducted at the Department of Seed Science and Technology, College of Agriculture, University of Agricultural Sciences, Raichur. Thirty rice genotypes were subjected to five salinity treatments comprising 0 (control), 40, 60, 80 and 100 mM NaCl, arranged in a factorial completely randomized design with four replications. Germination and seedling performance were assessed using the paper towel method in accordance with ISTA guidelines. Increasing salinity levels resulted in a significant decline in seed germination percentage, root and shoot length, seedling dry weight, and seedling vigour indices, while the proportion of abnormal seedlings increased. The control treatment recorded the highest germination (90.92%) and seedling vigour, whereas exposure to 100 mM NaCl reduced germination to 82.15%, indicating an overall reduction of approximately 9%. Considerable genotypic variation was observed in response to salinity stress. Genotypes NVSR 6494, NVSR 6489, CSR 23, CSR 104-10-2 and RP 6688-16-397 exhibited better performance by maintaining higher germination and vigour under saline conditions, whereas GNV 10-89, BPT 5204 and RP 6684-CGR 13 showed pronounced sensitivity. The findings demonstrate substantial variability among rice genotypes at the germination stage and identify promising lines for utilization in salinity tolerance breeding programmes.

Keywords: Salinity stress; seed germination; NaCl and genotypic variability.

1. Introduction

Rice (*Oryza sativa* L.) originated in present-day China, particularly the Yangtze River basin, where archaeological evidence indicates domestication commenced about 10,000 years ago (Singh et. al., 2023; Guo et al., 2014). From China, rice cultivation spread across Asia and later to Africa, Europe and the Americas through trade and human migration. Today, rice is a major staple food for almost half of the global population, especially in Asia, and is cultivated widely under diverse agro-climatic conditions.

Rice played a central role in the expansion of ancient civilizations in China, India and Southeast Asia, supporting population growth and influencing cultural practices (Miyamoto, 2009). In India, rice has been cultivated since the Indus Valley Civilization (2600–1900 BC) and has become deeply embedded in agricultural traditions (Higham, 1989). The crop exhibits substantial genetic diversity, with *Indica* and *Japonica* being the two major subspecies cultivated in India, adapted to tropical and temperate regions, respectively (Lu et al., 2009).

India is one of the world's leading rice producers, with diverse agro-climatic conditions supporting a wide range of traditional and improved varieties. Major rice-growing states include West Bengal, Uttar Pradesh, Odisha, Andhra Pradesh, Tamil Nadu, Punjab and Karnataka. In Karnataka, important rice-growing regions include Mysuru–Mandya and Gangavati–Koppal, where rice cultivation holds significant cultural and economic importance.

Rice belongs to the family Poaceae and is an annual grass cultivated under flooded or well-drained conditions. It shows wide variation in grain characteristics, nutritional composition and stress tolerance (Kovach et al., 2007). Rice grains primarily consist of carbohydrates (72–75% starch), with moderate protein content and low fat. Milling reduces nutrient content by removing the bran and germ, making polished rice poor in minerals and vitamins.

Globally, rice is cultivated on about 167.1 million ha with a production of 782 million tonnes and an average productivity of 4.67 t/ha (Anonymous, 2023–24). India accounts for the largest area under rice cultivation, producing 137 million tonnes with an average productivity of 4.3 t/ha. Large germplasm resources conserved worldwide, particularly at IRRI and in India, provide valuable genetic material for crop improvement.

Rice production is influenced by numerous biotic and abiotic factors that affect yield, quality and sustainability. Advances in breeding, agronomy and crop management have significantly enhanced rice productivity, contributing to global

food security. Salinity is one of the most severe abiotic stresses limiting rice production worldwide, ranking second only to drought (Kakar *et al.*, 2019). Nearly 20% of the world's land and about 50% of irrigated land are affected by salinity. Asia, which contributes over 90% of global rice production, accounts for approximately 21.5 million ha of salt-affected soils, including 12 million ha saline and 9.5 million ha sodic lands (Mohammadi *et al.*, 2013).

High soil salinity adversely affects rice germination, seedling establishment, growth and yield by reducing tillering and causing stunted plant development. Excess accumulation of sodium (Na^+) and chloride (Cl^-) ions disrupts ionic homeostasis, leading to ion toxicity, nutrient imbalance and impaired physiological processes such as water uptake and photosynthesis. Salinity also induces osmotic stress, reducing cell turgor and metabolic activity, ultimately lowering productivity (Ismail and Horie, 2017). Some rice genotypes mitigate salt injury through ion exclusion and sequestration into vacuoles, thereby protecting cellular functions (Munns and Tester, 2008).

The present study was undertaken to evaluate the effect of different salinity levels on seed germination and seedling establishment in thirty rice genotypes.

Expected output: Identification of rice genotypes with superior tolerance to salinity stress at germination and seedling stages.

2. Materials and Methods

The seed quality parameters analysis on Standardization and Comparative Evaluation of Salinity Stress Levels for Rice Seed Germination using the Paper Towel Method Under Laboratory Conditions was conducted in the seed testing laboratory of Department of Seed Science and Technology, College of Agriculture, University of Agricultural Sciences, Raichur. The College of Agriculture, Raichur is situated in North Eastern Dry Zone (Zone 2) of Karnataka at a latitude of 16.21° North and longitude 77.34° East with an elevation of 389 mean sea level, The seed material of 30 different rice genotypes required for the present experiment was collected from the Senior Rice Breeder, Agricultural Research Station, Gangavathi. University of Agricultural Sciences, Raichur.

Table 1. Preparation of various salt concentrations

NaCl (g)	Distilled water (ml)	NaCl (mm)	dS/m (EC)
2.33 g	1000 ml.	40 mM	4 dS/m EC
3.50 g	1000 ml.	60 mM	6 dS/m EC
4.67 g	1000 ml.	80 mM	8 dS/m EC
5.84 g	1000 ml.	100 mM	10 dS/m EC

Treatment imposition: For treatment imposition, the different salinity levels (factor-I) were created by preparing the required NaCl salt concentrations as given in 1.1 and the germination papers were soaked in the respective salt solution for 30 minutes later the germination papers were drained thoroughly and kept it on polythene sheet for germination test. The germination test was conducted as per ISTA procedure to screen 30 rice genotypes for salinity tolerance based on seed germination and seedling vigour. The details of the treatment were as furnished below.

Factor-I: Salinity level (S)

S_1: 0
S_2: NaCl @ 40 mM
S_3: NaCl @ 60 mM
S_4: NaCl @ 80 mM
S_5: NaCl @ 100 mM

Table 2. Factor-II: Genotypes (G)

G_1: NVSR 6489	G_{11}: CSR 116-10-2	G_{21}: FL 478
G_2: RNR 28361	G_{12}: RP 6682- CGR 11	G_{22}: RP 6711-MS-SS-20-2-9-5-23-6-1
G_3: NVSR 6526	G_{13}: CSR 104-10-2	G_{23}: Local Check (LC)
G_4: KPS 6343	G_{14}: NVSR 6494	G_{24}: DRR Dhan 53
G_5: CSR 36	G_{15}: CSR 10	G_{25}: RNR 15048
G_6: CSR 103-10-2	G_{16}: IIRRH 163	G_{26}: GNV 1109
G_7: RP 6684-CGR 13	G_{17}: RNR 29325	G_{27}: GNV 10-89
G_8: CSR 141-11-107	G_{18}: CSAR 9-29-2021	G_{28}: GGV-0501 (Gangavati Sona)
G_9: RP Bio 4919- NSR 85	G_{19}: CSR 141-11-112	G_{29}: MTU 1010
G_{10}: CSR 23	G_{20}: RP 6688-16-397	G_{30}: BPT 5204

Design of the experiment: The experiment consisted of 150 treatments were laid out in 2 Factorial Completely randomized design in four replications with five salt concentrations as factor I and thirty genotypes as factor II.

Seed germination (%): The standard germination test was carried out by following between paper method (ISTA, 2013). Hundred seeds in each replication from each treatment were placed on germination paper uniformly. The roll towels were kept in germination chamber maintained at 25 ± 2°C temperature and 90 ± 5 per cent relative humidity. Then the first count was taken on 5th day and the final count on 14th day. The number of normal seedlings from each replication were counted and the mean germination was expressed in percentage.

$$Seed\ Germination\ (\%) = \frac{Number\ of\ normal\ seedlings}{Total\ number\ of\ seed} \times 100$$

Abnormal seedlings (%): From germination test seedlings which do not have all the essential structures or damaged, deformed and decayed that prevents normal development of the seedlings were recorded on 14th day and the mean was expressed in percentage.

Shoot length (cm): From the germination test ten normal seedlings were selected randomly from each treatment replication wise on the day of final count (14th day). The shoot length was measured from the base of the primary leaf to the base of hypocotyl and the mean was expressed in centimeter.

Root length (cm): The root length was measured from the same ten seedlings used for measuring shoot length from the tip of primary root to the base of hypocotyls and the mean was expressed in centimeter.

Seedling dry weight (mg): The ten normal seedlings selected randomly from the germination test, were kept in a butter paper and dried in a hot air oven maintained at 70 ± 2°C for 24 hours. Thereafter, the seedlings were removed and weighted in an electronic balance and the average was expressed in milligram.

Seedling vigour index-I: The seedling vigour index-I is computed using the formula as suggested by Abdul- Baki and Anderson (1973).

Vigour index – I = Germination (%) x Mean seedling length (cm)

Seedling vigour index-II: The seedling vigour index-II is computed by multiplying the germination (%) with seedlings dry weight (mg).

Vigour index-II = Germination (%) x Dry weight of seedlings (mg).

3. Results and Discussion

Seed germination (%): The seed germination (%) of rice was significantly influenced by salinity levels (S), genotypes (G) and their interactions (G × S), Table 3 and Fig.1.

Seed germination decreased significantly with increasing NaCl concentration. The highest germination (90.92%) was recorded under control (S_1, 0 mM NaCl), which was statistically on par with S_2 (40 mM NaCl), while the lowest germination (82.15%) occurred at S_5 (100 mM NaCl), representing an overall reduction of ~9%. Salinity, genotypes and their interaction significantly influenced germination. Among genotypes, NVSR 6494 (G_{14}), RP 6688-16-397 (G_{20}), CSR 23 (G_{10}) and MTU 1010 (G_{29}) maintained higher germination, whereas RP 6684-CGR 13 (G_7), RNR 29325 (G_{17}) and GNV 10-89 (G_{27}) were highly sensitive. Reduced germination under salinity may be attributed to osmotic stress and ionic toxicity affecting water uptake and metabolic activity.

The tolerant genotypes likely maintained higher germination by better osmotic adjustment and enhanced enzyme activity, whereas sensitive genotypes were more adversely affected. Similar genotypic variability in salt stress tolerance Gill *et al*. (2003) in sorghum. These findings are in line with the reports of Begum *et al*. (2000) in maize and Jamil *et al*. (2006) in rice, who also reported significant reduction in germination under NaCl stress due to reduced water uptake and ion toxicity.

Root length (cm): Root length declined progressively with increasing salinity. The maximum root length was recorded at S_1 (18.53 cm), while the minimum occurred at S_5 (16.58 cm), showing a reduction of about 10.5%. Genotypic differences were significant, with NVSR 6489 (G_1), RNR 29325 (G_{17}) and CSR 104-10-2 (G_{13}) exhibiting superior root growth, whereas GNV 10-89 (G_{27}) showed the lowest root length. Root growth was highly sensitive to salinity due to direct exposure to saline conditions.

Salinity-induced root inhibition is mainly attributed to osmotic stress, reduced water uptake, and ion toxicity which ultimately disturb

cell elongation and proliferation (Van Zelm, 2020 and Ashraf and Harris, 2004). Neumann (1993) and Hakim *et al*. (2010) also confirmed that root growth is one of the most sensitive traits to salinity stress due to its close contact with the growth medium.

Shoot length (cm): Shoot length showed a significant and consistent reduction with increasing salinity. The highest shoot length (16.41 cm) was observed under control conditions, while S_5 recorded the lowest value (14.44 cm), indicating a 12% reduction. NVSR 6489 (G_1), RP 6682-CGR 11 (G_{12}) and RNR 29325 (G_{17}) maintained longer shoots, whereas BPT 5204 (G_{30}) and GNV 10-89 (G_{27}) were highly sensitive. Reduced shoot growth under salinity was mainly due to osmotic stress, ion toxicity and impaired photosynthesis.

These findings clearly establish an inverse relationship between salinity concentration and seedling growth. Similar results were reported by Islam and Karim (2010), who observed that salinity at 150 mM NaCl reduced seedling length in rice. Ali *et al*. (2014) also demonstrated that salinity stress significantly hampered seedling elongation due to ionic toxicity, osmotic stress, and unbalanced nutrient uptake, which ultimately reduced photosynthetic activity. Salinity also enhances respiration, leading to a shortage of assimilates for developing tissues, thereby suppressing elongation growth (El-Hendawy *et al*., 2005).

Table 3. Impact of salinity levels on seed germination (%) of rice genotypes using paper towel method

Treatments	S_1 (0 mM)	S_2 (40 mM)	S_3 (60 mM)	S_4 (80 mM)	S_5 (100 mM)	Mean G
G_1: NVSR 6489	89.25	87.50	84.25	80.25	79.75	**84.20**
G_2: RNR 28361	91.50	90.25	87.75	86.00	83.25	**87.75**
G_3: NVSR 6526	90.75	89.00	82.00	80.00	79.00	**84.15**
G_4: KPS 6343	90.25	91.00	85.50	83.25	81.00	**86.20**
G_5: CSR 36	92.50	92.00	89.25	86.00	82.00	**88.35**
G_6: CSR 103-10-2	91.50	90.25	87.75	85.50	80.50	**87.10**
G_7: RP 6684-CGR 13	80.25	79.75	78.50	78.25	75.50	**78.45**
G_8: CSR 141-11-107	92.50	89.50	86.50	82.00	80.75	**86.25**
G_9: RP Bio 4919- NSR 85	86.50	85.25	85.00	84.00	83.75	**84.90**
G_{10}: CSR 23	97.00	96.75	92.00	90.25	86.75	**92.55**
G_{11}: CSR 116-10-2	92.75	91.75	90.50	89.25	85.25	**89.90**
G_{12}: RP 6682- CGR 11	92.25	91.25	90.50	90.25	85.25	**89.90**
G_{13}: CSR 104-10-2	95.25	94.25	94.00	93.50	83.50	**92.10**
G_{14}: NVSR 6494	96.25	95.00	94.75	92.25	92.25	**94.10**
G_{15}: CSR 10	86.25	85.00	82.50	80.50	79.75	**82.80**
G_{16}: IIRRH 163	95.00	94.75	92.00	90.00	85.00	**91.35**
G_{17}: RNR 29325	80.25	79.00	78.00	76.50	78.50	**78.45**
G_{18}: CSAR 9-29-2021	96.00	92.00	93.50	90.00	85.25	**91.35**
G_{19}: CSR 141-11-112	90.50	89.25	87.50	86.25	86.00	**87.90**
G_{20}: RP 6688-16-397	97.50	96.25	93.25	90.00	87.50	**92.90**
G_{21}: FL 478	92.00	89.25	87.50	86.50	84.00	**87.85**
G_{22}: RP 6711-MS-SS-20-2-9-5-23-6-1	92.25	91.25	90.25	84.25	84.25	**88.45**
G_{23}: Local Check (LC)	91.00	90.00	88.75	86.25	76.50	**86.50**
G_{24}: DRR Dhan 53	90.25	89.50	88.25	85.00	84.75	**87.55**
G_{25}: RNR 15048	84.00	83.25	83.00	80.50	80.50	**82.25**
G_{26}: GNV 1109	87.25	86.50	85.00	82.00	74.50	**83.05**
G_{27}: GNV 10-89	86.50	83.25	85.00	77.00	73.25	**81.00**
G_{28}: GGV-0501	91.50	90.00	86.50	85.00	75.00	**85.60**
G_{29}: MTU 1010	94.25	93.25	92.00	90.25	87.75	**91.50**
G_{30}: BPT 5204	94.50	92.50	90.00	88.75	83.50	**89.85**
Mean S	**90.92**	**89.62**	**87.71**	**85.32**	**82.15**	
		S.Em ±			**CD @1%**	
Factor G		**0.46**			**1.69**	
Factor S		**0.18**			**0.69**	
Interaction (G x S)		**1.03**			**3.79**	

Legend: G: genotypes; S: salinity levels; NS: Non-significant

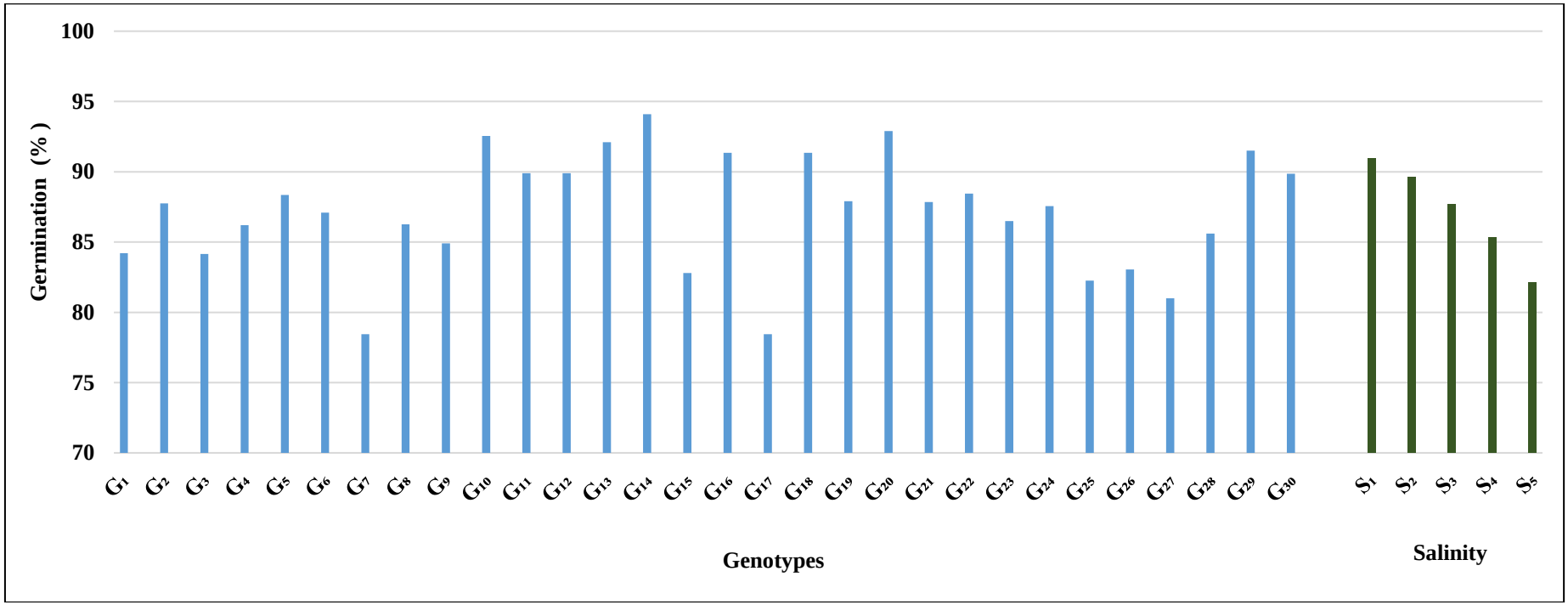

Fig. 1. Impact of salinity levels on seed germination (%) of rice genotypes using paper towel method

Legend:

Genotypes (G): *G_1: NVSR 6489; G_2: RNR 28361; G_3: NVSR 6526; G_4: KPS 6343; G_5: CSR 36; G_6: CSR 103-10-2; G_7: RP 6684-CGR 13; G_8: CSR 141-11-107; G_9: RP Bio 4919- NSR 85; G_{10}: CSR 23; G_{11}: CSR 116-10-2; G_{12}: RP 6682- CGR 11; G_{13}: CSR 104-10-2; G_{14}: NVSR 6494; G_{15}: CSR 10; G_{16}: IIRRH 163; G_{17}: RNR 29325; G_{18}: CSAR 9-29-2021; G_{19}: CSR 141-11-112; G_{20}: RP 6688-16-397; G_{21}: FL 478; G_{22}: RP 6711-MS-SS-20-2-9-5-23-6-1; G_{23}: Local Check (LC); G_{24}: DRR Dhan 53; G_{25}: RNR 15048; G_{26}: GNV 1109; G_{27}: GNV 10-89; G_{28}: GGV-0501 (Gangavati Sona); G_{29}: MTU 1010; G_{30}: BPT 5204;*

Salinity level (S): *S_1: 0; S_2: NaCl @ 40 mM (4 dS/m EC); S_3: NaCl @ 60 mM (6 dS/m EC); S_4: NaCl @ 80 mM (8 dS/m EC); S_5: NaCl @ 100 mM (10dS/m EC)*

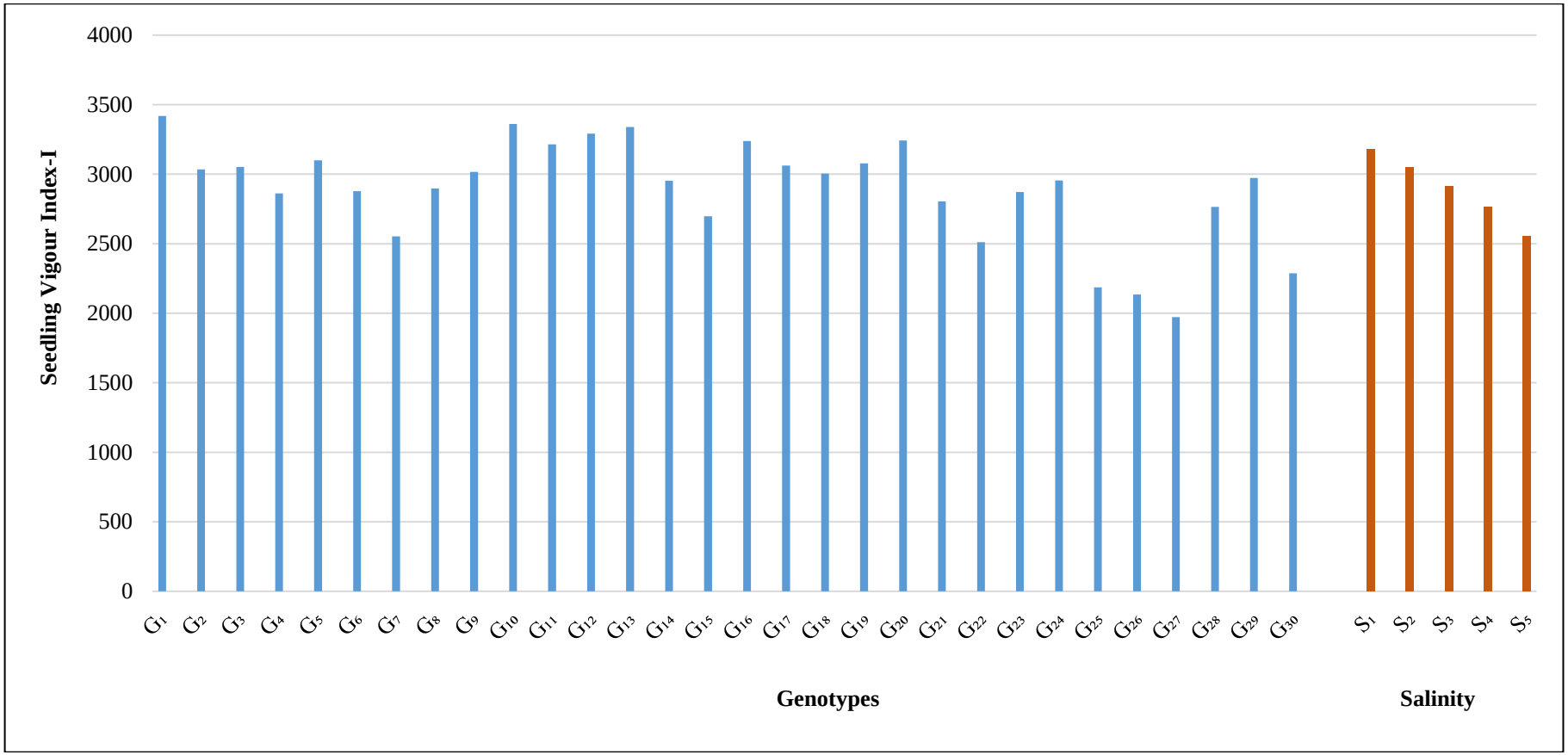

Fig. 2. Impact of salinity levels on seedling vigour index -I of rice genotypes using paper towel method

Legend:

Genotypes (G): *G_1: NVSR 6489; G_2: RNR 28361; G_3: NVSR 6526; G_4: KPS 6343; G_5: CSR 36; G_6: CSR 103-10-2; G_7: RP 6684-CGR 13; G_8: CSR 141-11-107; G_9: RP Bio 4919- NSR 85; G_{10}: CSR 23; G_{11}: CSR 116-10-2; G_{12}: RP 6682- CGR 11; G_{13}: CSR 104-10-2; G_{14}: NVSR 6494; G_{15}: CSR 10; G_{16}: IIRRH 163; G_{17}: RNR 29325; G_{18}: CSAR 9-29-2021; G_{19}: CSR 141-11-112; G_{20}: RP 6688-16-397; G_{21}: FL 478; G_{22}: RP 6711-MS-SS-20-2-9-5-23-6-1; G_{23}: Local Check (LC); G_{24}: DRR Dhan 53; G_{25}: RNR 15048; G_{26}: GNV 1109; G_{27}: GNV 10-89; G_{28}: GGV-0501 (Gangavati Sona); G_{29}: MTU 1010; G_{30}: BPT 5204*

Salinity level (S): *S_1: 0; S_2: NaCl @ 40 mM (4 dS/m EC); S_3: NaCl @ 60 mM (6 dS/m EC); S_4: NaCl @ 80 mM (8 dS/m EC); S_5: NaCl @ 100 mM (10dS/m EC)*

Abnormal seedlings (%): Abnormal seedling percentage increased significantly with salinity stress. The lowest abnormal seedlings were recorded at S_1 (1.15%), while the highest were observed at S_5 (4.00%). Among genotypes, NVSR 6526 (G_3), CSR 23 (G_{10}) and RP Bio 4919-NSR 85 (G_9) recorded fewer abnormalities, whereas NVSR 6489 (G_1) and DRR Dhan 53 (G_{24}) showed higher abnormal seedling percentages. Increased abnormalities under salinity were associated with ionic toxicity and disruption of normal metabolic processes.

These findings confirm that salinity stress adversely affects seedling quality by inducing abnormalities. Similar results were reported by Ali *et al.* (2014), who observed that salinity-induced osmotic stress and ion toxicity caused structural deformities in seedlings. Salinity has been shown to disrupt hormonal regulation, cell division, and elongation, ultimately increasing abnormal seedling incidence (El-Hendawy *et al*., 2005).

Seedling dry weight (mg): Seedling dry weight decreased significantly with increasing salinity. The highest dry weight (13.30 mg) was recorded under control, while the lowest (12.45 mg) occurred at 100 mM NaCl. NVSR 6489 (G_1) and RNR 29325 (G_{17}) maintained higher dry matter accumulation, whereas BPT 5204 (G_{30}) recorded the lowest dry weight, indicating susceptibility.

Seedling Vigour Index-I (SVI-I): SVI-I declined progressively with increasing salinity. The highest SVI-I was recorded at S_1 (3179), while the lowest was observed at S_5 (2552). Among genotypes, NVSR 6489 (G_1), CSR 23 (G_{10}) and CSR 104-10-2 (G_{13}) exhibited higher vigour, whereas GNV 10-89 (G_{27}) and GNV 1109 (G_{26}) showed poor performance, indicating high sensitivity to salinity stress. Seedling vigour index–I (SVI–I) was significantly influenced by salinity levels and genotypes, while their interaction (G × S) was found to be non-significant (Table 4) and Fig. 2.

Seedling Vigour Index-II (SVI-II): SVI-II was significantly reduced under higher salinity levels, decreasing from 1209 at S_1 to 1023 at S_5. Genotypes CSR 23 (G_{10}), CSR 104-10-2 (G_{13}), RP 6688-16-397 (G_{20}) and NVSR 6489 (G_1) maintained higher vigour, while BPT 5204 (G_{30}) and GNV 10-89 (G_{27}) recorded the lowest values.

Table 4. Impact of salinity levels on seedling vigour index -I of rice genotypes using paper towel method

Treatments	S_1 (0 mM)	S_2 (40 mM)	S_3 (60 mM)	S_4 (80 mM)	S_5 (100 mM)	Mean G
G_1: NVSR 6489	3769	3598	3421	3194	3110	3418
G_2: RNR 28361	3282	3157	3027	2934	2772	3034
G_3: NVSR 6526	3359	3248	2974	2887	2792	3052
G_4: KPS 6343	3150	3165	2839	2668	2489	2862
G_5: CSR 36	3323	3253	3123	2975	2822	3099
G_6: CSR 103-10-2	3285	3150	2883	2770	2298	2877
G_7: RP 6684-CGR 13	2777	2596	2541	2474	2373	2552
G_8: CSR 141-11-107	3235	3080	2917	2669	2583	2897
G_9: RP Bio 4919- NSR 85	3170	3092	3004	2937	2882	3017
G_{10}: CSR 23	3704	3641	3422	3273	2765	3361
G_{11}: CSR 116-10-2	3739	3265	3167	3046	2852	3214
G_{12}: RP 6682- CGR 11	3458	3363	3324	3258	3052	3291
G_{13}: CSR 104-10-2	3720	3572	3487	3431	2485	3339
G_{14}: NVSR 6494	3143	3067	2922	2831	2802	2953
G_{15}: CSR 10	2911	2819	2657	2575	2522	2697
G_{16}: IIRRH 163	3493	3422	3275	3114	2893	3239
G_{17}: RNR 29325	3218	3128	3042	2938	2983	3062
G_{18}: CSAR 9-29-2021	3303	3097	3043	2879	2696	3004
G_{19}: CSR 141-11-112	3268	3184	3065	2973	2897	3077
G_{20}: RP 6688-16-397	3703	3491	3295	3130	2595	3243
G_{21}: FL 478	3169	2943	2809	2687	2410	2804
G_{22}: RP 6711-MS-SS-20-2-9-5-23-6-1	2795	2624	2564	2304	2266	2511
G_{23}: Local Check (LC)	3127	3032	2947	2802	2447	2871
G_{24}: DRR Dhan 53	3255	3103	2971	2767	2680	2955
G_{25}: RNR 15048	2422	2338	2239	2066	1872	2187
G_{26}: GNV 1109	2379	2292	2188	2039	1774	2134

Treatments	S_1 (0 mM)	S_2 (40 mM)	S_3 (60 mM)	S_4 (80 mM)	S_5 (100 mM)	Mean G
G_{27}: GNV 10-89	2252	2116	2087	1776	1635	1973
G_{28}: GGV-0501	3166	3016	2816	2618	2203	2764
G_{29}: MTU 1010	3256	3142	3046	2789	2628	2972
G_{30}: BPT 5204	2549	2417	2275	2206	1989	2287
Mean S	3179	3047	2912	2767	2552	
		S.Em ±			**CD @1%**	
Factor G		**11.93**			**43.67**	
Factor S		**4.87**			**17.82**	
Interaction (G x S)		**26.69**			**NS**	

Legend: G: genotypes; S: salinity levels; NS: Non-significant

4. Conclusion

The study conclusively demonstrated that salinity adversely affects seed germination, seedling growth, vigour, biomass and chlorophyll stability, with wide genotypic variability in response. Laboratory, paper towel consistently identified CSR 104-10-2, CSR 23, BPT 5204, NVSR 6489 and RP 6682-CGR 11 as relatively tolerant, while genotypes like RP 6684-CGR 13, GNV 10-89, NVSR 6526 and RNR 29325 were highly sensitive.

Disclaimer (Artificial Intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

Competing Interests

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

Abdul-Baki, A. A., & Anderson, J. D. (1973). Vigor determination in soybean seed by multiple criteria. *Crop Science, 13*(6), 630–633. https://doi.org/10.2135/cropsci1973.0011183X001300060013x

Ali, M. N., Yeasmin, L., Gantait, S., Goswami, R., & Chakraborty, S. (2014). Screening of rice landraces for salinity tolerance at seedling stage through morphological and molecular markers. *Physiology and Molecular biology of plants*, *20*(4), 411-423.

Anonymous. (2023–24). Area, production and productivity of rice in Karnataka. https://www.stat.org

Ashraf, M., & Harris, P. J. C. (2004). Potential biochemical indicators of salinity tolerance in plants. *Plant Science, 166*(1), 3–16. https://doi.org/10.1016/j.plantsci.2003.10.024

Begum, N. M., Khan, M. J., & Islam, K. M. S. (2000). Feeding rations containing road side grass, maize silage or water hyacinth in bull calves. *Pakistan Journal of Biological Sciences, 3*(10), 1730–1732. https://doi.org/10.3923/pjbs.2000.1730.1732

El-Hendawy, S. E., Hu, Y., Yakout, G. M., Awad, A. M., Hafiz, S. E., & Schmidhalter, U. (2005). Evaluating salt tolerance of wheat genotypes using multiple parameters. *European Journal of Agronomy, 22*, 243–253. https://doi.org/10.1016/j.eja.2004.03.002

Gill, P. K., Sharma, A. D., Singh, P., & Bhullar, S. S. (2003). Changes in germination, growth and soluble sugar contents of *Sorghum bicolor* (L.) Moench seeds under various abiotic stresses. *Plant growth regulation*, *40*(2), 157-162.

Guo, L., Gao, Z., & Qian, Q. (2014). Application of resequencing to rice genomics, functional genomics and evolutionary analysis. *Rice, 7*(1), 4. https://doi.org/10.1186/s12284-014-0004-7

Hakim, M. A., Juraimi, A. S., Begum, M., Hanafi, M. M., Ismail, M. R., & Selamat, A. (2010). Effect of salt stress on germination and early seedling growth of rice. *African Journal of Biotechnology, 9*, 1911–1918. https://doi.org/10.5897/AJB09.1526

Higham, C. (1989). *The archaeology of mainland Southeast Asia: from 10,000 BC to the fall of Angkor*. Cambridge University Press. https://archive.org/details/archaeologyofmai0000high

Islam, M. M., & Karim, M. A. (2010). Evaluation of rice (*Oryza sativa* L.) genotypes at germination and early seedling stage for their tolerance to salinity. *The Agriculturist, 8*(2), 57–65. https://doi.org/10.3329/agric.v8i2.7578

Ismail, A. M., & Horie, T. (2017). Genomics, physiology, and molecular breeding approaches for improving salt tolerance. *Annual Review of Plant Biology, 68*, 405–434. https://doi.org/10.1146/annurev-arplant-042916-040936

ISTA, 2013, Available online: https://www.seedtest.org/api/rm/36KM8RHD6DGM336/sti146-autumn-2013.pdf

Jamil, M., Bae, L. D., Yong, J. K., Ashraf, M., Lee, S. C., & Rha, E. S. (2006). Effect of salt (NaCl) stress on germination and early seedling growth of four vegetables species. Journal of Central European Agriculture, 7(2), 273–282. https://doi.org/10.5513/jcea.v7i2.370

Kakar, N., Jumaa, S. H., Redoña, E. D., Warburton, M. L., & Reddy, K. R. (2019). Evaluating rice for salinity using pot-culture provides a systematic tolerance assessment at the seedling stage. *Rice, 12*(1), 57. https://doi.org/10.1186/s12284-019-0317-7

Kovach, M. J., Sweeney, M. T., & McCouch, S. R. (2007). New insights into the history of rice domestication. *Trends in Genetics, 23*(11), 578–587. https://doi.org/10.1016/j.tig.2007.08.012

Lu, H., Zhang, J., Liu, K. B., Wu, N., Li, Y., Zhou, K., ... & Li, Q. (2009). Earliest domestication of common millet (Panicum miliaceum) in East Asia extended to 10,000 years ago. *Proceedings of the National Academy of Sciences*, *106*(18), 7367-7372. https://doi.org/10.1073/pnas.0900158106

Mohammadi, R., Mendioro, M. S., Diaz, G. Q., Gregorio, G. B., & Singh, R. K. (2013). Mapping quantitative trait loci associated with yield and yield components under reproductive stage salinity stress in rice (*Oryza sativa* L.). *Journal of Genetics, 92*(3), 433–443. https://doi.org/10.1007/s12041-013-0285-4

Munns, R., & Tester, M. (2008). Mechanisms of salinity tolerance. *Annual Review of Plant Biology, 59*, 651–681. https://doi.org/10.1146/annurev.arplant.59.032607.092911

Neumann, P. M. (1993). Wall extensibility and the growth of salt-stressed leaves. In M. B. Jackson & C. R. Black (Eds.), Interacting Stress on Plants in a Changing Climate (Vol. 16, pp. 13-19). Springer. https://doi.org/10.1007/978-3-642-78533-7_39

Singh, S., Singh, A. K., Singh, S., & Singh, A. K. (2023). Evaluation of rice varieties (*Oryza sativa* L.) on the basis of physiological and morphological traits. *International Journal of Environment and Climate Change, 13*(8), 78–82. https://doi.org/10.9734/ijecc/2023/v13i81933

Van Zelm, E., Zhang, Y., & Testerink, C. (2020). Salt tolerance mechanisms of plants. *Annual review of plant biology*, *71*(1), 403-433. https://doi.org/10.1146/annurev-arplant-050718-100005

Peer-review history:
The peer review history for this paper can be accessed here:
https://pr.sdiarticle5.com/review-history/150607