

RESPONSE OF RICE GENOTYPES TO SALINITY UNDER HYDROPONIC CONDITIONS

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ABSTRACT

The experiment was aimed at assessing the response of 30 rice genotypes to different levels of salinity using NaCl concentration as salt stress at early seedling stage under hydroponic conditions. The experiment was replicated three times in a Completely Randomized Design for two years. The 30 rice genotypes evaluated for root length, fresh root weight, dry root weight, shoot length, fresh shoot weight, dry shoot weight, seedling biomass and shoot/root length ratio. The four salinity treatments/levels (0, 4, 6 and 12 dS/m) significantly affected the response of the 30 rice genotypes for all the traits evaluated. The interaction between salinity treatments and the genotypes was significant for all traits except fresh root weight, shoot length and dry shoot weight. The genotypic response revealed reduction in performance as the salinity level increases for all the traits, 10 genotypes were tolerant at all salinity levels. The most affected seedling trait due to salinity stress was seedling biomass at 6 dS/m (54.84%) and was expressed by genotype IR29 (susceptible check), followed by ROK 24 at 12 dS/m (54.43%). Eight rice genotypes; CK73, ITA212 (FARO 35), ITA222 (FARO 36), OG0315, OG250315, OW0315, TOG 5681 and Pokkali (Tolerant Check) were classified highly tolerant by both Stress Tolerance Index (SST) and Stress Susceptible Index (SSI), while FARO 61 (NERICA L – 34) and IR72 were moderately tolerant. These rice genotypes have good potentials for further salt tolerance breeding.

Key words: salt stress, genotypes, seedling traits, tolerance index, susceptible index

INTRODUCTION

Salt-affected soils are distributed throughout the world and every continent is faced with this problem (Brandy and Weil, 2002; Dubey and Singh, 1999). A total land area of 831 million hectares is salt-affected, globally, and African countries with growing concern of salinity problems of varying degrees includes; Kenya (8.2 Mha), Nigeria (5.6 Mha), Sudan (4.8 Mha), Tunisia (1.8 Mha), Tanzania (1.7 Mha) and Ghana (0.79 Mha) of land (FAO, 2000). Rice is one of the most important world food crops, which serves as staple food for over one-third of the world's population (Khush, 1997). Salinity is considered as one of the most important physical factors influencing rice production. At present, salinity is the second most widespread soil problem in rice growing countries after drought and is considered as a serious constraint to increasing rice production worldwide (Gregorio, 1997). Several rice-growing countries, both in the tropics and the temperate regions, are

facing high soil salinity as a major problem which is more severe in the arid, semiarid, and coastal rice-producing areas of the tropics (Lee *et al.*, 2003). The use of hydroponic evaluation of rice has been identified to be free of soil-related difficulties. Thus, this method can reliably assess the response of genotypes to salt stress and, therefore, identify salt-tolerant genotypes (Ashraf *et al.*, 1999; Bhowmik *et al.*, 2009). Evaluation of plant response to salt stress in different crop species in hydroponic cultures has been well documented (Xie *et al.*, 2000, Akram *et al.*, 2010, Shahzad *et al.*, 2012). According to the United States Department of Agriculture (USDA) Salinity Laboratory, saline soils can be defined as soil that has electrical conductivity of saturated paste extract (ECe) over 4.9 dS m⁻¹ measured at a temperature of 25 °C (Kanawapee *et al.*, 2013). Salinity increases when there are a lot of mineral salts dissolved in water such as NaCl, Na₂SO₄, NaNO₃, MgSO₄, MgCl₂, K₂SO₄, and CaCO₃ (Gao *et al.*, 2007). The

susceptibility of rice to salinity stress varies with developmental stages (Yoshida, 1967). Heenan *et al.* (1988) and Lutts *et al.* (1995) reported that rice is extremely sensitive to salinity during the following stages of development; germination, young seedling and early developmental stages for most commonly used rice varieties. The effect of salinity has been reported to be associated with all stages of plant development, thus, understanding the nature, concentrations and duration of salinity effects on rice is very important in rice improvement (Aslam *et al.*, 1993; Zeng *et al.*, 2001). The main aim of this study was to evaluate the performance of the rice seedlings under different salinity levels, identify and select the tolerant genotypes which could be used in future breeding programmes.

MATERIALS AND METHODS

Germplasm

Thirty diverse genotypes were used in this study, including some newly improved ones. These rice genotypes with their peculiar descriptors originated from Agricultural Research Institute of Guinea (IRAG) Guinea, Federal University of Agriculture, Abeokuta, (FUNAAB) and Africa Rice Centre (ARC) Nigeria, Senegalese Agricultural Research Institute (ISRA) Senegal, Sierra Leone Agricultural Research Institute (SLARI) Sierra Leone, International Rice Research Institute, Philippines (IRRI) Philippines and Indian Agricultural Research Institute (IARI) India (Table 1).

Rice Screening under Hydroponic Condition

The experiment was conducted in the screen house of the Bioscience Laboratory at the International Institute of Tropical Agriculture (IITA), Ibadan (Latitude 3° 54' N and longitude 7° 30' W), Nigeria across 2 cropping seasons. The greenhouse temperature was maintained at 25 ± 1°C, 12 h daylight with relative humidity at 70%. There was a regular and adequate sunlight periods needed. Seeds of the 30 rice genotypes were germinated in sterilized field soil while seedlings were grown for 14 days. Plastic containers of 40 × 25 × 20 cm were prepared for the screening purpose. A Styrofoam sheet was cut to fit the top of each container. Four rows with four holes each were made on each Styrofoam sheet and nylon net was placed at the bottom of each Styrofoam sheet to prevent the seedling from falling into the solution following the method described by Gregorio *et al.* (1997). Each Styrofoam sheet was floated in a container filled with 4 liters of distilled water.

Establishment of Plant in Nutrient Solution

After two weeks, the seedlings (at two to three leaf stages) were uprooted, rinsed with sterilized

deionised water to remove the soil and were transferred to the prepared containers. Each container had five rows consisting of five genotypes (one genotype per row), and each hole had one seedlings. The seedlings were grown in distilled water for 72 h and was replaced by a nutrient solution prepared using 1ml/L of working solution (Gregorio *et al.*, 1997). The working solution was prepared using the following stocks: NH₄NO₃ (91.4 g/L), Na₂HPO₄ (35.6 g/L), CaCl₂ (117.4 g/L), MgSO₄ (324 g/L) and KSO₄ (70.65 mg/L) for macronutrient stocks and a combination of MnCl₂ (1.5 g/L), H₃BO₃ (0.934 g/L) ZnSO₄ (0.035 g/L), FeSO₄ (7.7 g/L), CuSO₄ (0.031 g/L), (NH₄)₆Mo₇O₂₄ (0.13 g/L) and H₃C₆H₈O₇ (11.9 g/L) was used to make stock solution for required micronutrients (Gregorio *et al.*, 1997; Yoshida *et al.*, 1976). Seedlings were cultured in the nutrient solution for 14 days prior to salinization to allow proper establishment. The nutrient solution was renewed after every 8 days and the pH of 5.0 was maintained daily by adding either sodium hydroxide (NaOH) or hydrochloric acid (HCl).

Salinisation

Laboratory graded sodium chloride (NaCl, Qualikems Laboratory reagent) was added to the nutrient solution after proper establishment of the seedlings. The 30 genotypes were arranged in a Randomized Complete Block Design (RCBD) with four levels of salinity 0 dS/m (control), 4 dS/m, 6 dS/m and 12 dS/m, and three replications. The appropriate salinity levels were raised in a stepwise procedure until the final concentration was attained. The salinity levels were monitored using a portable EC meter (HI96304 HANNA instruments).

Data Collection

The following data were collected 10 days after the maximum desired stress level was achieved; shoot length (SL), root length (RL), shoot fresh weight (SFW), Root fresh weight (RFW), Shoot dry weight (SDW) and Root dry weight (RDW) under both control and salt stressed conditions.

Statistical Analysis

The salinity injury index evaluation was done using modified Standard Evaluating Score (SES) in rating the visual salt injury at seedling stage following the method proposed by Gregorio *et al.*, (1997). All the data were tested for normality while the data were subjected to analysis of variance (ANOVA) with 3 levels of classification (Salinity, Genotype and salinity × genotype), mean separation was done using Least Significant Difference (LSD) test at 5% probability. The data were analyzed using GENSTAT release 10.3 computer package. The harmful effects induced by

salinity were computed in percent reduction over control (% ROC or % R) for above cited plant attributes by the following formula: $\%R = [(V_c - V_s)/V_c] \times 100$, Salt/Stress Susceptibility Index (SSI) was obtained according to $(1 - V_s/V_c)/SI$, Stress Intensity (SI), $SI = 1 - (V_s/V_c)$, $STI = (V_c \times V_s)/V_c^2$, Where V_c is measured value under control and V_s is measured value under stress.

RESULTS AND DISCUSSION

Table 1 reveals the Mean Squares of traits among the 30 rice genotypes, there was highly significant differences among the rice genotypes for all the traits measured. The salinity levels as treatment was also highly significantly different as obtained in all traits measured. Thus, this result showed that the rice genotypes reacted differently to the level of salinity stress imposed. The 30 rice genotypes expressed their inherent and appreciable genotypic variability in their differential responses while under stress. The interaction effect was highly significant for root length, shoot length, salinity injury and seedling vigour index. The significant differences observed among all the rice genotypes suggested the presence of genetic variability in the materials used and provides good opportunity for salinity tolerance improvement. Significant genotype \times salinity treatment interaction revealed the differential effect of stress on root and shoots length and injury symptoms. The non significant genotype \times salinity interaction in fresh root weight, fresh shoot weight and dry shoot weight could be due to late physiological salt injury recovery rate. The mean performance of the 30 rice genotypes in stress and non stress environments using hydroponic methods is presented in Table 3. The least root length was recorded for V26 (13.00 cm) at 12 dS/m and the longest root length was 30.00 cm for V14 at 4 dS/m. There was gradual reduction in root length as the salinity dosage increases. The differential genotypic responses expressed in Table 3 was due to the effect of salinity on root cell size, the rate of cell production and elongation, consequently leading to shorter roots in rice. Similar report was documented by Azaizeh *et al.* (1992), Rodriguez *et al.* (2002) and Momayezi *et al.* (2009) that root length reduction was due to the effect of high concentration of salt. 16, 14 and 19 rice genotypes had higher fresh root weight than their genotypic average at 4 dS/m, 6 dS/m and 12 dS/m respectively. V2, 3, 4, 5, 6, 7, 8, 11, 12, 15, 23, 24 and 30 consistently had higher fresh root weights than other genotypes evaluated across the 3 salinity levels of stress imposed. Although, there

are variable genotypic responses to the salinity treatments, there was appreciable reduction in the fresh root weight as the salt concentration increases. Twelve rice genotypes performed better than the other genotypes by having higher dry root weight than their genotypic means under 4, 6 and 12 dS/m salinity treatments. Genotypes V5, 6, 11 and 23 were outstandingly tolerant to salinity in their root traits. These genotypes were consistently better than all the other genotypes in the expression of their root traits as indicator traits for salinity tolerance (root length, fresh root weight and dry root weight) across the salinity concentration levels. V23 and V24 performed better at higher concentration of salt, thus indicating salt tolerance at high concentration. V7 and V8 performed better at low concentration of salt (4 and 6 dS/m) for the entire root traits measured, thus, these 2 genotypes showed initial or early root salt tolerance. In Table 4, V10 has the least shoot growth (20.33 cm) as affected by salinity at 12 dS/m and V30 had the highest shoot length of 44.00 cm at high salt concentration (6 and 12 dS/m). Some 15, 14 and 13 genotypes had higher fresh shoot weight than their genotypic mean under 4, 6, and 12 dS/m salt concentration respectively. V1 and 4 performed well for the shoot trait measured (shoot length, fresh shoot weight and dry shoot weight) at 4 and 6 dS/m of salt concentration respectively. V6, 11, 12, 17, 22 and 24 were better performers at high salt concentrations (6 and 12 dS/m), thereby, indicating salt tolerance at high concentration of salinity. V13, 21, 23, 28 and 30 were outstanding genotypes across the 3 levels of salt treatment for all the shoot traits measured. These five genotypes were consistently good and showed very little reduction in the traits measured under salt stress when compared to the control treatment. According to Cramer and Nowak (1992), Perez-Alfocea *et al.* (1996), Purnendu *et al.* (2004), Maiti *et al.* (2006) and Janmohammadi *et al.* (2008), salinity stress affect the roots of some genotypes more than the shoot, due to varietal differences in root capacity to exclude Na^+ and Cl^- negative ions. At the highest salinity level (12 dS/m) there were only two mortalities (OG0315 and IR29), these genotypes were among the most affected by high concentration of salt stress.

Seedling biomass and percent decrease or reduction as influenced by different salinity level are presented in Table 5. Four genotypes (V1, 16, 17 and 23) and four genotypes (V11, 13, 26 and 30) had less than 5 and 10% biomass reduction, respectively at 4 dS/m salt concentration.

Table 1: Pedigree of varieties used and their responses to stress

Code	Genotype	Origin/Source	Response to stress
V1	CK73	Guinea	Salinity tolerant
V2	FARO 44 (SPI 690233)	Nigeria	Blast resistant
V3	FARO 52 (WITA 4)	Senegal	Drought and iron toxicity tolerant
V4	FARO 60 (NERICA – L19)	Senegal	Blast, drought and iron toxicity resistance
V5	FARO 61(NERICA L – 34)	Senegal	Drought and iron toxicity resistant
V6	ITA212 (FARO 35)	Nigeria	Salinity Tolerant
V7	ITA 222 (FARO 36)	Nigeria	Salinity tolerant
V8	ITA306	Nigeria	High yielding
V9	IR64	Philippines	Low input tolerant
V10	IR72	Philippines	Undetermined
V11	NERICA L7	Senegal	Drought, cold and iron toxicity resistant
V12	NERICA L8	Senegal	Drought, cold and iron toxicity resistant
V13	NERICA L12-	Senegal	Drought, cold and iron toxicity resistant
V14	NERICA L53	Senegal	Drought cold and iron toxicity resistant
V15	NERICA L20	Senegal	Drought, salt, cold and iron toxicity resistant
V16	NERICA L45	Senegal	Drought, cold and iron toxicity resistant
V17	NERICA L48	Senegal	Drought, cold and iron toxicity resistant
V18	NERICA L50	Senegal	Drought, cold and iron toxicity resistant
V19	NERICA L54	Senegal	Drought, cold and iron toxicity resistant
V20	OG0315	Nigeria	Drought tolerance
V21	OG250315	Nigeria	Drought tolerance
V22	OG300315	Nigeria	Drought tolerance
V23	OW0315	Nigeria	Undetermined
V24	OW100315	Nigeria	Undetermined
V25	OW250315	Nigeria	Undetermined
V26	ROK 5	Sierra Leone	Salinity tolerant
V27	ROK24	Sierra Leone	Iron toxicity tolerant
V28	TOG 5681	Nigeria	Landrace
V29	IR29 (Susceptible check)	Philippines	Resistant to biotic stress; blast, tungro, gall midge.
V30	Pokkali (Tolerant check)	India	Salinity resistant

The following genotypes; V1, 3, 8, 11, 13, 15, 16, 17, 21, 22 and 30 showed less than 20% biomass reduction when 6 dS/m salt concentration was applied. Under the highest salt concentration of 12 dS/m, 5 rice genotypes (V13, 21, 23, 26 and 30) that showed tolerance with less than 30% biomass reduction. The different genotypic responses of rice at different salt concentration revealed that V13, 21, 23 and 30 have high seedling tolerance to salt, while V11, 15, 16, 17 and 26 were mildly tolerant to salt stress. Genotypes with increased root fresh and dry weight but decreased in shoot fresh and dry weight may be due to inability of ionic movement of salt through the apoplectic pathway from the root to the shoot thereby resulting in higher accumulation of these salt in the root than the shoots (Hu *et al.*, 2012; Ali *et al.*, 2014; Usatov *et al.*, 2014 and Aliyu *et al.*, 2016). Salinity tolerance ranking (STR), salt susceptible index (SSI), percent root, shoot reduction and percent ratio at 12 dS/m are presented in Table 6.

The shoot is more affected than the root under salt stress as seen by the ratio and percent ratio of root length to shoot length. The root and shoot ratio, and percent ratio do not give a definite pattern showing salt tolerance. The SSI value of genotypes that are < 1 are considered tolerant, the lower the value the better the tolerance (Zeng *et al.*, 2001; Aliyu *et al.*, 2016). Here 15 genotypes were classified tolerant by SSI (SSI values less than 1), the least SSI value was 0.50 for OW0315 followed by 0.60 for OG0315, and the standard tolerant check Pokkali (0.63). The STR for all the rice genotypes evaluated at the 3 levels of salt concentration showed differential response of the genotypes at the 3 levels of salt stress. 21, 12 and 4 rice genotypes showed high salt tolerance at 4, 6 and 12 dS/m of salt concentration respectively. Six rice genotypes (V6, 7, 20, 21, 23 and 30) were highly tolerant, 8 genotypes (V1, 5, 10, 15, 16, 17, 22 and 28) were moderately tolerant and 3 genotypes (V3, 11 and 26) were slightly tolerant to salt stress.

Table 2: Mean squares of traits among thirty genotypes of rice under salinity stress

SV	DF	Mean Squares							
		^a RL	RFW	RDW	SL	SFW	SDW	SI	BIOM
Salinity (S)	3	1748.96**	0.74136**	0.040194**	1199.12**	4.4086**	0.16905**	237.28**	0.3714**
Year	1	0.0213 ^{ns}	0.1005 ^{ns}	0.0094 ^{ns}	1.0033 ^{ns}	0.9244 ^{ns}	1.0128 ^{ns}	0.0093 ^{ns}	0.0071 ^{ns}
Genotype (G)	29	121.445**	0.05419**	0.005300**	354.438**	0.4597**	0.03426**	14.731**	0.0458**
S x G	87	21.512**	0.00660 ^{ns}	0.000234 ^{ns}	28.012**	0.0387 ^{ns}	0.00155 ^{ns}	4.2117**	0.0019 ^{ns}
Residuals	238	6.853	0.00635	0.002405	6.654	0.0448	0.00255	0.0467	0.0034
CV%		11.8	25.1	39.6	8.1	22.9	22.1	8.9	20.2

*: significant at 5%; **: significant at 1%; ns: non significant ^aRL = root length, RFW = root fresh weight, RDW = root dry weight, SL = shoot length, SFW = shoot fresh weight, SDW = shoot dry weight, SI = stress intensity and BIOM = total biomass

Table 5: Mean values of seedling biomass and percentage decrease as affected by salinity concentrations

Genotypes	% Decrease of Biomass (g) at diff. Salinity levels							
	Control	4 dS/m		6 dS/m		12 dS/m		
		Salinity treatment	% Decrease	Salinity treatment	% Decrease	Salinity treatment	% Decrease	
V1	0.35	0.34	3.16	0.29	15.80	0.23	33.91	
V2	0.38	0.31	16.71	0.28	25.73	0.20	45.89	
V3	0.40	0.36	10.15	0.33	17.57	0.21	47.28	
V4	0.29	0.24	16.21	0.21	27.93	0.16	43.79	
V5	0.40	0.35	10.83	0.28	30.48	0.23	42.07	
V6	0.39	0.32	17.53	0.30	21.65	0.27	31.19	
V7	0.33	0.24	28.83	0.25	24.02	0.23	30.93	
V8	0.30	0.27	10.20	0.25	16.78	0.19	36.51	
V9	0.27	0.21	22.26	0.19	30.66	0.16	40.15	
V10	0.35	0.31	11.27	0.27	21.97	0.18	48.84	
V11	0.43	0.38	9.86	0.35	18.54	0.28	33.33	
V12	0.39	0.28	27.81	0.25	35.46	0.23	42.09	
V13	0.36	0.33	9.09	0.31	13.77	0.27	24.79	
V14	0.35	0.30	15.01	0.28	21.81	0.17	50.71	
V15	0.40	0.36	10.00	0.32	19.85	0.25	37.22	
V16	0.31	0.31	0.00	0.26	14.43	0.21	30.16	
V17	0.38	0.37	2.92	0.32	14.32	0.25	32.89	
V18	0.37	0.30	18.50	0.27	28.69	0.20	45.58	
V19	0.39	0.33	15.76	0.28	26.87	0.26	33.59	
V20	0.20	0.17	15.84	0.11	47.52	-	-	
V21	0.37	0.33	10.81	0.30	20.00	0.26	28.92	
V22	0.34	0.30	10.36	0.29	14.20	0.23	32.84	
V23	0.40	0.38	3.28	0.36	8.33	0.32	19.19	
V24	0.46	0.29	35.60	0.29	36.04	0.26	42.64	
V25	0.40	0.35	12.59	0.28	28.72	0.24	40.30	
V26	0.44	0.40	9.71	0.35	20.54	0.32	27.77	
V27	0.32	0.18	42.09	0.16	48.42	0.14	54.43	
V28	0.38	0.34	11.58	0.30	21.05	0.26	32.37	
V29	0.31	0.18	43.23	0.14	54.84	-	-	
V30	0.44	0.40	9.50	0.36	18.55	0.33	24.66	
Range	0.20-0.46	0.17-0.4	0.00-43.23	0.11-0.36	8.33-54.84	0.14-0.33	19.19-54.43	
Mean	0.36	0.31	15.36	0.27	24.82	0.23	36.93	
LSD 0.05	0.11	0.10	-	0.09	-	0.08	-	

Table 6: Response of 30 rice genotypes under 12 dS/m salt in hydroponic conditions at seedling stage

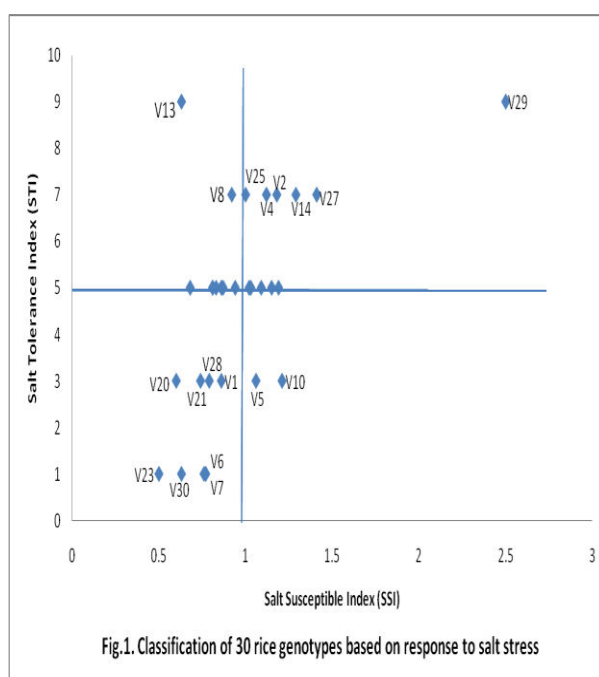
Genotype code/Genotypes	% Root decrease @ 12 dS/m	% Shoot decrease @ 12 dS/m	^a RL:SL percent ratio @ 12 dS/m (%)	Salt susceptible index @ 12 dS/m	Salinity tolerance ranking		
					4 dS/m	6 dS/m	12 dS/m
V1 CK73	36.00	24.08	1:1.7 (41.2)	0.86	1	1	3
V2 FARO 44 (SPI 690233)	31.01	24.24	1:1.5 (33.3)	1.18	1	3	7
V3 FARO 52 (WITA 4)	31.58	24.77	1:1.5 (33.3)	1.19	1	5	5
V4 FARO 60 (NERICA-L19)	31.09	15.38	1:1.9 (47.4)	1.12	1	3	7
V5 FARO 61 (NERICA L-34)	35.71	11.47	1:1.6 (37.5)	1.06	1	1	3
V6 ITA212 (FARO 35)	23.69	24.77	1:1.3 (23.1)	0.77	1	1	1
V7 ITA 222 (FARO 36)	31.48	8.77	1:1.7 (41.2)	0.76	1	1	1
V8 ITA306	36.35	21.88	1:1.3 (23.1)	0.92	1	5	7
V9 IR64	36.07	13.53	1:1.3 (23.1)	1.02	3	5	5
V10 IR72	35.91	35.11	1:1.5 (33.3)	1.21	1	1	3
V11 NERICA L7	39.99	25.24	1:1.2 (16.7)	0.87	1	3	5
V12 NERICA L8	33.33	17.18	1:1.5 (33.3)	1.03	3	5	5
V13 NERICA L12	36.99	13.46	1:1.6 (37.5)	0.63	1	7	9
V14 NERICA L53	45.91	25.98	1:1.4 (28.6)	1.29	1	5	7
V15 NERICA L20	44.12	24.54	1:1.5 (33.3)	0.94	1	1	5
V16 NERICA L45	26.54	17.77	1:1.9 (47.4)	0.81	3	3	5
V17 NERICA L48	30.00	8.43	1:1.8 (44.4)	0.86	1	1	5
V18 NERICA L50	32.53	19.35	1:1.3 (23.1)	1.15	3	3	5
V19 NERICA L54	29.83	21.70	1:1.7 (41.2)	0.83	1	5	5
V20 OG0315	-	-	-	0.60	1	1	3
V21 OG250315	26.45	22.41	1:3.1 (67.7)	0.74	1	1	3
V22 OG300315	25.26	21.73	1:3.4 (70.6)	0.81	1	3	5
V23 OW0315	33.32	15.93	1:3.3 (69.7)	0.50	1	1	1
V24 OW100315	36.55	13.12	1:3.0 (66.7)	1.09	3	5	5
V25 OW250315	30.48	20.18	1:4.4 (77.3)	1.00	3	7	7
V26 ROK 5	48.00	15.30	1:4.7 (78.7)	0.68	3	3	5
V27 ROK24	28.77	22.97	1:2.9 (65.5)	1.41	3	5	7
V28 TOG 5681	47.63	29.93	1:3.3 (69.7)	0.79	1	1	3
V29 IR29 (Susceptible check)	-	-	-	2.50	7	7	9
V30 Pokkali (Tolerant check)	20.03	12.00	1:4.0 (75.0)	0.63	1	1	1

^aRL:SL is Root Length to Shoot Length ratio Salt Tolerance Ranking (STR) value means 1-2 = Highly tolerant, 3-4 = Tolerant, 5-6 = Moderately tolerant, 7-8 = Susceptible and 9 = Highly susceptible. Salt Susceptible Index (SSI) value means Low value (<1) = Least susceptible and high value (≥1) = Highly susceptible

The effect of 4 dS/m salinity level was not profound with respect to all parameters considered, thus, almost all the genotypes appeared to be highly tolerant or mildly tolerant. However, as the salinity level increased to 6 and 12 dS/m the genotypes started showing gradual deviation from their previous salt tolerant ranking.

Therefore, salt concentration at 6 and 12 dS/m is a better determinant of salinity tolerance in rice as obtained in this study. These observations are in agreement with Muscolo *et al.* (2003), Maggio *et al.* (2007), and Noreen and Ashraf (2008) that reported variability in rice germplasm assessed under varying concentrations of salinity.

Figure 1 reveals the classification of 30 rice genotypes based on Salt Tolerance Index (STI) and SSI under 12 dS/m salt concentration; the highly tolerant rice genotypes are in quadrant C, consisting of V1, 6, 7, 20, 21, 23, 28 and 30. Moderately tolerant genotypes are found on the divide line (STI average) in quadrants C and D (V5, 10, 15, 16, 17 and 22). Genotypes exhibiting slight tolerance are in quadrant A, while susceptible genotypes are in quadrant B (V2, 4, 14, 25, 27 and 27). Genotypes in quadrant C, A and D are most important for salt tolerance breeding and further crop improvement. According to Lee *et al.* (2003), Gao *et al.* (2007), Soubir *et al.* (2009) and Momayezi *et al.* (2009) screening, classification and selection of rice accessions at seedling stages is necessary for salt stress tolerance improvement and possible deployment of outstanding genotypes at a much faster rate under hydroponic condition than field conditions.



CONCLUSION

Salinity at 12 dS/m contributed greatly to variations among rice genotypes under hydroponic condition for identification of tolerance genotypes. OG0315 and IR29 had high mortality at this salinity level, thus, the most harmful salinity stress level. It is, therefore, recommended that these genotypes be cultivated in non-saline environments. This study was able to identify genotypes CK73, ITA212 (FARO 35), ITA222 (FARO 36), OG0315, OG250315, OW0315, TOG 5681 and Pokkali (Tolerant Check) as consistently tolerant at all stress levels. These genotypes offer valuable genetic resources for both local and international rice improvement for salt tolerance. Therefore, these genotypes could be deployed as appropriate, and included in further rice breeding programmes.

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