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Research Article

Effect of Salinity on Final Growth Stage of Different Rice (*Oryza sativa* L.) Genotypes

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Abstract

Background and Objective: Rice is one of the important cereal crops satisfying the carbohydrate need of one third of the world population. Rice is recently introduced crop in Ethiopia but its production is expanding very fast. However, its production is tackled by many factors in which salinity is one of the problem. The objective of this study was to identify high yielding, salt tolerant rice genotypes. **Methodology:** The experiment was evaluated 13 genotypes along with two checks (one tolerant and one susceptible) at four salinity levels in a factorial combinations Completely Randomized Design (CRD) with three replications in a lath house pot experiment at Werer Agricultural Research Center, Eastern part of Ethiopia from August, 2014 to February, 2015. **Results:** The ANOVA for these two experiments revealed very highly significant difference between the genotypes in all studied traits witnessing the genetic variability which can be used in breeding rice for salinity tolerance. Salinity levels affected yield and its components during the final growth stage. The genotype by salinity interaction was also very highly significant for all traits showing the inconsistency of the performance of genotypes across the salinity levels that also caused change in rank genotypes. In the experiment salinity caused decreased grain yield by 0.16 g for every dS m^{-1} increase of salinity between 0 and 12 dS m^{-1}. **Conclusion:** Genotypes, IR 70023 and IR 71810 of rice (*Oryza sativa* L.) were found tolerant. A breeding program should be developed for the improvement of salt tolerant genotypes.

Key words: Genotype, grain yield, trait, variability

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Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Rice is one of the most strategic crops in the world, Africa and particularly in Ethiopia[1]. In Ethiopia, the second most populous nation in Sub-Sahara Africa, rice is one of the target commodity that have received due emphasis in promotion of agricultural production and is considered the "Millennium crop". Ethiopia has considerably vast suitable ecologies for rice production but unsuitable for production of other food crops[2].

The expansion of rice production in Ethiopia is tackled by many different constraints, with salinity as the major one. According to Hawando[3], 36% of the land in Ethiopia is affected by salinity. About 40% of the irrigable area in middle awash is out of production due to salinity[4]. The most efficient strategy which can increase the productivity of the saline land is the use of tolerant varieties[5,6].

Even though rice is known to be highly susceptible to salinity there are genotypes that can survive and produce grain at high salinity level[7]. The effect of salinity depends on the type of crop, environmental condition, biotic stress and growth stage[5]. Salinity causes stress through osmotic and specific ion effect[8] that results in low germination, stunted seedling growth, high sterility, dried leaf and low grain yield of rice[9-11].

Even though Ethiopia is an ideal country for production of rice, the amount of arable land under rice cultivation is very small as compared to the potential and a large quantity of rice is still imported annually[12]. Since, salinity is expanding in irrigated agriculture of Ethiopia[4] access to new varieties tolerant to soil stress conditions, especially to salinity is an urgent task to be undertaken. Therefore, the present study was proposed to identify high yielding, salt tolerant rice genotypes.

MATERIALS AND METHODS

Description of the study site: The study was conducted at Werer Agricultural Research Center (WARC) in lath house from August-February, 2015. Werer is located 9°27' N and 40°15' E in North Eastern part of Ethiopia about 280 km from Addis Ababa. The soil in the region is predominantly vertisol with the porosity and bulk density (0-25 cm depth) of 49.06% and 1.35 g cm^{-2}, respectively[3].

Treatments and designs: Factorial experiment consists of 15 rice genotypes including one susceptible check and one tolerant check at 4 levels of salinity (0, 4, 8 and 12 dS m^{-1}). The salt concentrations were selected based on the experiment by Dawit[13]. The genotypes were developed by IRRI (International Tice Research Institute) for salt tolerance and distributed for testing for the year 2012 growing season.

Soil collection and preparation: Soil was collected from WARC research field. The soil was air dried for 10 days followed by gently dispersing and mixing thoroughly then sieving through a 2 mm sieve. The pH value, CEC and EC of the soil were 8.1, 18 mEq/100 g soil and 1.01 dS m^{-1}. The texture of the soil was silty clay containing 40% clay, 49% silt and 11% sand.

Pot experiment management: The experiment was conducted by sowing rice seeds in plastic pots of 22 cm top diameter, 15 cm bottom diameter and 23 cm depth filled with 5 kg soil in 3:1 ratio of the collected soil and sand, respectively. Each pot was sown with 10 seeds and lined with double layer of cotton to restrict seepage of the solution. Then the pots were kept in the lath house under sunlight. Then after, the soil in the pots were moisturized with water and commercial NaCl with 12.8, 25.6 and 38.4 g were added to obtain 3 salinity levels (4, 8 and 12 dS m^{-1}). Salt solution seepage from each pot was collected every 24 h and returned to the pot to avoid loss of salts. The soil was fertilized with 50 N and 25 P mg kg^{-1} of soil according to IRRI recommendation[14]. Watering and other agronomic managements were done according to the requirement of the plant.

Data collection: The data collected was based on both individual plant and pot basis.

Data collected on pot basis: The weight of 100 selected grains from each pot was taken and conversion was made to 1000 grain weight; for pots having less number of grains conversion was made according to the number of seed available. The grain weight of each pot (from central spike and tiller spike) was taken after the moisture content was adjusted to 14% moisture content using moisture content meter (Agratronix, Japan).

Data recorded on individual plant basis: Data of the following traits were recorded from five plants in the pot. Plant height was measured from the ground level to the tip of central panicle. Panicle length was measured from the bottom of the panicle to the top most fertile spikelet on the main axis. Total number of spikelets from each selected central panicles were counted and number of unfilled spikelets were counted from the same panicles. Then spikelet fertility percentage was calculated by dividing the mean number of filled spikelets to the total number of spikelets multiplied by hundred. Total number of tillers were counted from randomly selected plants and then from the same plants effective number of tillers were counted by identifying tillers that have grains.

To compare the response of different genotypes for salinity stress, various indices have been used, such as tolerance index (Tol)[15], Mean Productivity Index (MPI)[15], geometric mean productivity index (GMP)[16], Stress Tolerance Index (STI)[16], Stress Susceptibility Index (SSI)[17], Yield Index (YI)[18] at stress condition and Yield Stability Index (YSI)[19]:

$$\text{Tol} = \text{Ypi} - \text{Ysi}$$

$$\text{MPI} = \frac{\text{Ysi}+\text{Ypi}}{2}$$

$$\text{GMP} = \sqrt{\text{Ypi} \times \text{Ysi}}$$

$$\text{STI} = \frac{\text{Ysi} \times \text{Ypi}}{\text{Yp}^2}$$

$$\text{SSI} = \frac{1-\text{Ysi}/\text{Ypi}}{1-\text{Ys}/\text{Yp}}$$

$$\text{YI} = \frac{\text{Ysi}}{\text{Ys}}$$

$$\text{YSI} = \frac{\text{Ysi}}{\text{Ypi}}$$

where, Ypi is the mean yield of each cultivar in the control treatment, Ysi is the mean yield of each cultivar in 12 dS m^{-1} saline treatment, Yp is the mean yield of all cultivars in control treatment and Ys is the mean yield of all cultivars in 12 dS m^{-1} saline treatment.

Data analysis: The data was subjected to analysis of variance (ANOVA) of the two factors Completely Randomized Design (CRD) using GLM procedure of Statistical Analysis System (SAS) version 9.0. Based on the grain yield data univariate stability parameters such as Wricke's ecovalence and Shukla's stability using SAS[20]. Multivariate analytical tool GGE biplot were also employed to asses similarity and dissimilarity among four salinity levels and interaction patterns between genotypes and salinity levels.

RESULTS AND DISCUSSION

The names of some genotypes had been shortened for simplification. Computations of regression analysis between the mean of the parameters and the salinity levels and data between the correlations of the stress indices were not showed.

Analysis of variance: The analysis of variance showed that there is very highly significant difference between the salinity levels, the genotypes and their interaction for the parameters taken.

Yield and yield components

Plant height: The analysis of variance showed the plant height of different rice genotypes were significantly affected by the different salinity levels. This result showed the increase in salinity concentration affected the plant height negatively, that caused 21-61% decrease at 12 dS m^{-1} even 100% for some susceptible genotypes (Fig. 1a) in agreement with the study of Hakim *et al.*[9], who stated that the reduction in plant height is proportional with the increment in salinity concentration but tolerant genotypes can retain their height even at higher salinity concentration by outperforming the sensitive ones. It also complies with the experimental observation of Dawit[13]. Generally, it was observed that salinity caused the decrease in plant height in all the genotypes that could be the cumulative effect of salinity in delaying emergency, the decrease in shoot and root biomass. The reduction in plant height in the increased salinity level could be due to lower water potential and reduction in leaf water content which results stomatal closure that limits carbon dioxide assimilation and reduced photosynthetic rate[12]. A disturbance in mineral supply (excess/deficiency) which induce changes in the concentration of specific ions that affect the growth[10] might be the other reason for reduction of plant height.

Number of tillers: Grain yield of rice is highly dependent on the number of panicle producing tillers. All the genotypes in this experiment were highly affected by the increase in salinity on total and effective number of tillers. In case of genotype IR 29 (susceptible check), IR 59418, IR 72593, IR 73055 and NERICA 4 showed 100% loss at 12 dS m^{-1} (Fig. 1b). Minimum reduction of effective tillers were observed in IR 71810, IR 71901, IR 71991 and IR 70023 across the four salinity levels (Fig. 1b). As the salinity concentration becomes higher and higher the reduction in number of effective tillers per plant was also higher[21]. The same was true for this experiment, which at higher salinity concentration the number of effective tillers decreased significantly over the control. This result is supported by the study of Putech and Modal[21].

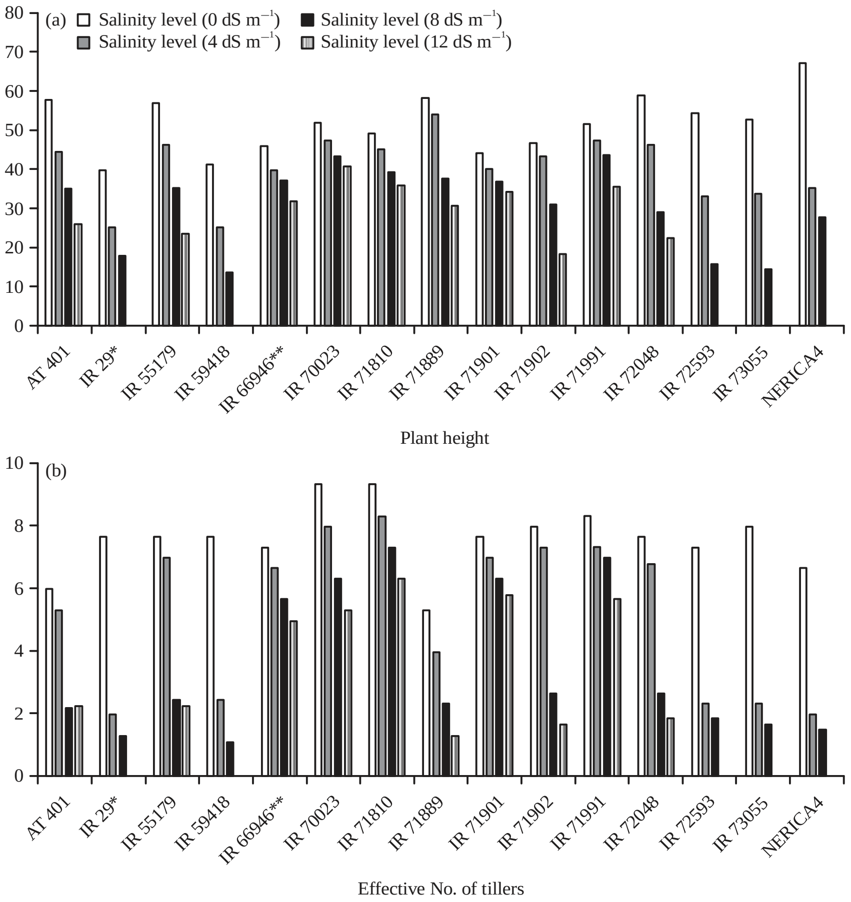

Fig. 1(a-b): (a) Plant height of the 15 rice genotype in four salinity levels and (b) Number of tillers of the 15 rice genotype in four salinity levels, *Susceptible, **Tolerant

Panicle length: This experiment revealed that panicle length of the different rice genotypes was greatly affected by salinity. The highest and the lowest panicle length was registered in IR 71889 (Control) and the four genotypes (12 dS m^{-1}), respectively. Salinity has negative effect on the length of panicle, thus there is a decrease in the length of the panicle with an increase in the concentration of salinity. The same thing was observed in this experiment but the decreasing rate was varied with genotypes. There was very little reduction of panicle length in the tolerant genotypes like IR 70023 and IR 71810 which lost 23% at the higher salinity level and much higher in the susceptible ones like NERICA 4 and IR 59418 (Fig. 2a). This finding is supported by the experiment of Hakim *et al.*[10], Rad *et al.*[22] and Mahmood *et al.*[23] where the major cause of reduction in panicle length was the reduction in seedling survival rates and stunted growth caused by salinity.

Spikelet fertility percentage: Spikelet fertility is important component of grain yield. Generally, all the genotypes showed decrease in spikelet fertility with increasing of salinity concentration. It was severe in IR 59418 (52-100%), IR 72593 (58-100%), IR 73055 (62-100%) and NERICA 4 (51-100). The IR 70023, IR 71991, IR 71901 and IR 71810 were relatively tolerant (8-30% reduction) for change in spikelet fertility with the increase in concentration of salinity (Fig. 2b). The percentage fertility of spikelet was negatively affected by the increase in salinity concentration. The same was true in all most all the genotypes in this experiment where the increase in salinity level severely affected the spikelet fertility percentage. This result is in line with the results of Dawit[13] where the reduction in spikelet fertility was reported at higher salinity concentrations.

Thousand kernel weight: The IR 73055, IR 72593, IR 59418 and NERICA 4 had the lowest thousand kernel weight ranging from 7.17-10.10 g (Table 1). These genotypes could not resist the salinity concentration and did not produce any grain at 12 dS m^{-1} but IR 71901, IR 70023, IR 71810, AT 401 and IR 71991 were tolerant with 22-37% reduction over the

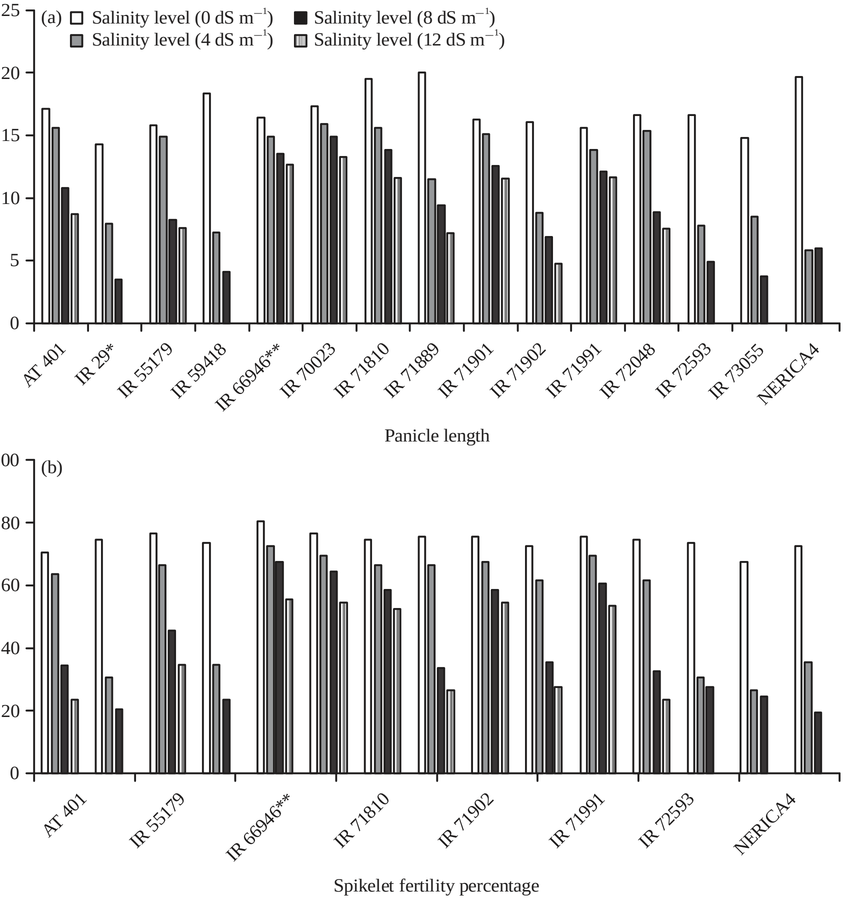

Fig. 2(a-b): (a) Panicle length of the 15 rice genotype in four salinity levels and (b) Spikelet fertility of the 15 rice genotype in four salinity levels, *Susceptible, **Tolerant

control. The highest amount of reduction at 12 dS m^{-1} was registered in IR 59418, IR 72593, IR 73055 and NERICA 4 where their reduction in thousand kernel weight at 8 dS m^{-1} was more than 50%. At 8 and 12 dS m^{-1} the lowest reduction was registered in IR 70023, IR 71810 and IR 71901 with the range of 12-18 and 22-29%, respectively (Table 1). Generally, in every addition of 1 U (dS m^{-1}) salinity between 0-12 dS m^{-1} decreased the grain weight by 0.74 g. The influence of salinity on thousand grain weight was high in this experiment and it is in line with the result of Puteh and Mondal[21] and Aref[24] where grain weight decreased significantly with increasing salinity concentration.

Grain yield: Grain yield is the final sum of all components at different stage thus, the salinity effect on each traits may directly or indirectly affect the final grain yield. The increment of salinity form the control to 12 dS m^{-1} significantly reduced the grain yield of all the genotypes. In all the salinity levels IR 59418, IR 72593, IR 73055 and NERICA 4 showed the susceptibility of salinity reducing form 59-100% yield loss between the control and the highest salinity levels (Table 1). But at 12 dS m^{-1} IR 70023, IR 71810, IR 71901 and IR 71991 can be recommended as tolerant genotype which only showed 37-46% yield loss compared to the control. The IR 55179, IR 71889, IR 71902 and IR 72048 were moderately tolerant which showed relatively good performance at lower salinity levels (4 and 8 dS m^{-1}) by losing 12-26% at 4 dS m^{-1} and 41-47% for IR 55179 and IR 71889 at 8 dS m^{-1} (Table 1).

The analysis of variance also showed that there was very highly significant ($p<0.001$) difference between the four salinity levels of the rice genotypes on their grain yield. The highest mean grain yield (10.31 g) was registered at the control salinity treatment (0 dS m^{-1}) and the lowest mean grain yield (2.94 g) was registered at 12 dS m^{-1}. The increase in salt concentration at each salinity level caused a significant reduction of grain yield, the increment from 0 dS m^{-1} (control) to 4, 8 and 12 dS m^{-1} caused a loss of 31, 56 and 71% in grain yield, respectively.

In this experiment salinity caused a decrease in grain yield especially when the concentration becomes higher. This

Table 1: Thousand kernel weight and grain yield of rice genotypes on different salinity levels

	Salinity level (dS m^{-1})									
	Thousand Kernel Weight (TKW)					Grain Yield (GY)				
Genotype	0	4	8	12	Mean	0	4	8	12	Mean
AT 401	23.67	21.35	18.33	16.00	19.84	11.27	8.30	3.33	2.80	6.43
IR 29*	21.80	14.13	11.93	0.00	11.97	9.83	4.50	0.73	0.00	3.77
IR 55179	24.00	18.37	11.43	10.23	14.75	13.20	11.60	6.97	4.13	8.98
IR 59418	18.90	11.43	9.67	0.00	10.00	8.53	3.67	1.30	0.00	3.38
IR 66946**	24.32	18.60	17.70	17.00	18.26	8.80	7.23	6.63	5.73	7.10
IR 70023	24.77	22.67	20.20	19.00	21.66	11.60	9.13	7.87	6.23	8.71
IR 71810	23.67	21.67	19.43	16.80	20.39	11.07	9.53	8.13	6.67	8.85
IR 71889	22.67	20.47	11.40	10.30	16.21	8.77	7.60	5.17	2.30	5.96
IR 71901	21.00	19.33	18.40	16.33	18.77	9.77	8.83	7.13	6.03	7.94
IR 71902	21.93	20.73	11.50	9.10	15.82	11.20	9.40	5.00	1.90	6.88
IR 71991	24.97	21.33	19.63	15.67	20.40	9.30	7.80	6.43	5.87	7.35
IR 72048	21.63	20.00	10.47	9.00	15.28	12.00	10.13	3.70	2.53	7.09
IR 72593	22.57	13.13	9.00	0.00	11.18	7.53	3.10	2.00	0.00	3.16
IR 73055	22.33	13.30	7.17	0.00	10.70	11.73	2.40	1.00	0.00	3.78
NERICA4	24.67	13.73	10.10	0.00	12.13	10.13	3.40	1.27	0.00	3.70
Mean	22.22	18.02	13.76	9.30	15.82	10.32	7.11	4.44	2.95	6.20

*Susceptible check, **Tolerant

Table 2: Wricke's ecovalence and Shukla's stability variance for grain yield per pot

Genotype	Gen. mean	W	Shukla (σ^2i)
AT 401	6.42	3.39	1.12
IR 29*	3.76	5.72	2.01
IR 55179	8.97	5.55	1.95
IR 59418	3.37	1.57	0.42
IR 66946**	7.09	11.64	4.29
IR 70023	8.71	3.17	1.03
IR 71810	8.85	5.87	2.07
IR 71889	5.96	3.34	1.09
IR 71901	7.94	7.92	2.86
IR 71902	6.87	5.63	1.97
IR 71991	7.35	8.74	3.17
IR 72048	7.09	9.55	3.48
IR 72593	3.15	1.36	0.34
IR 73055	3.78	21.26	7.99
NERICA4	3.70	7.47	2.68
	TSS$^{\#}$	102.18	

*Susceptible check, ** Tolerant, $^{\#}$Total sum of square due to heterogeneity among variance

agrees with the Hakim *et al.*[10] and Aref[24] that observed all the tested rice varieties were inversely influenced by salinity. The study by Grattan *et al.*[25] showed the reduction of grain yield by 12% for every unit of increase in ECe above 3 dS m^{-1}. Hakim *et al.*[9] explained that the reduction in grain yield was due to the manifestation of the cumulative reduction of the yield components. Although, salinity caused yield loss. There were genotypes which lost less than 40% of their grain yield of their control. These genotypes are tolerant and moderately tolerant to salinity according to the study of Puteh and Mondal[21].

Stability analysis: Wricke's[26] defined ecovalence as the contribution of each genotype to genotype by environment interaction. Genotype with lower Wricke's ecovalence (W_i) had smaller deviation from the environmental mean indicting the stability of the genotype. Higher W_i indicates the a higher contribution of a genotype for the genotype by environment interaction which indicates the instability in the performance of the genotype across the environments.

According to Wricke's[26] IR 73055, IR 66946 (tolerant check), IR 72048 and IR 71991 had the highest contribution to genotype × salinity interaction due to their higher ecovalence value (Table 2). The IR 72593, IR 59418, IR 70023, AT 401, IR 71902 had relatively very small ecovalence which indicate the stability of these genotypes. But IR 72593 and IR 59418 had lower mean yield.

According to Shukla[27] a genotype is called stable if the stability of variance (σ^2i) is equal to the environmental variance (σ^2e) which means that $\sigma^2 i = 0$. A relatively large value will indicate thee grater instability of the genotype.

According to Shukla[27] IR 73055 and IR 66946 (tolerant check) showed the greatest instability (Table 2). The IR 72593, IR 59418, IR 70023 and IR 71889 were relatively stable genotypes. But also IR 72593 and IR 59418 had lower mean yield.

Multivariate analysis: The GGE biplot (Fig. 3) grouped the four salinity environments in two sectors, environments in the same sector considered as a single mega environment so the lower salinity levels 0 and 4 dS m^{-1} grouped under one mega environment and the higher salinity levels 8 and 12 dS m^{-1} grouped in another mega environment but 8 and 12 dS m^{-1} are more closer. The winning genotype at 0 dS m^{-1} (control)

Table 3: Mean values of stress tolerance indices for rice genotypes at 12 dS m^{-1}

Genotype	TOL	MP	GMP	STI	SSI	YSI	YI
AT 401	8.47	7.03	5.62	0.30	1.05	0.25	0.95
IR 29*	9.83	4.92	0.00	0.00	1.40	0.00	0.00
IR 55179	9.07	8.67	7.39	0.51	0.96	0.31	1.40
IR 59418	8.53	4.27	0.00	0.00	1.40	0.00	0.00
IR 66946**	3.07	7.27	7.10	0.47	0.49	0.65	1.95
IR 70023	5.37	8.92	8.50	0.68	0.65	0.54	2.12
IR 71810	4.40	8.87	8.59	0.69	0.56	0.60	2.26
IR 71889	6.47	5.53	4.49	0.19	1.03	0.26	0.78
IR 71901	3.73	7.90	7.68	0.55	0.54	0.62	2.05
IR 71902	9.30	6.55	4.61	0.20	1.16	0.17	0.64
IR 71991	3.43	7.58	7.39	0.51	0.52	0.63	1.99
IR 72048	9.47	7.27	5.51	0.29	1.10	0.21	0.86
IR 72593	7.53	3.77	0.00	0.00	1.40	0.00	0.00
IR 73055	11.73	5.87	0.00	0.00	1.40	0.00	0.00
NERICA4	10.13	5.07	0.00	0.00	1.40	0.00	0.00

TOL: Tolerance index, MP: Mean productivity index, GMP: Geometric mean, productivity index, STI: Stress tolerance index, SSI: Stress susceptibility index, YSI: Yield susceptibility index, YI: Yield index, *Susceptible check, **Tolerant

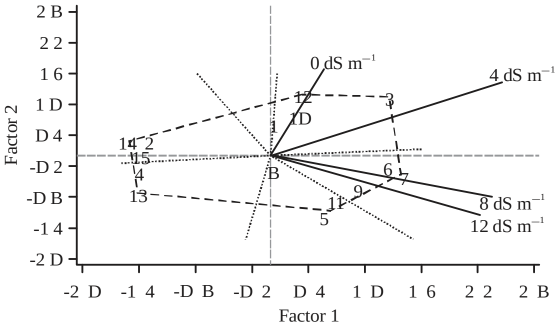

Fig. 3: GGE (Genotype main effect plus genotype by environment interaction) biplot analysis of grain yield, 1: AT 401, 2: IR 29, 3: IR 55179, 4: IR 59418, 5: IR 66946, 6: 70023, 7: IR 71810, 8: IR 71889, 9: IR 71901, 10: IR 71902, 11: IR 71991, 12: IR 72048, 13: IR 72593, 14: IR 73055 and 15 NERICA 4

was IR 72048 whereas at 4 dS m^{-1} it was IR 55179. At 8 and 12 dS m^{-1} the wining genotypes were IR 71810, IR 71901 and IR 70023. The IR 71889 was found to be unresponsive genotype. The low yielding genotypes in all salinity levels were IR 73055, IR 72593, NERICA 4, IR 29 and 4 (Fig. 3).

Generally, the at lower salinity level IR 72048, IR 55179, IR 71901, AT 401 performed good and at the higher salinity level IR 71810, IR 70023, IR 71901, IR 71991 and IR 66946 (tolerant) performed good. Therefore, these genotypes could be considered tolerant at each mega environments.

Stress tolerance indices: Genotypes having higher STI show higher grain yield stability across different environments[15]. Therefore, IR 70023 and IR 71810 with STI of 0.68 and 0.69, respectively were the most stable genotypes across the salinity levels. However, IR 59418, IR 72593, IR 73055 and NERICA 4 with STI value of 0 were the most sensitive ones (Table 3).

According to Khan and Kabir[28] lower SSI value (SSI<1) for a given genotype indicates the higher stability of the genotype in stress and non-stress environments. The IR 71991, IR 71901, IR 71810 and IR 70023 showed lower SSI value of 0.52, 0.54, 0.56 and 0.65, respectively (Table 3). Therefore, these genotypes were the most stable genotypes among tested genotypes in stress environments. Beside this, Nouri *et al.*[29] reported that genotypes that show lower TOL values and high MP values are more tolerant to stress. So based on the lowest TOL and the highest MP values, IR 71991, IR 71901, IR 71810 and IR 70023 were found to be tolerant.

The GMP used to determine the degree of susceptibility under both stress and non-stressed conditions; genotype with higher GMP considered tolerant and high yielding[16]. The GMP value of IR 59418, IR 72593, IR 73055 and NERICA 4 were 0 which indicted the susceptibility of these genotype in stress environment (12 dS m^{-1}). The IR 70023 and IR 71810 had higher GMP value that shows tolerance of these genotypes for stress environment. The YSI and YI used to discriminate tolerant genotypes in stress conditions and high value shows the tolerance of the genotype[28]. Therefore, IR 71810, IR 70023, IR 71901 and IR 71991 were found tolerant in stress condition.

All of the indices had strong, significant and positive correlation with grain yield in exception of SSI and TOL which had negative but strong correlation. This indicates all indices are useful in discriminating genotypes that are both tolerant and stable in both stressed and non-stressed condition. The YI, YSI, YSI and SSI had more strong correlation even perfect correlation in YI with grain yield which shows this indices are more powerful. The correlation of MPI, GMP and STI was found strong and significantly positive.

The results of correlation of this study is supported by Dawit[13] who reported that MP, GMP and STI are highly and positively correlated with the grain yield in stress and non-stress environments. Also significant and positive correlation was found among MPI, GMP and STI by Khan and Kabir[28] on the study of heat tolerance in bread wheat. Therefore, these indices are a good indicators in identifying high yielding genotypes in saline and non-saline environments.

CONCLUSION

In conclusion, IR 70023 and IR 71810 were found tolerant. As a recommendation, the 15 rice genotypes should further be evaluated in field experiments to confirm their salinity tolerance in the real environment. Moreover, studying the tolerance mechanism of these genotypes could simplify the selection and the variability creation method. Also, there should be a breeding program that improves the salt tolerant genotypes.

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SIGNIFICANCE STATEMENTS

- Since salinity is becoming a major problem in crop growing areas of Ethiopia, there should a way to solve this problem. Along many measures to control salinity using resistant genotypes is often the best and cheapest solution. So, this experiment able to identify some tolerant genotypes with comparable salinity levels to the ground problem
- Variety shortage especially rice varieties is also one of the problem in the irrigated regions of the country so this experiment can add up on high yielding genotypes for the irrigated areas
- It also create a good chance for other breeders in variety improvement programs by identifying promising lines for variety development
- Since, rice is good source of carbohydrate and essential proteins, it can has a great impact health in related issues especially for the poor community in need

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