

Full Length Research Paper

Genotype and Environment Interaction for yield performance of 12 Advanced Tongil rice genotypes with Doubled Haploid Background under Salts tress conditions in Tanzania

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Rice (*Oryza sativa L.*) is an important global food commodity crop. Its yield was affected by genotype, environment, and the interaction between genotype and environment that demands the development of diverse tolerant rice to increase yields and adaptation. Genotype and Environment interaction for yields of rice Tongil types with doubled haploid (DH) were evaluated in three locations. A randomized complete block design replicated three times was used. The additive main effects and multiplicative interaction (AMMI) analysis on grain yield revealed that genotypes Tong rt5 and Tong rt 10 were stable genotypes compared to check SATO 1. The genotype Tong rt7 performed poorly. Magozi had the highest mean yield while Chanzuru had the lowest mean yield. Genotypes were evaluated on Saline-Sodic that resulted in different performances. Significant differences were observed between genotypes and locations. Differences contributed to the difference in the sum of squares of grain yield. Scatter plot indicated positive correlation between Chanzuru and Magozi. Genotypes with shorter lines indicated stable genotypes. The experiment indicated two Mega-Environment, Chanzuru and Magozi share a single mega-environment. Small circle indicated greater stability performance of genotype. Performance differences in genotypes allowed the selection of superior genotypes for recommendation.

Key words: AMMI analysis, interaction, tongil rice, stable genotype, mega-environment.

INTRODUCTION

Rice (*Oryza sativa L.*) is an important global commodity crop. It is the third most preferred cereal in the world after maize and wheat (Bagati et al., 2016). It is a staple food for more than half of the world's population (Safdar et al.,

2019). The yield of the crop is influenced by the Genotypes, genotypes by environmental interactions (Smith et al., 2018). Jadhav et al. (2019) pointed out that to obtain consistent yield across diverse environments, a

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variety should have adaptability and stability to fit into various growing conditions.

Salinity contributes to one of the most serious ecological and environmental problems in rice production in Tanzania (Kashenge-Killenga et al., 2016). Amendment of the salt problem or development of salt-tolerant cultivars can be a solution to overcome the problem (Parmar et al., 2020). Several research has been done on the development of salt-tolerant rice crops worldwide (Reddy et al., 2017), but few research has been done based on Korean Tongil-type (Japonica - Indica cross) under Tanzania field conditions.

Yield variations in rice crops are attributable to the effect of the environment in which it is grown, the function of genes influencing the trait of genotypes, and the interaction between the two (Tiwari et al., 2019). Changes in the relative ranking of the performance of genotypes across environments and those that maintain their performance across sites or over the years are the results of the stability of genotypes on Genotype x Environment Interaction (GEI) (Oladosu et al., 2017). Multi-environment trials in rice breeding help to identify stable and high-yielding lines across and within environments (Kang, 2020). Various approaches are employed by plant breeders to evaluate and address the challenges posed by genotype by environment interaction (Guo et al., 2020). Efforts are made to suggest methods of mitigating the effects of genotype, genotype x environment interaction (Zaid et al., 2022). Genotypes tested in different locations show significant fluctuations in yield due to variations in soil fertility, the presence of biotic and abiotic stresses, and the interaction between genotypes with these factors (Debsharma et al., 2022; Teresa et al., 2021). Genotype and Environment interaction reduces the genetic progress in plants by minimizing the association between phenotypic and genotypic values (Pour-Aboughadareh et al., 2022). Genotype and Environment interaction must be exploited by selecting a superior genotype for each specific target environment or by selecting widely adapted and stable genotypes across a wide range of environments ((Oladosu et al., 2017). Through determining GEI effects, several methods of estimating phenotypic stability and adaptability are often used (Hashim et al., 2021). However, Sharifi et al. (2017) highlighted that the additive main effects and multiplicative interaction (AMMI) and the genotype main effects plus genotype by environment interaction effects (GGE-Biplot) are the two most frequently used tools for multi-environment trial data analysis.

Hence, the study was conducted to evaluate the performance and stability of newly introduced advanced rice genotypes Tongil type with Doubled Haploids (DH) background in three different locations of Tanzania for wider and/or specific recommendations for cultivation and use in the Country.

MATERIALS AND METHODS

Geographical descriptions of the experimental sites

Research experiments were conducted in three diverse geographical locations prone to salt conditions in Tanzania for one season from late November 2021 to mid-August 2022. The locations involved were Ndungu irrigation scheme in Same District, the Chanzuru irrigation scheme in Kilosa District Morogoro, and Magozi-Pawaga in Iringa District. The descriptions of the locations are summarized in Table 1.

Chemical characteristics of the experimental sites used in the study

Soil collection was conducted through a zigzag pattern (Otieno et al., 2022). The Soil characteristics had hydrogen concentration (p^H) of 8.47, electrical conductivity (EC) 5.28 μ S/cm, and exchangeable sodium percentage (ESP) 27.46 clay, saline-sodic at Ndungu; p^H of 8.31, EC 6.30 μ S/cm, and ESP 50.32 at Chanzuru; and p^H of 8.22, EC 3.63 μ S/cm, and ESP 25.62 at Magozi. Based on soil analysis results the genotypes have been tested on the clay soil, saline-sodic soils at Ndungu; sand-clay soil, saline-sodic soil at Chanzuru; and sand-clay saline-sodic at Magozi.

Experimental materials

Ten promising rice genotypes Tongil type (Tong rt 1-10) with DH background and two standard registered checks SATO1 as salt tolerant and IR 29 salt susceptible (Table 2) were sourced from TARI Dakawa and IRRRI Dakawa (Tanzania).

Experimental design

The trial at each location was laid out in a randomized complete block design with three replications. Seedlings having three weeks were transplanted following the (Pandey et al., 2021) recommendation. Plants were spaced at 20cm between lines and 20cm along transplanting holes. Each block had 5m² with five lines each line had 25 plants which gave 125 plants per plot. The agronomic practices were applied uniformly to all experimental plots. Fertilizer recommendations adopted by sub-Saharan Africa (SSA) recommendations of 100 kg N/ha (Tsujimoto et al., 2019) were used. Fertilizer was applied two weeks after transplanting and later 35 days after the first application. Two centered lines were harvested from each plot representing a sample for each genotype for further post-harvest analysis.

Data collection

Data on salt injury, plant vigor, Number of tillers per plant, plant height, 1000 grain weight, and spikelet fertility were measured from five randomly selected plants of each genotype as per (International Rice Research Institute, 2014).

Grain yield for two rows was determined in grams and yields per plot were measured in grams and converted into kilograms per hectare.

Data analysis

The data for each location were first analyzed independently using

Table 1. Geographical information of the experimental sites used in the study area.

Site	Longitude	Latitude	Elevation (m)	Average Temp (^o c)	Average Rainfall (mm)
Ndungu	38.08033 ^o E	4.37914 ^o S	503	20	66.7
Chanzuru	37.06555 ^o E	6.79729 ^o S	454	21	31.2
Magozi	35.47030 ^o E.	7.46134 ^o S	758	15	91.6

TMA-Tanzania meteorological Agency; Chanzuru had the lowest annual rainfall, while the highest average rainfall was experienced at Magozi Irrigation scheme.

Source: Global positioning system, TMA, 2022.

Table 2. The rice materials used during the experiment in the 2021/2022 season.

Na	Genotype breeding code	Genotype entry code	Type of genotype
1	SR23364-128-1-HV-1-1	Tong rt1	New genotype
2	PBR1000922-2	Tong rt2	New genotype
3	PBR1000653-2	Tong rt3	New genotype
4	SR34592-HB-1-HV-1	Tong rt4	New genotype
5	SR23364-133-184-1-HV-1-1	Tong rt5	New genotype
6	SR34042F3-22-1-1-5-3	Tong rt6	New genotype
7	SR35266-3-2-1	Tong rt7	New genotype
8	SR35266-2-7-3-1	Tong rt8	New genotype
9	SR35266-3-2-4-1	Tong rt9	New genotype
10	SR34054-1-21-4-1-2-3	Tong rt10	New genotype
11	SATO 1	SATO 1	Salt tolerant check
12	IR 29	IR 29	Susceptible check

GenStat statistical package 15th Edition at $p \leq 0.05$. Treatment means were separated by Duncan's multiple tests. Non-significant differences observed were tested using a combined AMMI analysis of variance across the locations. The stability to show the adaptability of genotypes and mega-environment was further confirmed by GGE biplot analysis (Yan et al., 2007).

Model equation

The analysis of variance (ANOVA) was performed using the following model, Thus, phenotypic expression exhibited by each population, l , in a specific environment, j , depends on three genotypic properties namely a mean expression, a linear response to the environment, and residual deviations from regression as illustrated by Eberhart and Russel, (1966) where: $Y_{ij} = \mu_i + \beta_i l_j + \delta_{ij}$ where: μ_i : is the mean of i^{th} variety over all environments. β_i is the regression coefficient that measures the response of the i^{th} variety to varying environments against the environmental index, l_j . δ_{ij} is the deviation from regression of the i^{th} variety in the j^{th} environment.

Stability analysis

The Genetic Environment Interaction sum of the square was done using the Additive Main effect and Multiplicative Interaction AMMI model which takes the following equation: $yge = \mu + \alpha g + \beta e + \sum \lambda n \gamma gn \delta en + \theta ge + \epsilon ger$, where yge = is the grain yield of variety g in the environment (e), μ is the grand mean, αg = the variety mean deviations (the variety means minus the grand mean), βe = are the environment mean deviations (the environment means

minus the grand mean), λn = the eigenvalue of n^{th} principal components analysis (PCA) axis n , γgn = the variety eigenvector value for IPC axis n , δen = is the environment eigenvector value for IPC axis n , ϵge = is the random error

RESULTS

Yield performance of rice for specific locations

Rice genotypes tested in three locations indicated that Tong rt5, Tong rt10, and Tong rt6 were leading in yield performance, with no significant difference observed between the three at the Ndungu irrigation scheme. Genotypes Tong rt9, variety IR 29, and genotype Tong rt7 respectively showed significant differences compared with highest yielding genotypes. No significant difference was observed in yield at the Chanzuru irrigation scheme instead SATO 1, Tong rt5, and Tong rt3 performed well compared to other genotypes. Genotypes Tong rt9, Tong rt6, and Tong rt4 performed poorly indicating poor adaptation at Chanzuru. Magozi irrigation scheme favored the performance of SATO 1 which showed significant differences with other genotypes. No significant difference in yield was observed from other genotypes at Magozi, while poor performance was observed from

Table 3. Yield performance and 1000gwt of genotypes for specific locations and combined performance for three locations 2022/23.

Genotype	Specific location			Combined	Specific location			Combined
	Ndungu (Yield Kg/ha)	Chanzuru (Yield Kg/ha)	Magozi (Yield Kg/ha)	Yield (Kg/Ha)	Ndungu 1000gwt (g)	Chanzuru 1000gwt (g)	Magozi 1000gwt (g)	1000gwt (g)
Tong rt1	3646bcd	1476ab	5478abc	3533bcd	20.00abc	18.67abcd	26.00e	21.56cde
Tong rt2	2247ab	1425ab	3066ab	2121ab	17.67a	16.33abc	21.00b	16.44ab
Tong rt3	3769bcd	1635ab	5728bc	3710cd	20.67abc	17.67abcd	21.67bc	20.00bcd
Tong rt4	2837abc	486ab	4390ab	2571abc	21.67abc	21.00bcd	27.00ef	23.22de
Tong rt5	5316d	2458ab	5538abc	4437d	22.33bc	21.00bcd	24.67d	22.67de
Tong rt6	3778bcd	1627ab	3601ab	2469abc	18.67ab	15.00ab	19.67a	17.78bc
Tong rt7	1696a	1310ab	2746a	1724a	19.00abc	17.62abcd	27.00ef	19.22bcd
Tong rt8	2758abc	2651ab	4388ab	2661abc	23.33c	23.89d	28.67g	19.89bcd
Tong rt9	1171a	1002ab	4958abc	2481abc	17.33a	13.05a	22.67c	13.33a
Tong rt10	4090cd	1458ab	4710abc	3419bcd	22.33bc	21.00bcd	27.67fg	23.67de
SATO 1	2463abc	3082b	7314c	4286d	22.33bc	22.00cd	31.33h	25.22e
IR 29	1588a	1726ab	2906a	1915a	20.00abc	19.83bcd	28.00fg	21.44cde
Grand Mean	2946	1695	4569	3070	20.44	18.92	25.44	20.37
%CV	31.2	34.6	31.4	46.7	11.1	17.4	3.1	10.5

Mean with similar letters indicates no significant difference while means with different letters indicate significant differences in performance. Gwt= Grain weight in grams, CV=Coefficient of variation, g=grams.

genotype Tong rt7, variety IR 29, and genotype Tong rt2 at Magozi. For combined analysis, significant differences in yields occur between genotype Tong rt 5, SATO 1 compared to genotype Tong rt 7 and IR 29 (Table 3)

Agro-morphological traits mean performance of rice varieties tested in three environments

Morphological performance across three environments indicated no significant difference in salt injury, plant vigor, and spikelet fertility for all genotypes. Tong rt 2 had significant differences in the number of tillers compared to other genotypes, for plant heights genotype Tong rt 2 and Tong rt 9 had significant differences compared

to other genotypes, while the plant vigor indicated non-significant differences between genotypes. Genotype Tong rt 9 significantly differs from genotype Tong rt 3, 6, 10, and SATO 1 in 1000 grain weights. Yield differences were observed between genotype tong rt 7 compared to genotype tong rt 3, rt 5, and SATO 1 (Table 4).

ANOVA for yield performance of twelve tested rice materials

The study indicated significant differences among genotypes and locations at the 95% level $P < 0.005$ with no significant difference (0.189) between interaction effects of Genotype with Location at

$P > 0.005$ (Table 5).

Percentages contribution to the total sum of squares of grains yield variation for the tested rice genotypes

Genotype, stress environment, and interaction effect can influence the ability of crops to reach their yield potential even if all inputs are non-limiting. Table 6 determines the percentage contribution of each factor that contributed to the deviation in the yield potential of rice crops. The study shows that the environment had a higher contribution to the differences in the total sum of squares (36.06%) compared to genotypes which

Table 4. Genotype and environment mean performance of rice at Ndungu, Chanzuru, and Magozi for the season of 2021/2022 using RCBD.

Na	Genotype entry code	SI	NT	PV	PH (cm)	SF	1000Gwt (g)	Yield (Kg/Ha)
1	Tong rt1	4.556ab	19.11ab	5.000a	68.89b	1.889a	21.56cde ⁵	3533bcd ⁴
2	Tong rt2	5.444ab	27.44c	5.111a	53.56a	3.222ab	16.44ab ¹⁰	2246abc ¹⁰
3	Tong rt3	3.889a	18.78ab	4.556a	68.33b	1.889a	20.00bcd ⁶	3710cd ³
4	Tong rt4	4.556ab	19.33ab	5.000a	70.33b	2.778ab	23.22de ³	2571abc ⁸
5	Tong rt5	4.111a	20.33ab	4.778a	67.11b	1.667a	22.67de ⁴	4437d ¹
6	Tong rt6	5.889ab	18.67ab	6.556a	68.67b	2.778ab	17.78bc ⁹	3002abcd ⁷
7	Tong rt7	5.889ab	15.78a	4.667a	61.33ab	2.444ab	19.22bcd ⁸	1917a ¹²
8	Tong rt8	5.889ab	22.00abc	6.333a	61.67ab	2.889ab	19.89bcd ⁷	3266abcd ⁶
9	Tong rt9	6.333b	17.67ab	5.444a	50.33a	4.000b	13.33a ¹²	2377abc ⁹
10	Tong rt10	3.889a	19.44ab	5.000a	67.11b	1.889a	23.67de ²	3419abcd ⁵
11	SATO 1	4.111a	24.00bc	4.556a	69.89b	2.111ab	25.22e ¹	4286d ²
12	IR 29	5.000ab	21.33abc	5.889a	61.00ab	3.444ab	21.44cde ⁶	2073ab ¹¹
	Mean	4.963	20.32	5.241	64.02	2.583	20.37	2907
	%CV	37.7	33.1	36.1	19.2	22.0	21.8	46.7

SI=Salt injury, NT=Number of tillers, PV=Plant vigor, PH=Plant Height centimeter (cm), SP=Spikelet fertility, Gwt=Grain weight in grams (g), CV= Coefficient of variation.

Table 5. ANOVA for yield performance of twelve tested rice materials.

No	Source of variation	Df	Sum of squares	Mean squares	F. ratio	Probability at 5%
1	Rep	2	10732548	5366274	2.61	
2	Genotype	11	70812467	6437497	3.13	<0.002
3	Location	2	149495855	74747927	36.39	<0.001
4	Genotype. Location	20	55084369	2754218	1.34	0.189
5	Residual	61	125308771	2054242		
	Total	96	380336662			

contributed (16.78) and (15.32%) contributed by the interaction effect respectively (Table 6).

Yield performance selections per environment of twelve rice materials tested in three sites.

Statistically additive main effect and multiplicative

interaction for tested rice materials showed the highest mean yield from Magozi and Ndungu with a low yield in Chanzuru. Tong rt5 and Tong rt3 were selected in three sites, and SATO 1 and Tong rt 1 were selected in two sites only while Tong rt 10 and Tong rt 6 were selected once from one location only (Table 7).

Genotype and Environment Score in GGE scatter plot

Scatter plot indicate positive correlation between performance in Chanzuru and Magozi, low correlation between performance between Chanzuru, Magozi and Ndungu (Figure 1).

Table 6. The analysis of the variance of grain yield of various genotypes using Additive Main effects and Multiplicative Interaction (AMMI).

Source variation	DF	SS	MS	F	F. prob	% SS contribution
Treatments	35	293361389	8381754	4.87	0.00000***	68.16
Genotypes	11	72207015	6564274	3.81	0.00037***	16.78
Environments	2	155207599	77603799	13.15	0.00002***	36.06
Block	6	35400641	5900107	3.43	0.00573***	8.23
Interactions	21	65946775	3140323	1.82	0.03691***	15.32
IPCA 1	12	38425174	3202098	1.86	0.059***	8.93
IPCA 2	10	27521602	2752160	1.6	0.12977ns	6.39
Residuals	59	101630502	1722551	*	*	
Total	107	430392532	4022360	*	*	

The block source of variation refers to blocks within environments. DF=Degree of freedom, SS= sum of square, MS=mean sum of square, IPCA=Interaction principal component analysis, ns=non-significant, and *** = Significant at $p \leq 0.01$.

Table 7. Yield performance selections per environment of twelve rice materials tested in three sites of the study during 2022/23.

Description		Four statistical ranking selections					
No.	Environment	Mean	Score	1	2	3	4
1	Chanzuru	1207	-9.23	SATO 1	Tong rt5	Tong rt3	Tong rt1
2	Magozi	4569	-35.79	SATO 1	Tong rt3	Tong rt5	Tong rt1
3	Ndungu	2947	45.02	Tong rt5	Tong rt10	Tong rt6	Tong rt3

Performance of genotypes and Environment indicate only two Mega-Environment, Chanzuru and Magozi share a single mega-environment while Ndungu are located in second Mega-Environment (Figure 2).

Ranking GGE biplot analysis for yield performance of rice in the tested environments

Genotype and genotype \times environment (GGE) biplot (Figure 3) displayed the first and third quadrants having genotypes with low yields below the average, and quadrants two and four displayed genotypes with high yields above the mean average. Genotypes with shorter lines aligned closer to the Centre of origin indicated stable genotypes.

Comparison genotype biplot

Compare performance of ideal environment or performance of ideal genotypes; small circle indicates greater stability performance hence Tongil rt 5 is more stable genotype than SATO 1 with large circle (Figure 4).

DISCUSSION

Genotypes and location showed a significant effect on grain yield. The location was observed to have the highest influence on yield differences of genotypes (p -value= $<.001$) followed by genotypes (p -value= $<.002$); the results aligned with (Balakrishnan et al., 2016), while these results go against (Akter et al., 2016) who found that genotypes had higher contribution than the environment. However, the interaction of the genotypes and the environment was not observed to have a statistical significance difference (p value=0.189). Non-significant on interaction is comparable results with the results obtained by Shrestha et al. (2020) in hybrid rice tested in different locations. Sheoran et al. (2021) on the other hand, observed reductions in yield-related traits in rice and wheat were associated with an increase in soil sodicity. This observation is similar to the differences observed among the yields of genotypes due to differences in levels of soil p^H , electrical conductivity, and exchangeable sodium percentage difference between the tested environments contributed to yield differences in this study. Differences in attitude, rainfall distribution, and temperature between the tested environments also

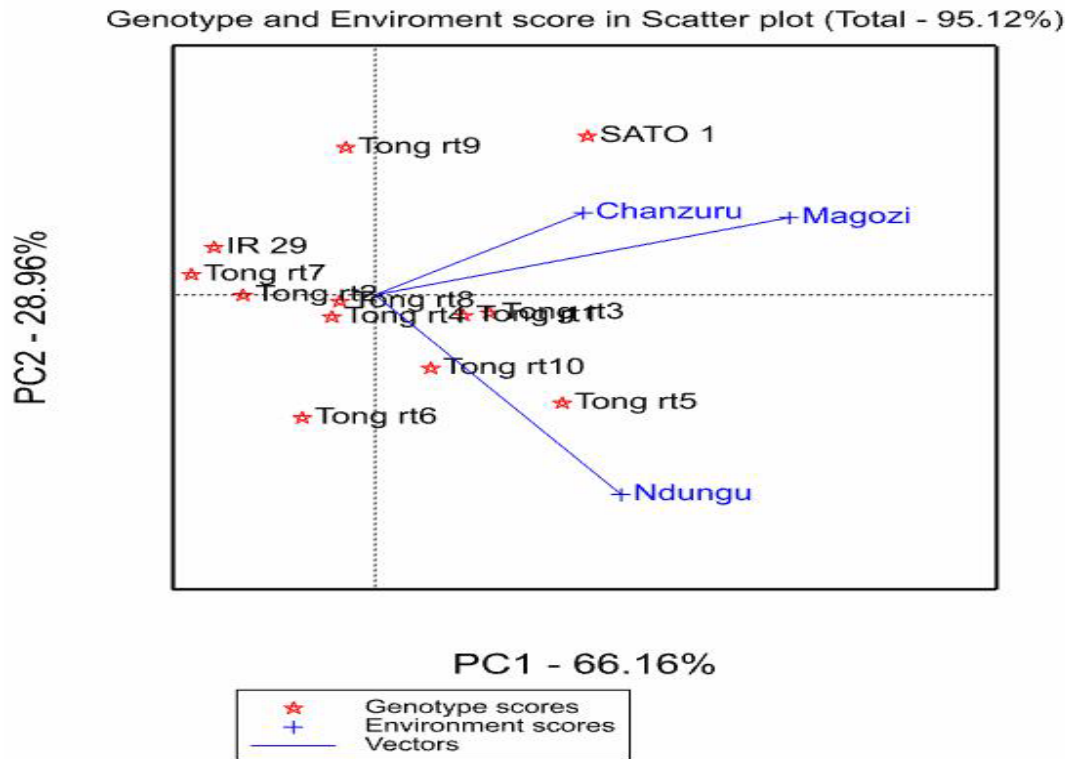


Figure 1. GGE Scatter plot in mega-environment.

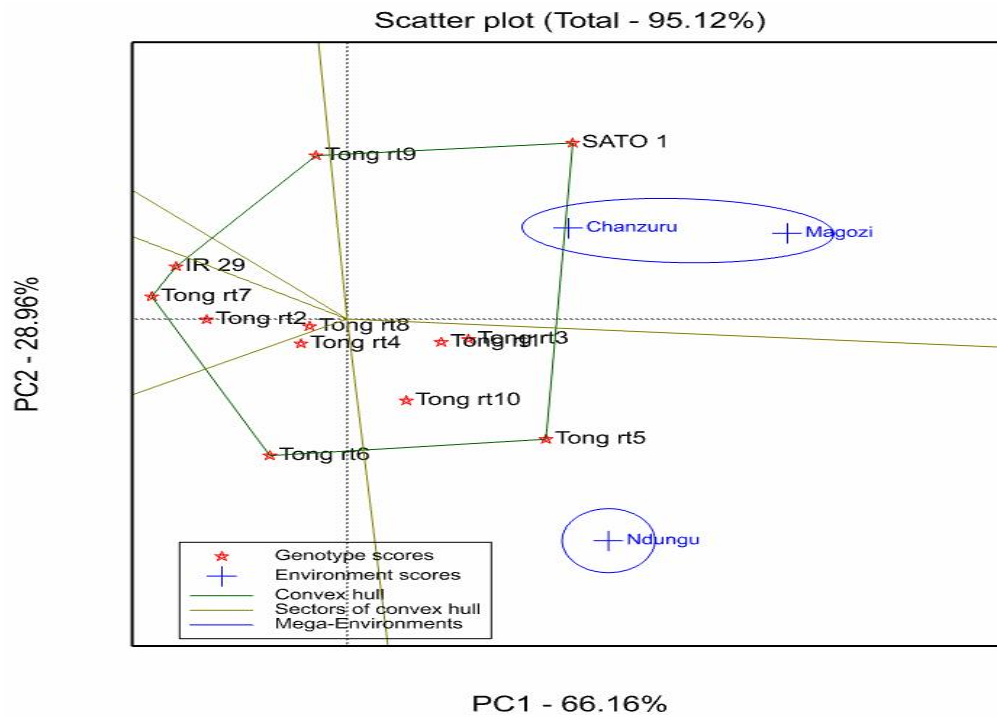


Figure 2. Genotype Score in Mega-Environment scatter GGE biplot
PC=Principal Component.

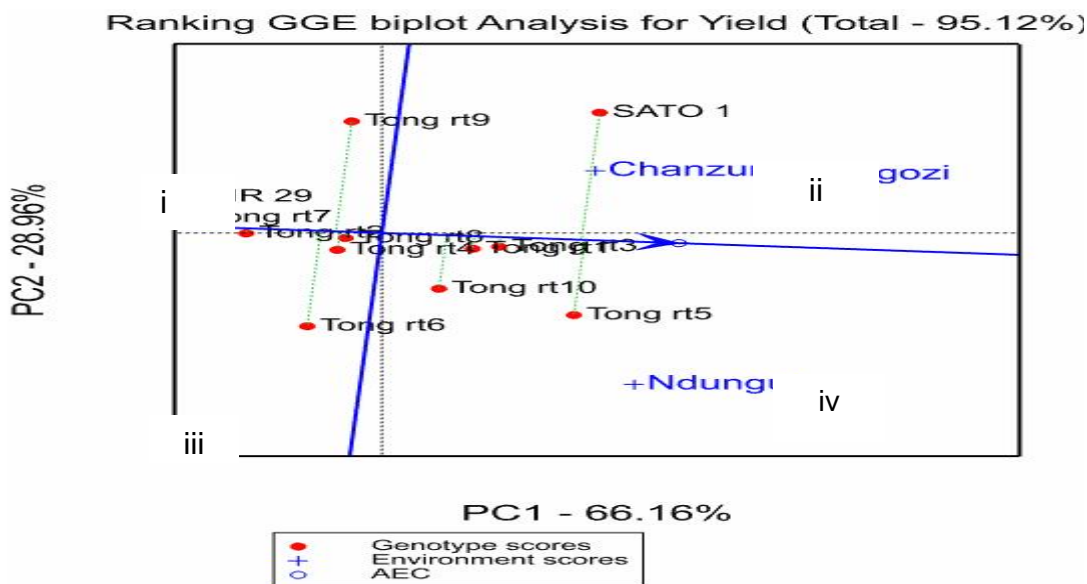


Figure 3. PC=Principal component.

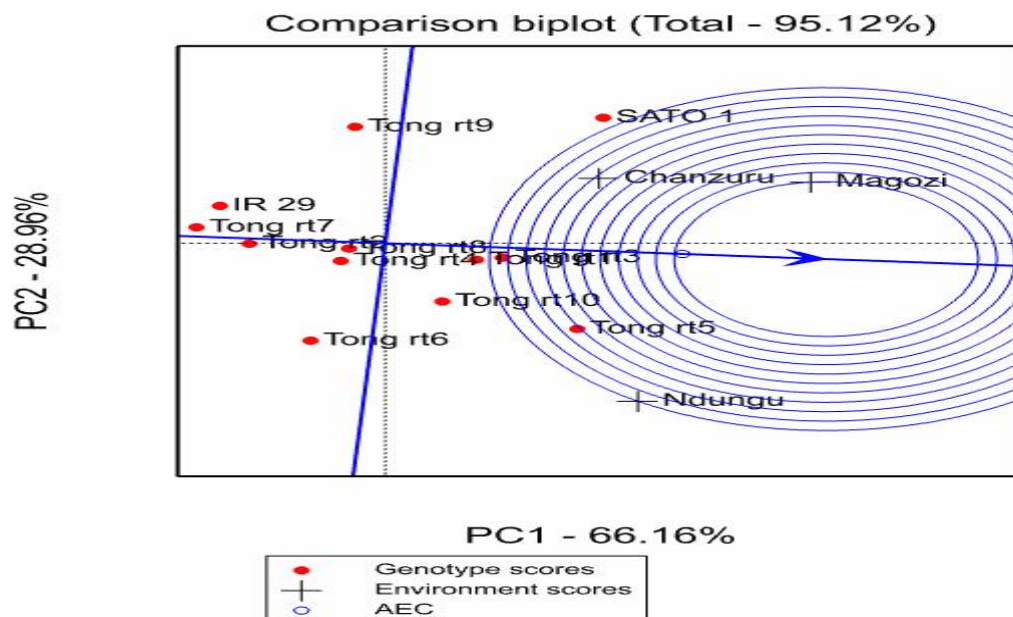


Figure 4. Comparison GGE Biplot.

accounted for genotypes' performance differences in yields across the environments that correspond with similar observations (Kanfany et al., 2021). Several methods have been developed to test genotypes with greater stability for different ranges of environments, which also help to estimate their performance under similar situations. Yield variation of genotypes which were observed invited stability analysis to discriminate

stable genotypes and unstable genotypes across environments. Furthermore; the additive main effects and multiplicative interaction (AMMI) model and GGE biplot were selected to rank the level of stability between genotypes (Yan et al., 2007).

The biological concept of the stable genotype is the one, whose phenotype shows little deviation from the expected character level when the performance of the

genotype is tested over several environments. An ideal genotype should have high mean yield performance and stability across environments. The Additive Main effects and Multiplicative Interaction (AMMI) is one of the best analyses for testing genotype stability. Using the model in this study; The AMMI analysis of variance applied on rice genotypes for grain yield in three environments revealed that environmental variation (36.06%), genotype difference effect (16.78%), and interaction between genotype and environment (15.32%) considerably contributed to the performance difference (Table 6). Each factor both environment, genotype, and interaction contributed to the difference in the sum of squares of the tested rice from which (28) presented similar results when different genotypes were tested across different environments.

The study showed that environment had a higher contribution to yield difference of genotypes, followed by genotypes contribution of which similar results were presented by Hashim et al. (2021). This means that the environment in which the experiment was undertaken, and the experimental materials involved were significantly different. The variation observed among genotypes for grain yield is largely contributed by environmental, and genotype inherent differences.

AMMI yield performance selections per environment (Table 7) indicate that two genotypes Tong rt5 and Tong rt3 were statistically selected in all environments. This implies that the genotypes were favored in all three environments while variety SATO 1 and genotype Tong rt1 where statistically selected in two environments only indicated their suitability in the selected areas. The first selected genotypes (Tong rt5 and Tong rt3) for this study can be recommended in all tested environments and genotypes selected in two locations can be recommended on the selected two sites only. This result is in agreement with (Huang et al., 2021) who pointed out the similar results of genotypes that genotypes breeding can be for specific predictable variation (locations) or unpredictable variation (changes within seasons).

A genotype is considered ideal if it has a high mean yield and is less variable across locations and seasons. Therefore, genotypes located closer to the virtual "ideal genotype" are more desirable. In the present study, different genotypes were found ideal in different locations, as shown in Figure 1 where the GGE biplot model was employed. Yue et al. (2022) reported that the ability of the GGE Biplot model to separate low-yielding genotypes below the average includes means allocated in quadrants one and three while those yielding above the average are means located in quadrants ii and iv of this study. When GEI is subjected to the effects of predictable components, breeding can either choose genotypes for a specific environment or extensively adjusted genotypes across several environments. For

the present study genotypes closer to a specific location in the GGE biplot; SATO 1 closer to Magozi and Chanzuru indicate better performance in those locations, shorter lines existing from genotype Tong rt10 and Tong rt5 from the biplot origin indicate stability genotypes and can be considered for wide adaptability while long lines from SATO 1 indicate unstable variety that can be recommended for specific locations under the study.

The partitioning of genotype main effect and genotype by environment (GGE) through GGE biplot analysis showed that PC1 and PC2 accounted for 67.87 and 27.89% of the GGE sum of squares respectively explaining a total of 95.76% variation, The large PC1 score represents high-yielding ability while the small PC2 score represents stability.

With no GEI, genotypes could perform equally in all locations. However, the presence of GEI discovered by the GGE biplot in this study also contributed to variations in the yield stability performance among rice genotypes tested across three testing environments which revealed that SATO 1 interacted positively at Magozi and Chanzuru while Tong rt 10 and Tong rt 5 had average interaction effect that indicates that the genotypes are stable in interacting with the environment.

The origin indicates the average mean performance of genotypes over the environment, the greater distance between the locations indicates the greater the differences between yield performances of the environment while the lower distance shows less difference between yield performances between environments.

Genotypes in the present study exhibited varying responses across different environments. Genotypes Tong rt5 and Tong rt10 displayed yield stability; these two genotypes are positioned near the origin and demonstrated a mean grain yield close to the overall average. Their IPC1 scores are close to zero. This observation is consistent with findings by Chandrashekhara et al. (2020) and Kumar et al. (2016), suggesting that these genotypes are less influenced by environmental interactions. These genotypes are considered the most stable among the tested genotypes for this study and they could be recommended for wide adaptability revealing the stability that contributes to a superior genotype on the environmental factors that facilitated the selection of genotypes.

Considering one season from this study; the genotype Tong rt5 is suggested for release as a variety for commercial purposes although, for consistency and accuracy, it should be repeated to test its stability over several seasons. The coefficient of variation invariably was found to be high in some of the tested parameters this is due to stress environments where some of the genotypes could die during the course of the field evaluation, this was also explained by Krishnamurthy et al. (2017) reported the similar information on how stress

may result into the unexpected high coefficient of variation.

Conclusion

The study through the AMMI model and GGE Biplot demonstrated that the yield difference of evaluated rice materials was highly contributed by genotype (G), and environment (E), and less from interaction effects between rice materials and location. The AMMI model and GGE Biplot combined made it possible to describe high-yielding and stable genotypes across the tested environment. Promising genotype Tong rt5 (4437kg/ha) outperformed the released check salt tolerant variety SATO 1 (4286kg/ha) and hence is a potential genetic resource for improving and stabilizing grain yield in salt-affected soils in Tanzania with similar soil types. The check susceptible IR 29 (2073kg/ha) and genotype Tong rt7 (1917kg/ha) had poor performance for grain yield in tested sites that qualify as a susceptible check on saline-sodic soil for further studies.

RECOMMENDATION

Since the study was conducted in one season it is recommended that the study can be repeated to test the consistency of performance of these genotypes in a different season to confirm if similar results in different seasons will be achieved.

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CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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