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Farmer's Perception on the Yield Performance of the Different Rice Genotypes under Field Conditions in Tanzania

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Abstract

The Participatory variety selection (PVS) for salt-tolerant rice genotypes with Tongil type rice was conducted in Ndungu, Chanzuru and Magozi irrigation schemes located in different agro-ecological zones in Tanzania during the 2021/2022. The study aimed to identify high-yielding and acceptable rice genotypes through farmers' selections. The experiment involved ten rice genotypes with Tongil types and two check varieties tested under saline-sodic soils. A Randomized Complete Block Design (RCBD) was used. Thirty farmers were invited to participate in the selection at the maturity stage before harvesting. Farmers selected three best and three poor-yielding genotypes. Genotypes Tong rt10 and Tong rt1 were selected by farmers as best genotypes in two locations, while Tong rt2, Tong rt3, Tong rt8, and SATO 1 were selected once by farmers in one location as best genotypes. No genotype was selected as best in all locations. Farmers' selections ranked Tong rt9 and Tong rt7 as poor-yielding genotypes. In order to compare farmers' selection and statistical results, yields of rice genotypes for each location were first analyzed independently and then combined analysis for the three locations using GenStat statistical package 15th Edition at $p \leq 0.05$; Treatment means separated by Tukey's 95% confidence intervals. Genotypes responded differently on salt injury; SATO 1, Tong rt 10, Tong rt 3, and Tong rt 5 scored the averages of 4 on a 1 – 9 scale, indicating that plant growth was normal, moderately tolerant to tolerant. In contrast, some genotypes scored an average of 5, indicating reduced growth and tillering, most leaves discolored, and few elongating. Other genotypes scored six (6), showing entire growth ceasing with most plants leaves dying. Based on farmers' preferences, genotypes Tong rt 10 and Tong rt 1 were selected. These genotypes are recommended for future rice variety trials and development.

Keywords: *Farmers selection, saline-sodic soils, rice genotypes*

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Introduction

Rice (*Oryza sativa L.*) is a staple food crop for more than half of the world's population (Safdar *et al.*, 2019; Atnafu Delele *et al.*, 2021). It is the third most preferred cereal in the world after maize and wheat (Bagirov *et al.*, 2020). Rice is among the top three crops with the highest production in the world (Fahad *et al.*, 2019). It is considered the predominant dietary energy source of seventeen countries in Asia and the Pacific, nine in North and South America, and eight in Africa (Rathna Priya *et al.*, 2019). In order to address the goal of widening the genetic base for salt-tolerant rice, it is ideal to pay attention to novel traits that farmers and consumers will prefer (Jiao *et al.*, 2019). Farmers' selection is employed to identify genotypes that incorporate farmers' knowledge to enhance the acceptability and diffusion of genotypes (Najeeb *et al.,* 2018). The approaches also combine conservation and crop improvement objectives of crops. The participatory variety selection (PVS) enables skilled traditional farmers to select the best-performing breeding lines and varieties from a group of pre-evaluated seeds selected by plant breeders (Belayneh and Chondie, 2022, Dyck and Silvestre, 2019). The participatory variety selection method is currently extensively adopted by plant breeders to improve rice crops (Weltzien and Christinck, 2017; Witcombe *et al.,* 2017). The genotypes selected through the joint effort of farmers and plant breeders improve the adoption rate of the new variety (Ceccarelli and Grando, 2019). It was highlighted by Suvi *et al.,* (2021) that farmers prioritize many different traits besides grain yield. Incorporating farmers' selection criteria in the advanced stage of new genotype development is useful in sub-Saharan Africa (Abady *et al.,* 2019). Individual farmers may have different selection concerns that require the availability of several cultivars within each society to meet different requirements, depending on their circumstances (Kholová *et al.,* 2021). The more selection criteria a farmer uses, the more landraces he or she will need to plant to meet all of his or her targeted requirements (Thiele *et al.,* 2021). Farmers' selection criteria are often based on several characteristics such as active participation in technology development, cropping system, and family uses of the crop and future market; however, they might differ depending on the gender and age of farmers, as well as socioeconomic situations (Worku *et al.,* 2020). The number of tillers, salt tolerance, thresh ability, seed size, shape, color, aroma, yield of harvested components, absence of insect damage, and maturity duration are all common crop characteristics employed by farmers in selecting best genotypes for their preference trait. Different cultivars are also chosen and planted as backups in case one fails due to environmental stress. Farmers may take advantage of different markets by selecting cultivars that are in high demand.

Stages of farmers' participation in variety selection depend on the crop, parent materials, target region, researcher capacity to assimilate farmer criteria, traits of interest, and scale of the breeding program/number of materials to be screened; farmer participation can be advantageous at various times. Farmers can play many roles in participatory plant breeding, including technical leadership, important social and organizational leadership, information dissemination, trainer/skill-building, field laborer, input supply, and landrace or farmer material for further breeding programs (Begna, 2022). Participatory variety selection model was employed for this on-farm experiment to evaluate the aforementioned salt-tolerant rice genotypes with tongil type background in three different locations of Tanzania and assess genotypes with preferred characteristics for increased adoption rate.

Materials and Methods

Geographical Description of Experimental Sites

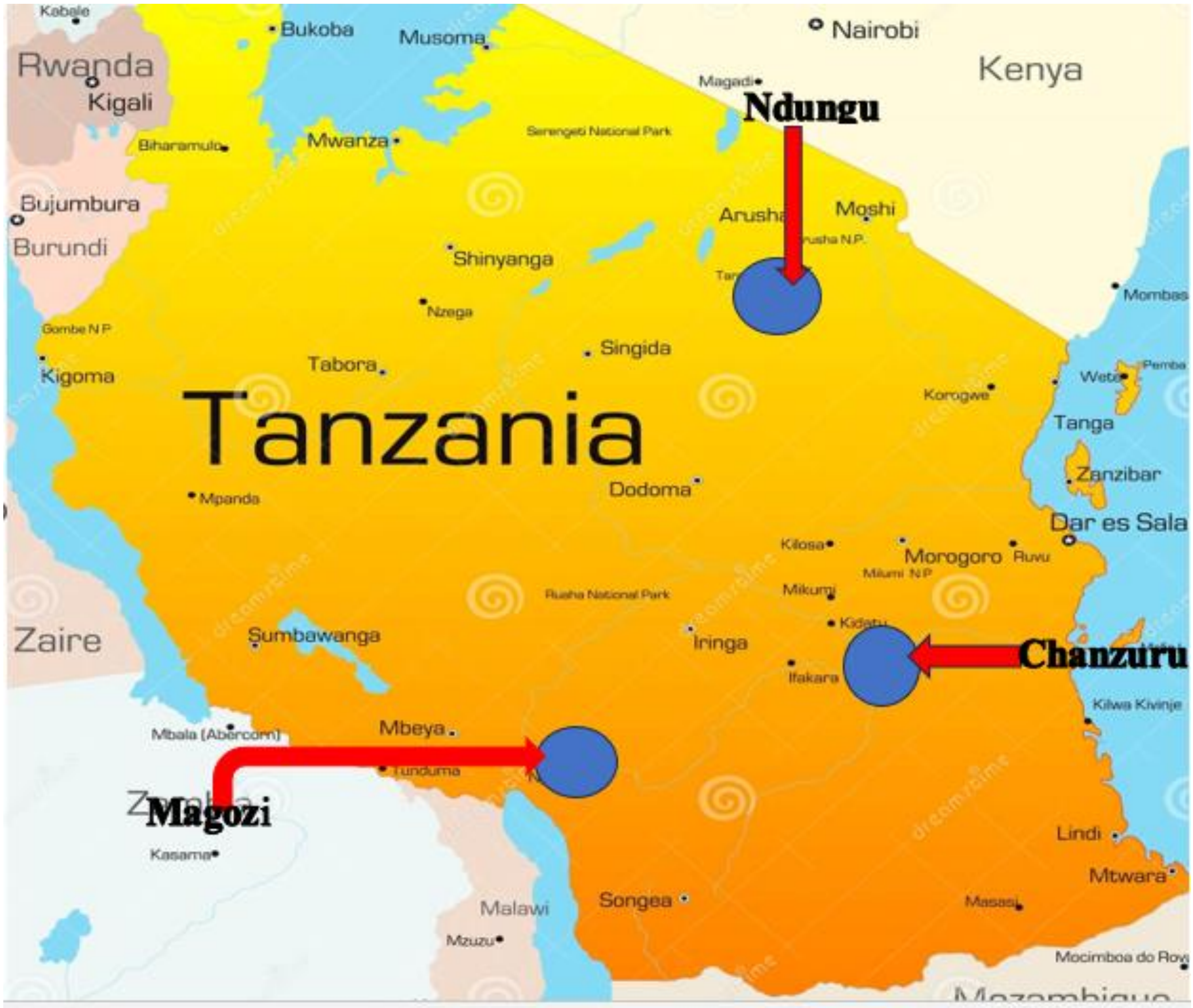
The experiment was conducted in three diverse geographical locations prone to salt conditions in Tanzania. It was done for one season from late November 2021 to mid-August 2022. The locations which participated in the study were the Ndungu irrigation scheme in Same District, the Chanzuru irrigation scheme in Kilosa District and Magozi irrigation scheme in Iringa District. Ndungu Irrigation Scheme is found at latitude -4.379140S and longitude 38.080330E, and situated at 503 m above sea level; Chanzuru irrigation scheme is found at latitudes -6.797290 S and longitude 37.065550 E, situated at 454m above sea level while Magozi Irrigation Scheme is located at latitudes -7.461340 S and longitude 35.470300 E and situated at 758m above sea level 65 km North West of Iringa town at Ilolo mpya Ward, in Iringa Rural District.

Soil sample collection design from experimental sites

Soil sample collection was conducted through a zigzag pattern as outlined by Otieno *et al.,* (2022). Soil samples were taken from 0–30cm depth and send to Sokoine University of Agriculture Laboratory for analysis. The samples were analyzed for soil pH, EC, ESP, and other parameters.

Figure 1

A map showing experimental sites where rice genotypes were tested



Experimental Materials

In this study ten (10) promising salt tolerant rice genotypes with Tongil-type backgrounds sourced from Tanzania Research Institute, Dakawa were used. These genotypes were previously sourced from Korea for performance evaluation in Tanzania. Tongil (IR667-98-1-2) rice was developed in 1972 as high-yielding rice variety derived from a three-way cross between indica and japonica varieties. Tongil rice contributed to self-sufficiency of staple food production in Korea during a period of Korean Green Revolution. Also, the experiment involved two standard checks, SATO 1 as a registered salt Tolerant variety in Tanzania and IR 29 as a registered salt susceptible variety for comparison. Different genotypes were used in this experiment to represent the diversity of materials among the rice populations to explore their potential for adaptability

Table 1

Rice genotypes evaluated in three different locations

No.	Genotype entry code	Type of genotype	Source
1	Tong rt1	New genotype	TARI Dakawa
2	Tong rt2	New genotype	TARI Dakawa
3	Tong rt3	New genotype	TARI Dakawa
4	Tong rt4	New genotype	TARI Dakawa
5	Tong rt5	New genotype	TARI Dakawa
6	Tong rt6	New genotype	TARI Dakawa
7	Tong rt7	New genotype	TARI Dakawa
8	Tong rt8	New genotype	TARI Dakawa
9	Tong rt9	New genotype	TARI Dakawa
10	Tong rt10	New genotype	TARI Dakawa
11	SATO 1	Salt tolerant check	TARI Dakawa
12	IR 29	Susceptible Check	TARI Dakawa

Study design

The experiment from each location was laid in a Randomized Complete Block Design with three replications. Seeds were planted in the nursery and then transplanted to the main field when three weeks old (Pandey *et al.,* 2021). Seedlings were spaced at 20 cm along transplanting holes and 20 cm between lines. Each block had 5m^2 with five lines. Each line had 25 plants. A plot had a total of 125 plants. Similar crop management was done in all three experimental sites. Yield data for analysis were collected as per Sumanth *et al.* (2017).

Thirty (30) farmers were invited for selection in each site making a total of 90 farmers who were involved in the genotype selection in the three sites. Of the respondents 49 were male and 41 were female. The protocol, as stipulated by Witcombe and Virk (2001) was used for preference score. Farmers were asked to move around the field at maturity and, through ballot voting, selected three best genotypes and three poor genotypes in terms of yield performance. After the voting, votes were tallied, and preference scores were computed for performance verification. The harvested yields per plot were converted into kilograms per hectare for easy computation and reporting.

Data Collection

Agronomic data for salt injury was scored using a scale of 1 – 9 (scale 1,3,5,7, 9), number of tillers per plant through normal counting, plant height representing actual measurement (cm) from the soil surface to tip of the tallest panicle of the rice plant, grain yield including area harvested per plot excluding border rows recorded in kilogram per hectare at 14% moisture content were collected as per International Rice Research Institute and International Network for Genetic Evaluation of Rice, (2014).

Data Analysis

The data on agronomic traits especially yield for each location were first analyzed independently using GenStat statistical package 15th Edition at $p \leq 0.05$; the treatment means were separated by Tukey's 95% confidence intervals. Farmers' preferences based on positive and negative scores were computed.

Model equation

Thus, phenotypic expression exhibited by each population, I, 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: $Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$ 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, I_j. δ_{ij} is the deviation from regression of the i^{th} variety in the j^{th} environment

Results

Soil chemical characteristics of the irrigation scheme used for experiment

The soil test results indicate the presence of saline-sodic soils in all tested environments with different Electrical conductivity (EC), Cation Exchange Capacity (CEC), and Exchangeable Sodium Percentage (ESP) that can limit plant growth and nutrient uptake by the plants. The soil characteristics at Ndungu had a pH of 8.47, electrical conductivity (EC) 5.28μS/cm, and exchangeable sodium percentage (ESP) 27.46 which indicate saline-sodic soils; at Chanzuru the soil for the experiment had a pH of 8.31, EC 6.30μS/cm, and ESP 50.32; and pH of 8.22, EC 3.63μS/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, sandy-clay, saline-sodic soils at Chanzuru, and sand-clay saline-sodic soils at Magozi. The genotypes were tested on the saline-sodic soils with a high P^H above eight (Table 2)

Table 2

Soil characteristics of the experimental sites

Site	Texture Class	P^H 1:02:05	EC μS/cm	CEC Cmol+/kg	ESP	Description
Ndungu	Clay	8.47	5.28	47.3	27.46	Saline-Sodic
Chanzuru	Sandy clay	8.31	6.3	31.3	50.32	Saline-Sodic
Magozi	Sand clay loam	8.22	3.63	26.7	25.62	Saline-Sodic

Note. PH = Logarithmic hydrogen ion concentration, EC=Electrical Conductivity, CEC=Cation Exchange Capacity, ESP=Exchangeable Sodium Percentage

The response of genotypes to salt injury across the three sites

Genotypes responded differently on salt injury; SATO 1, Tong rt 10, Tong rt 3, and Tong rt 5 scored the averages of 4, indicating that plant growth is nearly normal; still, tillering is reduced, and some leaves are discolored and rolled. In contrast, some genotypes scored an average of 5, indicating growth and tillering, which are reduced, most leaves discolored, and few elongating. Other genotypes scored six (6), showing growth entirely ceasing, most leaves dry, and some plants dying. An overall ANOVA on Salt injury showed a p-value of (0.036) that genotypes had significant differences in salt injury with no significant difference in location (0.387) and genotype by location (0.645) at p=0.005 (Table 3)

Table 3

Responses of genotypes to salt injury across locations

Genotypes	Chanzuru	Magozi	Ndungu	Mean
IR 29	4	5	6	5
SATO 1	4	3	5	4
Tong rt1	4	5	5	5
Tong rt10	4	5	3	4
Tong rt2	5	6	6	5
Tong rt3	4	4	3	4
Tong rt4	5	4	4	5
Tong rt5	4	5	3	4
Tong rt6	8	6	4	6
Tong rt7	6	5	6	6
Tong rt8	7	6	4	6
Tong rt9	8	5	6	6

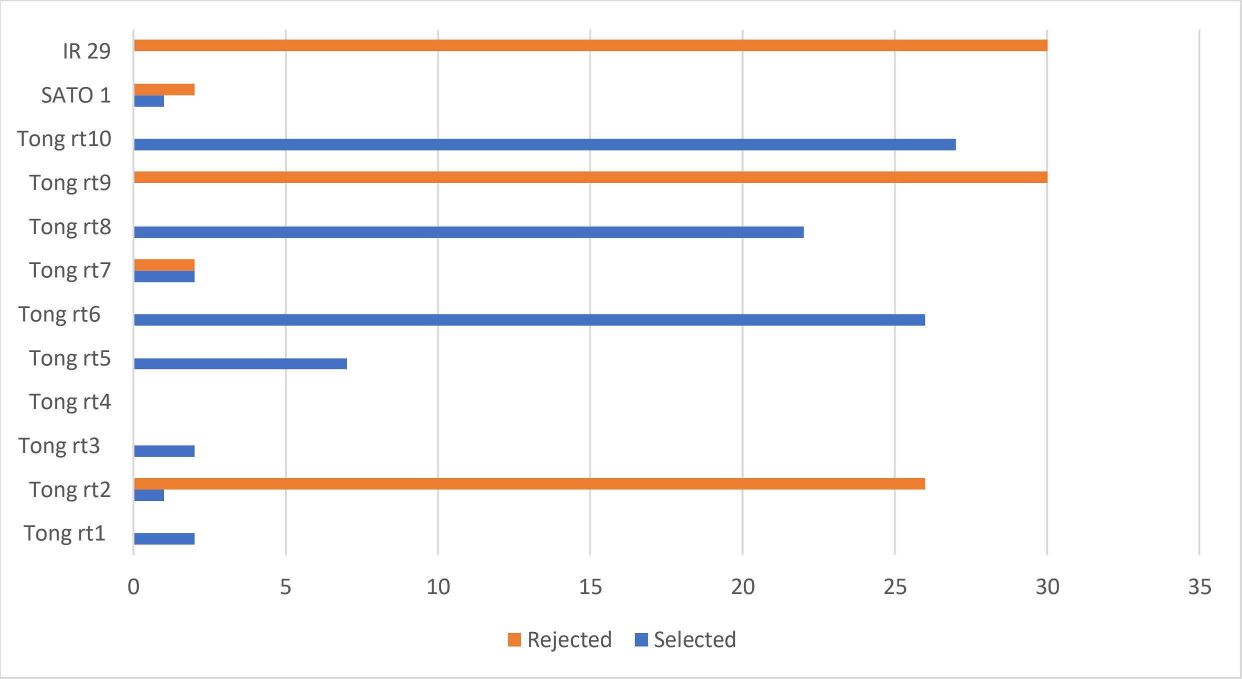
NOTE: 3=Growth nearly normal but there is some reduced in tillering and some leaves discolored and rolled, 5.- Growth and tillering reduced, most leaves discolored and few elongating, 7.- Growth completely ceases, most leaves dry and some plants dying

Farmer's selection and ranking on tested genotypes at the Ndungu irrigation scheme

Farmers at the Ndungu irrigation scheme selected genotypes Tong rt10, Tong rt 6, and Tong rt 8 as the best genotypes, while genotype Tong rt 9, variety IR 29, and genotype Tong rt 2 were rejected by farmers (Fig. 2). Promising new genotypes outweighed registered variety SATO 1 based on farmers' preferences selection at this site

Figure 2

Farmers' selection preferences at Ndungu irrigation scheme

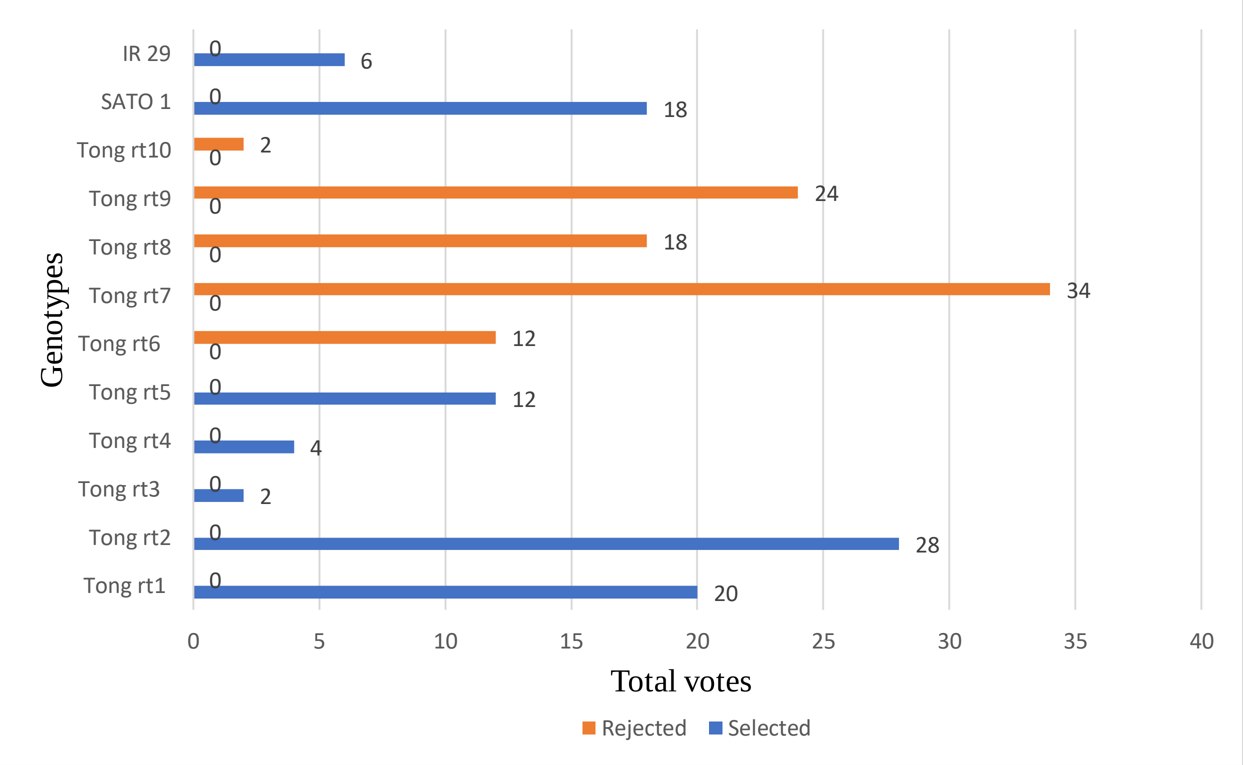


Farmers' selection and ranking genotypes at Chanzuru Irrigation Scheme

Promising genotypes Tong rt2, Tong rt 1, and salt tolerant SATO 1 were selected by farmers at the Chanzuru site, while genotypes Tong rt 7, Tong rt 9, and Tong rt 8 genotypes were rejected (Fig. 3). Two promising genotypes compete with a registered standard check SATO 1 based on the farmer's selection

Figure 3

Farmers' preference selection at Chanzuru irrigation scheme

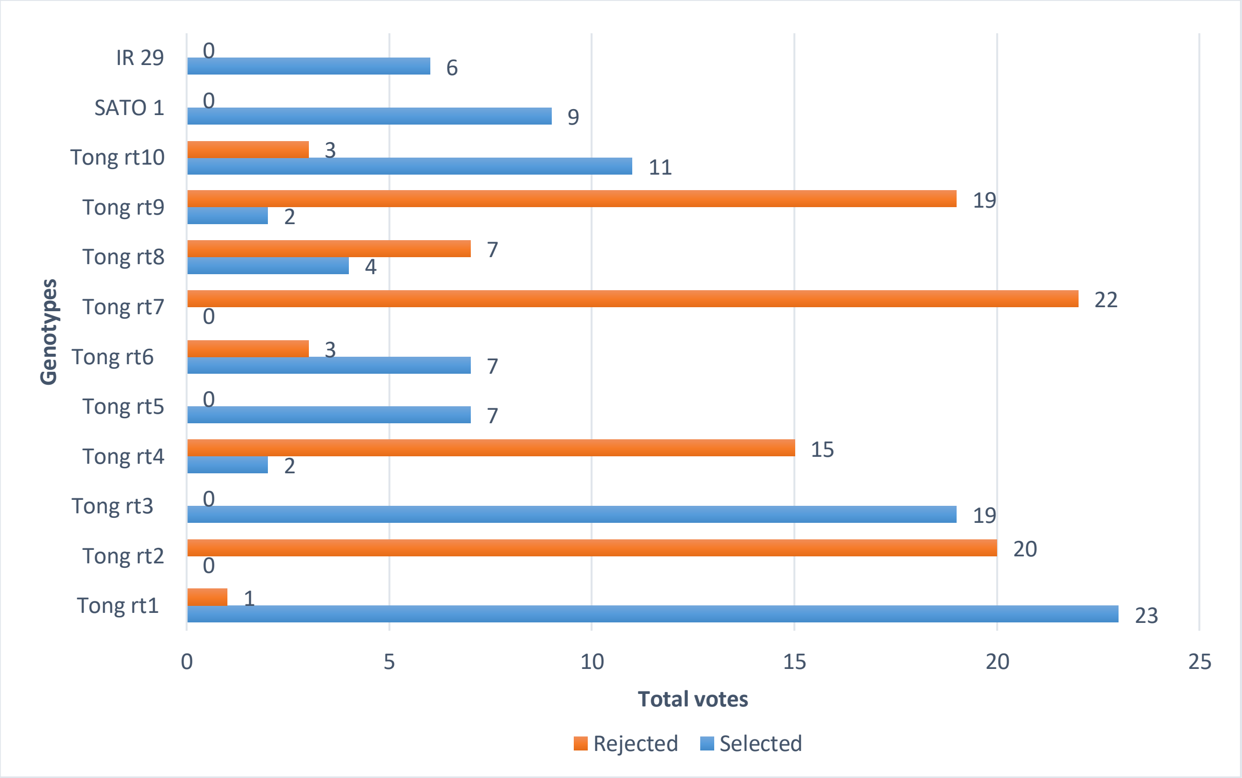


Farmer's selection and ranking on tested genotypes at Magozi Irrigation Scheme

Promising genotypes Tong rt1, Tong rt 3, and Tong rt 10 were selected by farmers at the Magozi site. Genotype Tong rt 7, Tong rt 2, and Tong rt 9 genotypes were rejected by farmers at Magozi. Standard check SATO 1 was not among the first three selected by farmers at the Magozi irrigation scheme (Fig. 4)

Figure 4

Farmer's preference selection at Magozi irrigation scheme

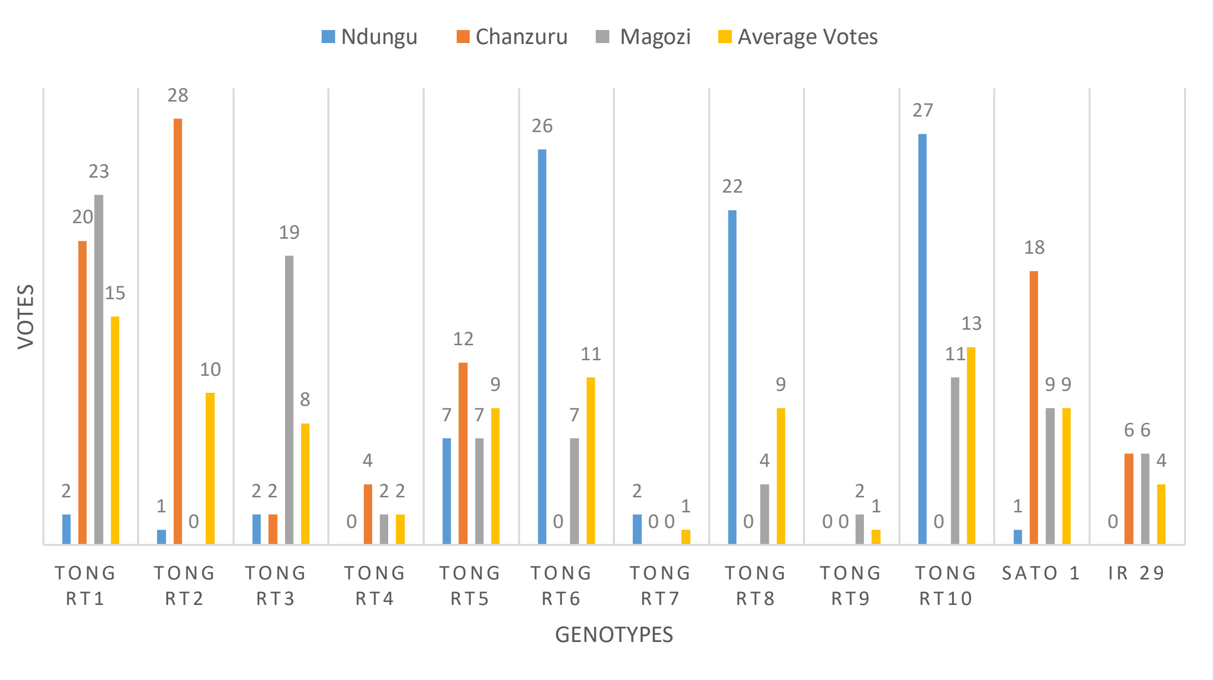


Mean preferences of farmer's selection and ranking for accepted and rejected genotypes across three locations

The average mean preference votes of farmers ranking based on positive scores across the three locations indicates that the leading accepted genotypes were Tong rt 1 with 15 average votes. The other leading accepted genotypes were Tong rt 10 with 13 positive votes and Tong rt 6 with eleven (11) votes. These genotypes outperformed the registered check-tolerant variety SATO 1, which obtained nine (9) votes. The average Mean preference selection votes of farmers ranking based on negative score votes across the three locations indicates that the leading rejected genotypes were Tong rt 9 with 24 average votes. The other leading rejected genotypes by farmers were Tong rt 7 with 19 negative votes and Tong rt 2 (negative 15 votes). These genotypes outperformed the registered check susceptible variety IR 29, which obtained ten negative votes. All these rejected genotypes were not preferred by farmers across the three locations (Fig. 5)

Figure 5

Mean Farmers' preference for selected genotypes

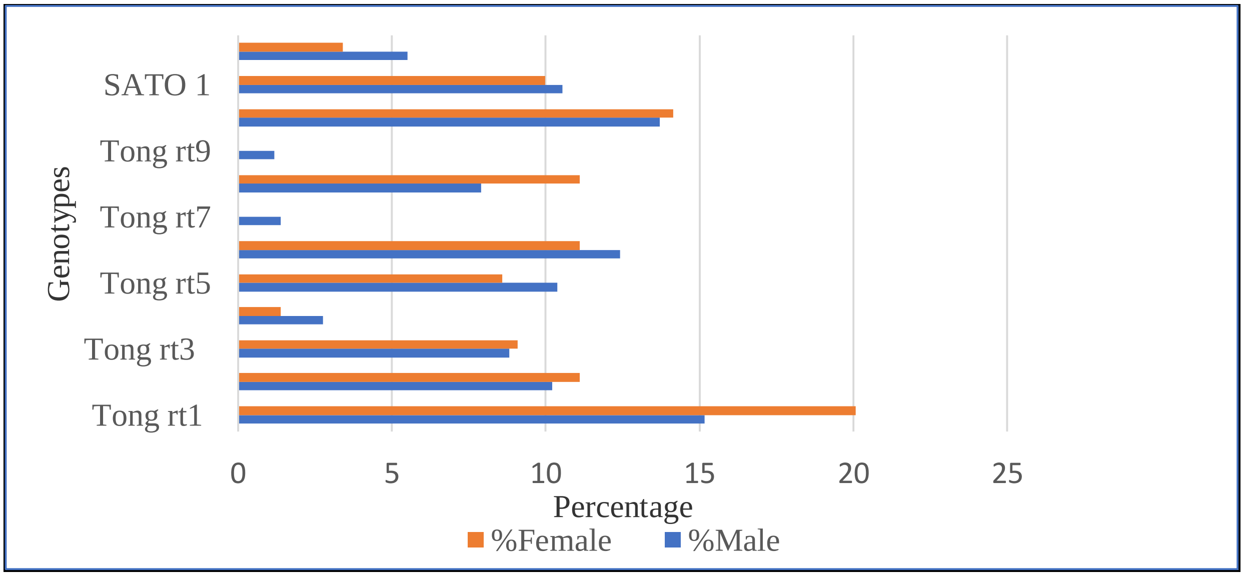


Percentages of farmers by Gender on the selected genotypes across three locations

A large number of female farmers selected genotypes Tongil rt 1 than males. There were equal percentages of male and female farmers who selected Genotype Tongil rt 10. Male farmers selected genotypes Tongil rt 5 and variety SATO 1, which statistically showed high-yielding performance compared to other genotypes (Fig. 6)

Figure 6

Percentage of farmers by gender for selected genotypes across locations



Yield performance of genotypes in kilogram per hectare for specific locations and across three locations

The yield performance results indicate that based on average yield performance across three locations, genotype Tong rt 5 (4437kg/ha) yielded higher than the registered check tolerant variety SATO 1 (4286kg/ha). The other leading genotypes after SATO 1 were Tong rt 3 (3710kg/ha), Tong rt 1 (3533kg/ha), and Tong rt 10 (3419kg/ha). The lowest-yielding genotypes were Tong rt 7 (1917 kg/ha), IR 29 (2073kg/ha), and Tong rt 2 (2246kg/ha)

Table 4

Yield performance of genotypes for specific and across locations

	Grain Yield for specific Location (Kg/Ha)			Average Yield
Genotypes	Ndungu	Chanzuru	Magozi	Kg/Ha
Tong rt1	3646bcd^{5}	1476ab^{5}	5478abc^{4}	3533bcd^{4}
Tong rt2	2247ab^{9}	1429ab^{7}	3066ab^{10}	2246abc^{10}
Tong rt3	3769bcd^{4}	1634ab^{4}	5728bc^{2}	3710cd^{3}
Tong rt4	2837abc^{6}	486ab^{9}	4390ab^{7}	2571abc^{8}
Tong rt5	5316d^{1}	2458ab^{2}	5538abc^{3}	4437d^{1}
Tong rt6	3778bcd^{3}	29a^{12}	3601ab^{9}	3002abcd^{7}
Tong rt7	1696a^{10}	1303ab^{8}	2746a^{12}	1917a^{12}
Tong rt8	2758abc^{7}	836ab^{11}	4388ab^{8}	3266abcd^{6}
Tong rt9	1171a^{12}	856a^{10}	4958abc^{5}	2377abc^{9}
Tong rt10	4090cd^{2}	1458ab^{6}	4710abc^{6}	3419bcd^{5}
SATO 1	2463abc^{8}	3082b^{1}	7314c^{1}	4286d^{2}
IR 29	1588a^{11}	1731ab3	2906a^{11}	2073ab^{11}
GM	2946	1398.16	4569	3070.
LSD	1554.3	2587.0	2430.8	2340.1
CV	31.2	34.6	31.4	46.7

Note. GM=Grand mean, CV=Coefficient of Variation, LSD=Least Significant difference. Mean with similar letters indicate no significant difference while means with different letters indicate significant differences in performances, numbers 1-12 indicate performance ranking of genotypes. 1-indicate genotype with high performance, 12 -indicate the genotype with the lowest performance.

Discussion

Rice crop has significant genetic diversity in salt stress tolerance. Combining superior alleles from various sites, the availability of multiple breeding tolerance sources, and gene exploration can further extend the genetic base and increase the degree of tolerance (Balakrishnan *et al.,* 2016). Crop diversity provides hope to society and the breeding program for crop diversification. The study on the identified ten new promising potential genotypes for salt tolerance makes an essential study in the rice breeding program. The diversity identified following this study shows a promising future in reducing crop failure on the targeted and accepted sites since diverse genotypes indicate the variability to adapt to climatic change that can be experienced in the experimental sites.

Genotypes under this study were not previously cultivated by farmers in the selected salt-affected areas. Field evaluation and farmers' selection of genotypes resulted in the development of information on salt-tolerant genotypes in a new geographical location. The resulting output also suggests varietal improvement with conventional breeding tools and a unique Quantitative Trait Locus (QTL) gene for molecular breeding. Genotypes under the study showed differences in saline-sodic tolerance levels that resulted in yield reduction and changes in farmer's preferences. The highest reduction in dry biomass yield per unit increase in salinity in test environments was also observed by Qureshi and Daba (2020) while evaluating the growth and yield parameters of five Quinoa plants. The differences in genotypes' performance could be grouped as sensitive, moderately sensitive, and tolerant genotypes to saline-sodic soil.

The highest yield performance of genotypes in mult-location was observed from genotypes Tong rt 5, SATO 1, Tong rt 3, and Tong rt 1. Magozi scored a higher yield, followed by Ndungu, while Chanzuru had the lowest average yield performance on the genotypes tested. The yield of rice decreased as the salt level increased, indicating the effect of salt on the growth of rice genotypes. This result is in agreement with models that presented similar trends in capturing the effect of the different gradients of salinity on rice biomass production and yield, as shown by Radanielson *et al.* (2018). The yield of most of the genotypes dropped at the Chanzuru irrigation scheme because the site showed a high concentration of salinity compared to other sites.

A variation in farmers' preference for the promising rice genotypes was revealed in all the locations. Based on farmers' preference selections for specific locations, Tong rt 10, Tong rt 6, and Tong rt 8 were the most preferred genotypes by farmers for the Ndungu site. Tong rt 2, Tong rt 1, and SATO 1 at Chanzuru, while Tong rt 1, Tong rt 3, and Tong rt 10 were the best genotypes selected by farmers at Magozi Irrigation schemes. The study conducted by Semahegn *et al.* (2021) demonstrated similar results that when farmers ranked the most preferred varieties, the ranking order was sometimes variable between locations and years. The study indicated that the top-selected genotypes in one location were not necessarily selected in other locations. The result was similar to the study conducted by Burman *et al.* (2018), who observed that the most preferred entries in their study differed across locations and years. The diversity of farmers' preferences observed in the three locations is an important observation, suggesting that more efforts are needed to increase genetic diversity in the field to meet farmer preferences. The problem of climate change can be alleviated by having a wide range of genotypes; this suggestion was similar to the observation made by Weltzien *et al.* (2019), who stated that the capacity to assess farmer preferences for varietal traits to guide breeding efforts in responding to specific users remains an open question. Suitable genotypes from the trial sites suggest that rice genotypes selected by farmers in particular locations meet farmers' needs and breeder objectives. The rejected genotypes from this study indicate that the genotypes do not meet farmer needs in specific locations, hence loose breeder objectives that are intended to meet the farmer's needs.

Participation of farmers in selection also has shown an important role in increasing the genetic diversity of rice in the field based on farmers' preferences across locations. It was reported by Studnicki *et al.* (2019) that cultivar recommendations based on mean performance conducted on research stations could be unreliable and ineffective for assessing the performance of genotypes if the study does not include farmers' assessment data. The study conducted by Tin *et al.* (2021) in sodic soils through cooperation between Can Tho University and nearby farmers organized in seed clubs confirmed the relevance and usefulness of participatory variety selection to develop and adopt new salt-tolerant lines. Appropriate cultivar recommendation calls for the combination of on-station and on-farm variety evaluation by farmers for quick adoption of new breeding materials. The genotype selected by farmers in the specific location under this study indicates that genotype will be adopted quickly by farmers in the selected site. In contrast, the rejected genotypes will not be rapidly adopted by farmers. Selection performance indicate that Tongil rt 1 had higher average vote performance of 15 followed by Tongil rt 10 which scored average votes of 13. It was also reported by Burman *et al.* (2018) that unsuccessful genotypes do not meet farmer needs and will affect their adoption rates since the participation of farmers in variety selection increases the diffusion of seeds of superior rice varieties.

Based on the preference scores analyzed on positive and negative votes given by the individual Farmer to the particular cultivar across three locations, the genotypes Tong rt10, Tong rt2, and Tong rt1 were ranked first, Tong rt6, Tong rt1, and Tong rt3 second while genotypes Tong rt8, SATO1, and Tong rt10 were the third farmers choice in different locations. Genotypes Tong rt10 and Tong rt1 were selected by farmers into two locations, suggesting wide adaptability and acceptability. Other genotypes, Tong rt2, Tong rt3, Tong rt8, and SATO 1, were selected once in one location, indicating narrow adaptation based on farmers' preferences.

The mean preference of farmers selected from three tested locations indicates that farmers highly preferred genotypes Tong rt1, Tong rt10, and Tong rt 6. In contrast, genotypes Tong rt 9, Tong rt 7, and Tong rt 2 were not selected by farmers. Statistical analysis of the study indicates genotypes Tong rt 5, SATO 1, and Tong rt 3 yielded higher than other genotypes at 5% level of significance. The genotype Tong rt 7, check susceptible variety IR 29, and Tong rt 9 had low yield compared to other rice genotypes tested. Positive mean selection compared to specific location farmer selection revealed that genotypes Tong rt10 and Tong rt1 had wide acceptability compared to different genotypes. Based on farmers' selection, these two genotypes can be recommended for further studies because farmers from the two sites out of three have shown interest in these two genotypes.

The results show that genotypes that had good yield performance in one location were low yielding in another location. On the same basis, farmer-preferred genotypes in one location were not necessarily preferred in other locations. Mitchell and Fukai (2014) reported comparable results that farmer-preferred genotypes are not necessarily the highest yielding genotypes; there were changes in farmers' preferences in specific and across locations. No genotype was selected in all three sites from this study, which suggests the need for rice diversity to meet various farmers' needs. Differences in farmer preferences concerning changes in genotype performance in varied environments also would attract more study effort on the stable genotypes. The more frequently the genotype is selected by farmers, the higher the adoption rate of the genotype from the areas where the genotype has been determined. The result of the study indicates that there was a relationship between preferred genotypes by farmers and tolerance to salt injury score. The average performance against salt injury was good for most of the selected genotypes. The study's interests are linked to farmers' interests at this point. These results align with the Tarekegne *et al.* (2019) study, which observed a similar response of farmer selection on disease response in finger millet.

The study indicated that 10% Male farmers selected genotypes Tongil rt 5 and 11% selected SATO 1 variety, which showed high-yielding performance compared to other tested genotypes. Indicating that male farmers managed to select genotypes with high-yielding genotypes which aligned with statistical results than females, and females' famers didn't manage to align with statistical results on selecting the top yielding genotypes, perhaps female farmers had other selection objectives rather than yield. This study indicates that Gender may change farmers' selection preferences; hence, it should be well incorporated in further studies to identify perceptions based on the target market regarding Gender. The results agree with Aristya *et al.* (2021) findings, who stated that differences in Gender, age, education, and farm size also influenced the adoption and farmers' acceptability of new rice varieties technology. Another study explained that any intervention to improve farmers' seed purchases should consider efforts to increase farmers' purchasing power, which is driven by preferences (Ohno *et al.,* 2018).

Conclusion

Participatory Varietal Selection combines the perceptions of farmers' and breeders' opinions in selecting promising rice genotypes. The adoption rate of the variety is predicted by the farmers' willingness to grow it after being released; hence, the farmer's selection takes advantage of the Genotype x Environment interaction that provides a selection of varieties that perform well in their farming locations. In the coming century, significant challenges to agriculture and biodiversity will be dominated by increased climatic variations, shifting species ranges, disruption to biotic interactions, nutrient limitation, and emerging pests and pathogens. Researchers are advised to pay attention to farmers' participation in the selection of suitable crop genotypes. Farmer's participation in selection encourages the adoption rate when the genotype reaches farmers after being released. Also, farmers' participation helps to reduce resources and time wastage when the genotype is rejected at the last stage of evaluation. The study opened an opportunity to realize the farmer's preferred traits within the promising Tongil-type rice genotypes. Compared to other genotypes evaluated in this study Tong rt 1 and Tong rt 10 have become the farmer's choice. The result indicates that the selected genotypes can be used as commercial varieties in the selected areas. This study adds valuable information on rice breeding programs. Differences in farmers' perceptions observed on rice genotypes tested in this study demand the development of several rice genotypes that will meet current and future farmers' preferences. The on-station trials without taking the data from the farmers' fields' evaluation are the reasons for the low adoption rate of new varieties. The Participatory variety selection (PVS) was employed to explore the local knowledge perception as an untapped source of information on the possible traits farmers prefer to accelerate the adoption rate of rice tested on salt-affected soils. Statistical result analysis indicates that Tong rt 5 and SATO 1 had higher yields than other genotypes during evaluation but the two genotypes were not among the most selected by farmers.

The two promising genotypes preferred by farmers under the study are recommended for further steps of evaluation that can lead to registration and release since they were selected with most farmers during participatory variety selection. These genotypes can also be used in rice improvement programmes targeting salt tolerance. Another recommendation is that this study be repeated to confirm the performance consistency of these genotypes across seasons in line with the farmer's selection preferences. Apart from performance consistency, genotyping should be included during further studies of these genotypes to identify the existence and the location of salt-tolerant genes in the genotypes that show outstanding performance across locations and seasons.

Acknowledgement

I acknowledge the Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI) for sponsoring this valuable study.

Conflicts of Interest

I declare no conflict of interest to this study; it is my original work undertaken in three different unique places with unique genotypes in Tanzania.

Ethical approval

This study did not include any human and vertebrate animal studies for ethical approval.

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