Sokoine University of Agriculture

MSc Dissertation

Characterization of Selected Rice Genotypes from Eastern and Southern Africa Tolerant To Salinity at Seedling Stage

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CHARACTERIZATION OF SELECTED RICE GENOTYPES FROM EASTERN AND SOUTHERN AFRICA TOLERANT TO SALINITY AT SEEDLING STAGE

Dissertation Submitted to Sokoine University of Agriculture in Partial Fulfillment of the Requirements for the Degree of Master of Science in Crop Science

By

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EXTENDED ABSTRACT

Soil salinity stands as a prominent abiotic stress significantly impacting rice production and food security within sub-Saharan Africa. A promising strategy to mitigate this challenge involves the development and deployment of salinity-tolerant rice varieties. The objective of this study was to identify salinity-tolerant rice genotypes suitable for integration into breeding programs, offering a viable solution to salinity-affected soils in Eastern and Southern African rice-growing areas. The investigation focused on both phenotypic and genotypic characterizations of selected rice genotypes at the seedling stage, coupled with the identification of salinity tolerance-associated quantitative trait loci (QTLs).

This research focused on analyzing a collection of 206 rice genotypes obtained from Tanzanian farmers' fields, along with other genotypes from Eastern and Southern Africa. genotypes were then subjected to phenotypic screening under a salinity level of 12 dS/m, utilizing a hydroponic system and following the established IRRI protocol. From this initial pool, 13 genotypes were carefully selected based on their SES scores to undergo more detailed evaluation of their growth and physiological characteristics. To identify the presence of the *Saltol* allele, a widely recognized QTL associated with salinity tolerance, genotypic analysis was performed using 1k-RiCA SNP markers.

Phenotypic screening revealed salinity's adverse effects on various growth parameters, particularly on root and shoot dry weights, indicative of osmotic imbalance. Correlation analysis identified sodium concentration, sodium-to-potassium ratio, and canopy temperature as strong indicators of salinity tolerance in rice genotypes. These variables hold as potential physiological markers for salinity tolerance screening in breeding programs. Principal Component Analysis (PCA) was employed to identify key variables for salinity tolerance, revealing potassium ratio, root dry weight,

shoot dry weight, shoot length, and survival as significant contributors. Based on PCA results, genotypes were classified into tolerant, moderately tolerant, and sensitive categories. Six moderately tolerant genotypes (Intsindagira Bigega, K5, SATO 1, Sukari, Terembele (LL 29), and ZX 117) exhibited promising phenotypic tolerance, making them potential candidates for enhancing salinity tolerance in rice varieties.

Concurrently, Genotypic evaluation at the seedling stage provided insights into the expression of salinity-tolerant traits among the rice genotypes. Remarkably, 36 rice genotypes were found to possess the *Saltol* allele, recognized for its role in conferring salinity tolerance. some *Saltol*-possessing genotypes exhibited inadequate performance under salinity stress conditions. Interestingly, 16 genotypes lacking the *Saltol* allele demonstrated salinity tolerance, suggesting the presence of other genetic factors (QTLs) contributing to this trait beyond *Saltol*. Additionally, the geographical distribution of *Saltol*-possessing genotypes within Tanzania revealed variations across different Agro-ecological zones. Notably, the Coastal Zone exhibited a higher proportion of phenotypically tolerant genotypes compared to other zones, suggesting local farmers' continuous selection pressure as a possible contributing factor. These findings highlight the potential for integrating diverse salinity-tolerant rice genotypes, possessing various genetic mechanisms, into breeding programs. This approach could lead to the development of novel rice varieties capable of thriving under salinity stress conditions.

ISIKIRI KUU

Chumvi ya udongo unachukua nafasi kubwa kama changamoto ya mazingira unaokinzana na uzalishaji wa mpunga na usalama wa chakula katika eneo la kusini mwa Jangwa la Sahara. Mkakati wa kushughulikia changamoto hii ni kuendeleza na kutumia aina za mpunga zinazostahimili chumvi. Lengo la utafiti huu lilikuwa kutambua aina za mpunga zinazostahimili chumvi zinazofaa kuingizwa katika programu za uzalishaji, kutoa suluhisho la udongo ulioathiriwa na chumvi katika maeneo ya kilimo cha mpunga ya Afrika Mashariki na Kusini mwa Afrika. Uchunguzi ulilenga sifa za kifeno na jeni za aina za mpunga zilizochaguliwa katika hatua ya miche, pamoja na kutambua maeneo ya jeni yanayohusiana na kustahimili chumvi (QTLs).

Utafiti huu ulijumuisha uchambuzi wa aina 206 za mpunga kutoka mashamba ya wakulima wa Tanzania, pamoja na aina nyingine kutoka Afrika Mashariki na Kusini mwa Afrika. Aina hizi zilipimwa kwa sifa za kifeno chini ya kiwango cha chumvi cha 12 dS/m, kwa kutumia mfumo wa hidroponiki na kufuata itifaki iliyowekwa na IRRI. Kutoka kwenye kundi hili la awali, aina 13 zilichaguliwa kwa makini kulingana na alama zao za SES ili kufanyiwa tathmini zaidi ya ukuaji wao na sifa za kifiziolojia. Kwa kutambua uwepo wa jeni ya Saltol, ambayo ni jeni inayohusiana na kustahimili chumvi, uchambuzi wa jeni ulifanywa kwa kutumia alama za SNP za 1k-RiCA.

Uchunguzi wa kifenotipiki ulifunua athari mbaya za chumvi kwenye vigezo mbalimbali vya ukuaji, hasa kwenye uzito mkavu wa mizizi na shina, ukiashiria usawa wa osmotiki. Uchambuzi wa kubainisha uhusiano ulitambua mkusanyiko wa sodiamu, uwiano wa sodiamu na potasiamu, na joto la jani kama ishara zenye nguvu za uvumilivu wa chumvi katika aina za mpunga. Vipengele hivi vinaweza kutumiwa kama viashiria vya kifiziolojia vya uvumilivu wa chumvi katika mipango ya uzalishaji. Uchambuzi wa Mipengo ya Kimsingi (PCA) ulitumika kutambua vipengele muhimu vya uvumilivu wa

chumvi, ukiashiria uwiano wa potasiamu, uzito mkavu wa mizizi, uzito mkavu wa shina, urefu wa shina, na uhai kama wachangiaji muhimu. Kulingana na matokeo ya PCA, aina ziligawanywa katika makundi ya zenye uvumilivu, zenye uvumilivu wa wastani, na zenye hisia kali. aina sita zenye uvumilivu wa wastani (Intsindagira Bigega, K5, SATO 1, Sukari, Terembele (LL 29), na ZX 117) zilionyesha uvumilivu wa kifeotipiki unaovutia, zikiwafanya kuwa wagombea wa kusababisha uvumilivu wa chumvi katika aina za mpunga.

Kwa kuongezea, tathmini ya kijenitopiki kwenye hatua ya miche ilionyesha ufahamu wa maonyesho ya sifa zenye uvumilivu wa chumvi miongoni mwa aina za mpunga. Kwa utofauti, aina 36 za mpunga zilipatikana kuwa na jeni ya Saltol, inayotambulika kwa jukumu lake la kusababisha uvumilivu wa chumvi. Baadhi ya aina zenye jeni ya Saltol zilionyesha utendaji usiofaa kwenye hali za msongo wa chumvi. Aina 16 zisizo na jeni ya Saltol zilionyesha uvumilivu wa chumvi, kupendekeza uwepo wa sababu nyingine za kijenetiki (QTLs) zinazochangia sifa hii mbali na Saltol. Aidha, usambazaji wa kijiografia wa aina zenye jeni ya Saltol ndani ya Tanzania ulionyesha tofauti katika maeneo tofauti ya kilimo. Kwa kutambua, Eneo la Pwani lilionyesha idadi kubwa ya aina zenye uvumilivu wa kifeotipiki ikilinganishwa na maeneo mengine, ikipendekeza shinikizo la uteuzi wa wakulima wa ndani kama sababu inayoweza kuchangia. Utafiti huu unaonyesha uwezekano wa kuunganisha aina mbalimbali za mpunga zenye uvumilivu wa chumvi, zenye sifa za kijenetiki tofauti, katika mipango ya uzalishaji. Mbinu hii inaweza kuongoza kwenye maendeleo ya aina mpya za mpunga zenye uwezo wa kustawi katika hali za msongo wa chumvi.

DECLARATION

I, **Kefrine Kennedy Lutambi** do hereby declare to the Senate of Sokoine University of Agriculture that this dissertation is my own original work done within the period of registration and that it has neither been submitted nor being concurrently submitted in any other institution.

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Kefrine Kennedy Lutambi **Date**
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DEDICATION

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LIST OF ABBREVIATIONS AND ACRONYMYS

DNA	Deoxyribonucleic Acid
EC	Electrical Conductivity
et al.,	and others
FAO	Food and Agriculture Organization
IRRI	International Rice Research Institute
MAS	Marker-Assisted Selection
NaCl	Sodium Chloride
NBS	National Bureau of Statistics
QTL	Quantitative Trait Loci
SAR	Sodium Adsorption Ratio
SES	Standard Evaluation System
SNP	Single Nucleotide Polymorphism
SSRs	Simple Sequence Repeats
SUA	Sokoine University of Agriculture
URT	United Republic of Tanzania
1K RiCA	1K-Rice Custom Amplicon

CHAPTER ONE

1.0 General Introduction, Justification and Objectives

1.1 General Introduction

Rice (Oryza sativa) is one of the most important crops grown and consumed globally (Huong *et al.,* 2020) and by 2030, 40 percent more rice will be needed to meet the growing demand in rice-consuming countries (Gregorio *et al.,* 2015). People depend on rice for food calories and protein, especially in developing countries (IRRI, 2010). Rice is a crucial staple crop in Eastern and Southern Africa, playing a vital role in ensuring food security and supporting the livelihoods of millions (Kalala *et al.,* 2017). With its high nutritional value and importance as a source of dietary energy, rice is particularly significant for vulnerable populations in the region (Rugumamu, 2014). The demand for rice in Tanzania and sub-Saharan Africa continues to rise due to population growth and changing dietary preferences, placing additional pressure on cultivation systems (Sekiya *et al*., 2020). In Tanzania rice is ranked second among preferred and widely grown staple food crops after maize (URT, 2014). It is a significant source of employment, income and food security for farming household. Per-capita consumption for rice in Tanzania is about 25kg, ranked as a third crop after Maize (73kg) and cassava (157kg) and contributes for about 8% of caloric intake among Tanzanians (URT, 2019). According to Kadigi *et al.* (2020), Tanzania is ranked second among rice producers in Eastern, Central, and Southern Africa, with Madagascar being the largest. However, rice production faces various challenges in these areas, including limited arable land, resource constraints, and unfavorable climatic conditions (Höllermann et al., 2021, Michael et al, 2023). Both biotic and abiotic stresses cause a significant yield loss in rice-growing areas, including high salinity, drought, heat, and floods. Among them, salinity stress is the main hazardous factor of rice productivity (Dolo *et al.,* 2017, Michael *et al.,* 2023).

Salinity stress, resulting from excessive salt in the soil or irrigation water, poses a significant threat to rice cultivation across the world, leading to reduced crop performance and yield losses (Hakim *et al.,* 2010; Krishnamurthy *et al.,* 2020; Tahjib-Ul-Arif *et al.,* 2018). Farm land is affected by the saline intrusion of over 400 million hectares, accounting for 1/3 of the world's cultivated land (Thị Lang *et al.,* 2019). Rice production in regions such as Eastern and Southern Africa faces various challenges, with salinity emerging as a significant issue that adversely affects different growth stages (Kashenge-Killenga *et al.,* 2014; Meliyo *et al.,* 2017a; van Oort, 2018). According to FAO (2003) projects that there is an estimate of 3.5 million ha of salt affected soils in Tanzania covering both the semi-arid, low land and irrigated and non-irrigated areas. A recent survey by (Omar *et al.,* 2022), has indicated that salt-affected soils are the foremost constraints restraining rice production in many irrigation schemes in the Northern and Southern highlands of Tanzania. The distribution of saline soils also spans from dry or semi-arid areas of the country (Meliyo *et al.,* 2017b) The main cause of salinization of soils have been previously reported to be accumulation of salt caused by improper drainage during irrigation, poor-quality irrigation water, or soils containing salt from salt-rich rocks, as well as the impacts of climate change (Meliyo *et al.,* 2017b). According to Kashenge-Killenga *et al.* (2012) Slightly to total yield losses of about 5 to 100% has been recorded in rice irrigation schemes of southwestern Tanzania (Kashenge-Killenga *et al.,* 2016).

Salinity stress exerts detrimental effects on plants, disrupting various physiological and biochemical processes (Afzal *et al.,* 2022; Tenório *et al.,* 2019). High salt concentrations in the soil or irrigation water disrupt water uptake and cause osmotic stress, leading to reduced plant vigor, stunted growth, and decreased nutrient absorption. Furthermore, salt accumulation in plant tissues can disrupt ion balance, impair metabolic pathways, and induce oxidative stress. To combat this problem, several means have been employed with

varying degrees of success. One approach involves the use of agronomic practices such as land leveling, water management, and the application of organic amendments, which aim to minimize the adverse effects of salinity on rice growth and yield. In parallel to these management approaches, breeding efforts have played a pivotal role in developing rice genotypes with enhanced tolerance to salinity stress. Through the identification and selection of naturally salt-tolerant varieties or the introgression of desirable traits from landraces, breeding programs have made significant strides in developing rice genotypes capable of withstanding salinity stress, particularly at the seedling stage. These efforts have contributed to the improvement of rice production in saline-prone areas, enhancing food security and sustainable agriculture across the world (Tabassum *et al.,* 2021).

In pursuit to combat salinity stress in rice cultivation, the identification of tolerant genotypes is a critical step towards enhancing crop productivity and resilience. Phenotypic screening, which involves assessing the performance of rice genotypes under salinity stress conditions, has been a widely employed approach (Kakar et al., 2019). This method allows for the evaluation of various morphological, physiological, and biochemical traits associated with salinity tolerance. Through careful observation and measurement of traits such as plant height, root length, leaf chlorophyll content, and sodium ion exclusion ability, promising genotypes with enhanced tolerance to salinity can be identified (Huong et al., 2020). Furthermore, genotypic screening using marker-assisted selection (MAS) techniques, such as quantitative trait locus (QTL) mapping, has proven to be a powerful tool in identifying salt-tolerant rice genotypes. QTL mapping involves the identification of genetic markers associated with salinity tolerance traits through linkage analysis and statistical modeling. By comparing the genetic profiles of different rice genotypes with their observed salinity tolerance levels, specific genomic regions or QTLs can be identified that contribute to salinity tolerance. These QTLs can then be utilized in

breeding programs to select and develop rice lines with improved salinity tolerance (Krishnamurthy *et al.,* 2020)

The integration of phenotypic screening and genotypic screening approaches offers a comprehensive strategy for identifying salt-tolerant rice genotypes. Phenotypic screening provides valuable insights into the actual performance of genotypes under salinity stress conditions, allowing for the selection of promising candidates. Genotypic screening, on the other hand, enables the identification of underlying genetic factors contributing to salinity tolerance, offering a more precise and targeted approach (Krishnamurthy *et al.,* 2020).

Phenotypic screening can be conducted at different stages of rice growth, such as seedling, vegetative, and reproductive stages, using various morphological, physiological, and biochemical traits as indicators of salinity tolerance (Tabassum *et al.,* 2021). Some of the commonly used traits are shoot length, root length, shoot dry weight, root dry weight, relative water content, chlorophyll content, proline content, Na+/K+ ratio, and yield components (Dolo *et al.,* 2017). Phenotypic screening can be performed in controlled environments, such as pot-culture or hydroponics, or in natural field conditions, depending on the availability of resources and the objectives of the study (Kakar *et al.,* 2019). Genotypic screening can be performed using molecular markers that are linked to quantitative trait loci (QTLs) or genes that confer salinity tolerance in rice. Molecular markers can facilitate the detection of genetic variation among rice genotypes and the identification of salt-tolerant donors or progenies. Molecular markers can also assist in marker-assisted selection (MAS) or genetic engineering to transfer salinity tolerance genes into elite rice varieties. Some of the widely used molecular markers for salinity tolerance in rice are simple sequence repeats (SSRs), single nucleotide polymorphisms (SNPs), and expression sequence tags (ESTs) (Kakar *et al.,* 2019, Krishnamurthy *et al*., 2020).

This study aims to find rice genotypes that have a high tolerance to salinity stress and to reveal their genetic characteristics. Salinity stress is a major abiotic factor that limits rice productivity and quality in many regions of the world. Therefore, finding and developing rice varieties that can cope with salinity stress is crucial for ensuring food security and sustainable agriculture in saline-affected areas. This study intends to provide useful information and materials for rice breeders who are interested in improving salinity tolerance in rice. The study will identify salinity-tolerant rice genotypes through phenotypic and genotypic screening methods, and will use them as donor parents for breeding new rice cultivars with enhanced salinity tolerance. This study will also identify the quantitative trait loci (QTL) that are associated with salinity tolerance in rice, and will elucidate their genetic mechanisms and effects.

The main hypothesis of this study is that there are significant differences in salinity tolerance among rice genotypes, and that some genotypes have superior salinity tolerance than others. The study expects to find these salinity-tolerant genotypes from East and Southern Africa Germplasm by measuring various morphological, physiological, biochemical, and molecular traits under salinity stress conditions. The study also expects to find the QTL that are responsible for salinity tolerance in rice by using molecular markers that are linked to these QTL. By finding and characterizing these salinity-tolerant genotypes and QTL, the study hopes to offer valuable genetic resources and insights for rice breeders who want to develop new rice varieties with improved salinity tolerance.

1.2 Justification

Agriculture is a sector that is closely linked to climate and that is thereby naturally prone to impacts of climate change (Soto and Bahri, 2012). Due to long-term adverse effects of climate change, the frequency, intensity and duration of abiotic stresses are expected to increase in the near future, posing serious threats to crop production and global food security (Dar *et al.,* 2021). Salt-

affected soils, characterized by high soluble salt content, pose a significant challenge to rice cultivation in irrigation schemes across Tanzania and Africa at large (Kashenge-Killenga *et al.,* 2016). When salt levels surpass the threshold detrimental to crop production, adopting salt-tolerant rice varieties and implementing soil salinity management strategies become crucial for enhancing rice productivity (Ismail *et al.,* 2012). To address this issue, the objective of this study is to identify salinity-tolerant rice genotypes that can be utilized in the breeding process, offering a potential solution to the problem of soil salinity.

Salt-affected soils dominantly Saline soils present a major constraint to rice production, leading to reduced yields in numerous irrigation schemes in Tanzania (Kashenge-Killenga *et al.,* 2016). Global trends indicate an escalating prevalence of salt-affected soils, with an increase from 45 million to 62 million hectares between 1990 and 2013, particularly in irrigated areas (Costantini *et al.,* 2017, van Oort, 2018). In Tanzania, irrigation schemes located in arid and semi-arid regions are already experiencing rising levels of salinity or sodicity due to improper drainage, poor-quality irrigation water, salt-bearing rocks, and climate change (Meliyo *et al.,* 2016). Surveys have shown that seven out of nine examined rice irrigation schemes in Tanzania have been impacted by high salt levels, with reported electrical conductivity (EC) values of up to 10.5 dSm-1 and sodium adsorption ratio (SAR) of 72, indicating extreme salinity and sodicity levels respectively (Kashenge-Killenga *et al.,* 2012, Omar *et al.,* 2022). Effectively managing saline soils is crucial to mitigate negative consequences and ensure the long-term sustainability of irrigated agriculture. The selection of the appropriate rice variety by farmers plays a vital role in boosting crop productivity. Consequently, screening for tolerant genotypes and development of new rice varieties with a high level of salinity tolerance is important for improving rice yields.

1.3 Objectives

1.3.1 Overall Objective:

This study aims to identify salinity tolerant rice genotypes that can be incorporated into the breeding process, thereby offering a viable solution to the issue of salinity in rice-growing areas of Eastern and Southern Africa.

1.3.2 Specific objectives

To accomplish the aforementioned overall objective, the following specific objectives have been established

i. To conduct phenotypic characterization of selected rice genotypes from Eastern and Southern Africa at the seedling stage.

ii. To perform genotypic characterization at the seedling stage and identify Saltol QTL associated with salinity tolerance in rice.

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CHAPTER TWO

Seedling Stage Phenotypic Screening for Salinity Tolerance in Rice Genotypes from Eastern and Southern Africa[1]

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Abstract

Rice production in Africa and many parts of the world is severely affected by soil salinity, which requires breeding to improve yield and quality, considering the complex physiological adaptations. Rice shows different levels of sensitivity across growth stages, especially in early seedling and reproductive phases. This study involved screening of 13 genotypes selected from the pool of 206 rice genotypes with the aim of evaluating their tolerance to salinity at the seedling stage at salinity level of 12 dS/M. This study evaluated effect of salinity on reduction of different growth parameters and found that salinity stress reduced the root and shoot dry weights of most rice genotypes, indicating the disruption of osmotic balance in both plant systems. Spearman's correlation indicated that variables that are most strongly associated with salinity tolerance in rice genotypes are sodium content, sodium to potassium ratio and canopy temperature at later stages of salinity stress. These

[1] The material contained in this chapter is in preparation for submission to rice journal.

variables can be used as indicators or markers for salinity tolerance screening in breeding programs. Principal component analysis (PCA) was used to reduce the dimensionality of the data and identify the key variables and sources of variation for salinity tolerance. Results indicated that potassium (K^+), ratio, root dry weight (RDW), shoot dry weight (SDW), shoot length (SL) and survival were the most important variables for salinity tolerance, as they had high loadings on the first principal component (PC1), which explained 56.95% of the total variation in the data. Based on the PCA results, the genotypes were classified into three categories: tolerant, moderately tolerant, and sensitive. This study identified six moderately tolerant genotypes (Intsindagira Bigega, K5, SATO 1, Sukari, Terembele (LL 29), and ZX 117) that showed promising phenotypic tolerance. These genotypes could be potential candidates for future breeding programs aimed at enhancing salinity tolerance in rice varieties. Further research, including genotypic screening and field evaluations, is recommended to deepen our understanding of the underlying mechanisms and validate these outcomes for practical applications

Keywords. Salinity, Tolerance, Phenotyping, Principal Component Analysis, Breeding

1.0 Introduction

Abiotic stresses, such as extreme temperatures, floods, drought, and soil salinity, contribute significantly to a decline of 50-70% in global crop production. Salinity being recognized as one of the primary environmental constraints on agricultural productivity (Razzaque *et al.,* 2017). Salinity refers to the soil condition with a high concentration of soluble salts, and soils are categorized as saline if their electrical conductivity of saturated paste extract (ECe) is 4 dS/m or greater (Munns & Tester, 2008). The primary sources of salinity are natural salt deposits present in the soil or bedrock, while secondary salinization can occur due to improper irrigation and drainage practices (Ismail *et al.,* 2007). According to Chen *et al*. (2021), over one billion hectares of land worldwide are affected by

soil salinity or sodicity, and around 25-30% of irrigated lands (equivalent to 70 million hectares) are unproductive due to salt accumulation. Soil salinity is a prevalent problem, particularly in arid and semiarid regions, which hinders plant growth and biomass production (Bayoumi *et al.,* 2014). According to (Osman, 2018), High levels of soluble salts have two significant impacts on plants. Firstly, is an increase in the osmotic potential of the soil, impeding water uptake, and secondly, is specific ion toxicity or effects. When salt builds up in the roots, it causes a reduction in osmotic potential hence water uptake, leading to a phase of stomatal closure and decreased shoot growth, known as ion-independent phase. Another ionic phase occurs more slowly once salt concentration in the leaves reaches cytotoxic levels, resulting in senescence of mature leaves (Stutsel *et al.,* 2021). As a result, salinity is a critical issue in agriculture, impacting crop yield and posing a threat to global food security.

Rice is a crop species that is severely affected by soil salinity in large regions of Africa, Southern and Southern-East Asia, leading to significant yield losses. To address this issue, researchers such as Li and Xu (2007) emphasize the importance of identifying the specific traits associated with salinity tolerance in rice plants and developing appropriate screening techniques for breeding programs. This is especially crucial as rice plants possess complex physiological mechanisms that help them adapt to salinity stress (Kakar et al., 2019). Furthermore, studies suggest that the sensitivity of rice plants to soil salinity varies across the growth stages, with greater sensitivity noted during the early seedling and reproductive stages (Noorzuraini *et al.,* 2021).

The physiological view of salinity tolerance during early vegetative stage includes salt exclusion, ion compartmentalization, vacuolar salt compartmentation, responsive stomata, antioxidant upregulation, and vigorous growth (Ismail et al., 2007). However, the growth of salinity-stressed crop plants is mostly limited by the

osmotic effect of salinity, irrespective of the crop's ability to exclude salt (Jabeen et al., 2019). The osmotic effect can be described as a water-deficit effect as a result of the presence of salts in the soil, as high concentrations of salts in the soil make it harder for the roots to extract water. This results in reduced growth rates and stomatal conductance (Sirault *et al.,* 2009). Therefore, sensing of salt and dehydration stresses is of utmost importance in the process of achieving cellular homeostasis in plants. The appropriate adaptation response is dictated through the regulation of genes in cells and tissues that alter plant metabolism and growth (Schmidt *et al.,* 2013)
In salinity prone areas, farmers are known to have adopted the use of rice landraces for generations even though these generally have poor agronomic traits including tall plant stature, long growth duration, low yield, and poor grain quality. Some landraces, as demonstrated by Razzaque *et al.* (2017), exhibit remarkable salinity stress tolerance attributed to physiological mechanisms including sodium exclusion, vacuolar compartmentation, and stomatal responsiveness. Additionally, specific salinity-tolerant genotypes like Pokkali, Nona Bokra, and Horkuch, as highlighted by Razzaque *et al.* (2017), indicate their tolerance to salinity stress through similar mechanisms of sodium exclusion, vacuolar compartmentation, and stomatal responsiveness.

The cheapest and easiest way to address the problem of salinity is through breeding for salinity tolerant rice genotypes (Razzaque *et al.,* 2017). For this, the foremost step is to screen the existing germplasms of rice to identify the potential breeding materials (Tahjib-Ul-Arif et al, 2018). In rice the screening can be done independently at its two salinity sensitive stages (Ali *et al.,* 2014). Screening of germplasm at the seedling stage is readily acceptable as it provides a rapid screening that is difficult at the vegetative and reproductive stages (Reddy *et al.,* 2017). A number of screening methods for different morpho-physiological traits have been used to measure salinity tolerance in rice including shoot weight, shoot Na^+ concentration, the ratio of shoot Na^+ /K^+, leaf injury and survival rate,

leaf area and others (Hairmansis *et al.,* 2014). Infrared thermography has also been used to measure leaf temperature, as a surrogate for stomatal conductance, to screen the osmotic tolerance of rice seedlings (Siddiqui *et al.,* 2014). Stomatal activity is one of the most important physiological traits for plant growth and development. It plays a crucial role in the carbon and water balance by controlling photosynthesis and transpiration (Pineda *et al.,* 2021). According to (Chen *et al.,* 2021) Na^+ and K^+ are the major monovalent ions affecting rice growth, with K^+ a major macronutrient for plant growth. In addition, the plant's ability to maintain Na^+ and K^+ balance is the key feature of tolerance under salt stress in rice The typical mechanisms of salinity tolerance in rice are Na^+ exclusion or reduced uptake, and increased absorption of K^+ to maintain a suitable Na^+/K^+ balance in shoots. Thus, understanding the accumulation of Na^+ and K^+ in rice is important for exploring the fundamentals of rice biology and should provide useful information relevant to rice adaptation to salinity stress.

This study involved screening a set of selected African rice genotypes for tolerance to salinity at seedling stage. Then further characterized the genotypes that performed best at the 12dS/m salinity level, in order to identify the physiological mechanisms that explained their salinity tolerance. The study aimed to provide information that could be useful in improvement programs for the development of new salinity tolerant rice cultivars. This study hypothesis postulates that the chosen rice genotypes sourced from eastern and southern Africa will exhibit significant diversity in morpho-physiological characteristics and tolerance mechanisms when subjected to salinity stress. This variability holds significant importance in the identification and selection of superior rice genotypes, thereby facilitating the utilization of desirable phenotypic variations in rice breeding programs aimed at enhancing salinity tolerance.

2.1Materials and Methods

2.1.1 Plant materials

Seeds of 206 rice genotypes (*Oryza sativa* L.) were collected including landraces and improved genotypes from different farmers' field across Tanzania as well as several research institutes including the International Rice Research Institute (IRRI) stations in Tanzania, Burundi, Kenya, and the Tanzania Agricultural Research Institute (TARI). Other countries where the genotypes came from include Malawi, Rwanda, Ethiopia, Mozambique and Uganda. Out of 206 genotypes, 102 were landraces and 99 were improved genotypes. Five genotypes obtained from IRRI, Philippines, namely Pokkali, FL 478, CSR 28, and Nona Bokra (known for salinity tolerance), along with IRRI 154 (a salt-sensitive genotype), were employed as tolerance and susceptibility checks in the study.

2.1.2 Experiments

This study comprised three distinct experiments. In the initial experiment, a total of 206 different genotypes were examined. The purpose of this stage was to narrow down the selection from a large pool of genotypes to a smaller, manageable group that could be more easily evaluated for their growth and physiological characteristics. The second experiment involved 13 genotypes selected from the initial pool based on their SES Scores, which indicated their tolerance and sensitivity to salinity. This step aimed to confirm the results of the first experiment and also included measurements of growth and physiological parameters like Sodium concentration, Potassium concentration, and the Sodium to Potassium ratio. The third experiment, also comprising 13 genotypes, concentrated on conducting further physiological measurements, particularly the evaluation of canopy temperature. The first and second experiments were conducted at Sokoine University of Agriculture in Morogoro, Tanzania, during August and September. Experiment 3 took place at the International Rice Research Institute (IRRI) in the Philippines in November.

2.1.3 Phenotypic Screening

Rice genotypes were screened for salinity tolerance at seedling stage in a hydroponic system using the IRRI standard protocol (Gregorio *et al.,* 1997). Initially, seeds were pre-heated at 500C in a convection oven for 5 days to break seed dormancy. The seeds were germinated in petri dishes containing moistened blotter paper for 2 days. The pre germinated seeds were sown on Styrofoam seedling floats and were established in trays filled with nutrient solution (Yoshida *et al.,* 1976) in the screen house. The experiment was conducted using a split plot design with three replications each with salinized and non-salinized set up. The 7-day-old seedlings were initially salinized using 6dS/M concentration of salt (NaCl), which was then increased to 12dS/m after two days to reduce immediate shock. During treatment, the EC (12 dS/m) and pH (5.5) of the nutrient solution were checked daily by EC and pH meters, and the nutrient solution was renewed weekly.

2.1.4 Salinity stress symptoms evaluation

The modified standard evaluation system (SES) was used in rating the visual symptoms of salt toxicity (IRRI, 1997). Visual rating of salinity tolerance was done according to Table 2.1. This scoring discriminated the susceptible from the tolerant and the moderately tolerant genotypes. Initial and final scoring was done at 14 days and 21 days after salinization, respectively. Survivability was determined by the percentage of survived plants after treatment. This measurement was conducted in all the three experiments.

Table 2.1: Modified standard evaluation score (SES) of visual salt injury at seedling stage

Score	Observation	Tolerance
1	Normal growth with no leaf symptoms	Highly tolerant
3	Nearly normal growth, but leaf tips of few leaves whitish and rolled	Tolerant
5	Growth severely retarded, most leaves rolled; only a few are elongating	Moderately tolerant
7	Complete cessation of growth; most leaves dry; some plants dying	Susceptible
9	Almost all plants dead or dying	Highly susceptible

Source: Gregorio *et al.* (1997)

2.1.5 Growth measurements

Shoot and root length of rice seedlings was measured in centimeters. For shoot and root dry weight at 21 days after salinization, three randomly chosen plants of each genotype from each replication were uprooted, washed carefully with distilled water and then blotted dry. The samples were then oven dried at 70 ^{o}C to constant weight. Lastly the dry weight was measured using a laboratory balance. These recordings were taken in both the salinized and non-salinized conditions for all the three experiments.

2.2 Physiological Study of Salinity Tolerance at Seedling Stage

2.2.1Sodium and Potassium determination in plant tissues

For determination of sodium and potassium concentrations, youngest fully expanded leaves were sampled at 21 days after salinization (DAS) and washed carefully with distilled water. Homogenized dried leaf samples (100 mg) were placed in tubes containing 10 mL of 0.1 mol/L N-acetic acid and heated in a water bath at 85 ºC for 2 h. and then filtered using Whatman filter paper No. 1. Sodium and potassium concentrations were determined using flame photometer. Sodium and Potassium was determined in all the three experiments.

2.2.2 Thermal Image Acquisition

Thermal images of seedlings (each genotype) were acquired between 1000 and 1200 hours on 7, 15 and 20 days after salinization. Images were taken on the salt treatment and the control treatment with infrared thermal camera (NEC Thermo Tracer TH7800). The IR camera was positioned at a distance of 0.7 m. Images were analyzed in InfRec analyzer NS9500 Lite. Emissivity for measurements of leaves and plant canopies was set at 1. For more accuracy, the span of auto adjusted thermal image was manually set. The images were captured throughout the replications to assess the difference in canopy temperature of leaves of different rice genotypes. Thermal images were obtained from experiment three only.

2.3 Statistical Analysis

Effects of salinity stress on rice growth parameters was evaluated by calculating and comparing the percentage reduction of each parameter under each salinity levels. Eq. 1 was used to calculate the percentage reduction of each growth parameter. One-way ANOVA was then performed on the percentage reduction data for each parameter and plotted a heatmap using the R packages tidyr, ggplot2, scales, and stringr:

$$\boldsymbol{Percentage\ Reduction} = \frac{\boldsymbol{Control - Saline}}{\boldsymbol{Control}} \textbf{ X 100} \ldots\ldots\ldots\ldots\ldots\ldots\ldots \textbf{Eq. 1.}$$

We assessed the effects of salinity and genotype on sodium, potassium, and Na to K ratio in plant tissues by conducting a two-way ANOVA for each parameter. We used the aov function in R and checked the normality and homogeneity of variances assumptions using the Shapiro test and bartlett.test functions in R, respectively. We visualized the data using bar plots with standard error bars.

The relationships among various growth and physiological variables of salinity-stressed plants were explored by computing the spearman rank correlation matrix for 13 variables of interest. We used the corr.test function from the psych package in R to calculate the

correlation coefficients and the p-values. We plotted the lower triangle of the matrix for significant correlations ($p < 0.05$) using the corrplot package in R.

Agglomerative hierarchical clustering was performed on the scaled variables (zero mean and unit variance) to identify groups of genotypes with similar responses to salinity stress. Euclidean distance and Ward's method as the distance measure and linkage method were utilized, respectively, using hclust and dendextend packages. We plotted a dendrogram to show the clusters and the genotype labels. Seven variables were used for clustering: SES scores, Survival, shoot length, root length, shoot dry weight, root dry weight, and root to shoot dry weight ratio.
Principal Component Analysis (PCA) was conducted on the data set to reduce the dimensionality and reveal the main sources of variation among the genotypes under salinity stress. FactoMineR package was utilized to perform PCA on 10 scaled variables: score, survival, shoot length, root length, shoot dry weight, root dry weight, RDW/SDW ratio, leaves Na^+ concentration, leaves K^+ concentration, and Na^+/K^+ ratio. Eigenvalues and percentages of the PCs were tabulated using the pca$eig object and obtained the variable loadings for each PC using the pcavarcoord object. We created a scatter plot of PC1 and PC2 scores and plotted the PCA results showing the individuals and variables on the same graph using ggplot2 and plot. PCA functions.

2.4 Results

2.4.1 Phenotypic and Physiological responses of rice genotype to induced salinity.

2.4.1.1 Growth parameter's response to salinity.

The results indicated a significant influence of salinity stress on all growth parameters of the rice genotypes, as demonstrated in Figure 2.1. Analysis of variance (ANOVA) highlighted notable distinctions among the genotypes concerning the percentage reduction of various growth parameters, including shoot length (SL %R), root

length (RL %R), shoot dry weight (SDW %R), root dry weight (RDWmg %R), and the ratio of root dry weight to shoot dry weight (RDWOVERSDW %R) ($p < 0.01$) (Table 2.2).

The heatmap visualization underscored divergent sensitivities of the genotypes to salinity stress, with certain types exhibiting higher percentage reductions across each parameter, as depicted in Figure 2.1. This heatmap explained distinct patterns of tolerance and susceptibility among the rice genotypes in response to salinity stress. A comparative assessment of the growth parameters highlighted that root and shoot dry weights experienced more substantial reductions across most genotypes, in contrast to root and shoot length, as well as the ratio of shoot length to shoot dry weight.

Within the category of tolerant checks, FL 478 exhibited the least percentage reduction in all parameters, except for RDW/SDW, suggesting its remarkable tolerance to salinity stress. In the case of Pokkali, the percentage reduction in shoot length (SL), root length (RL), and shoot dry weight (SDW) was low; however, there was a notable reduction in root dry weight (RDW) and RDW/SDW, implying a distinct salinity tolerance mechanism compared to other checks. Other genotypes such as Intsindagira Bigega, K5 Terimbele (LL 29), and ZX 117 displayed comparable lower reduction trends in growth parameters, resembling the tolerant checks, suggesting tolerance of those genotypes.

Conversely, IRRI 154 exhibited the highest percentage reduction across all parameters, except for RDW/SDW, designating it as the most sensitive genotype to salinity stress. Kijicho and Sukari exhibited similar patterns of percentage reduction, resembling the susceptible check, with pronounced reductions in SL, SDW, and RDW, while showing lower reductions in RL and RDW/SDW.

The findings validated the hypothesis that distinct genotypes manifest diverse responses to salinity stress during the seedling stage. However, the results did not corroborate the hypothesis that disparate growth parameters react uniformly to salinity stress. Certain parameters, notably root dry weight and root dry weight overshooting dry weight, demonstrated heightened percentage reductions compared to others, implying their heightened sensitivity to salinity stress.

Table 2.2: Analysis of Variance (ANOVA) results for percentage reduction of growth parameters in rice genotypes under salinity stress. Percentage reduction is indicated as %R

Variable	SL %R_ p-value	RL %R p-value	SDW %R p-value	RDW %R p-value	RDW/SDW %R p-value
Genotype	1.23E-08	0.00454	3.07E-10	1.32E-11	0.003217

Figure 2.1: Heatmap of percentage reduction of growth parameters of rice *genotypes* under salinity *stress*. The color scale indicates the percentage reduction of each parameter, with darker colors (Dark blue) representing *lower* reductions and lighter colors (Yellow) representing *higher* reductions. The parameters are shoot length (SL), root length (RL), shoot dry weight (SDW), root dry weight (RDW), and root dry weight over shoot dry weight (RDW/SDW).

2.4.1.2 Physiological Response: Leaves Sodium and Potassium Concentration

The results show the mean sodium concentration in the leaves of 13 rice genotypes at two salinity levels (0 and 12 dS/m). The results indicate that there was a significant main effect of salinity level on sodium concentration ($p < 0.01$), as the mean sodium concentration was much higher at 12 dS/m (1.67%) than at 0 dS/m (0.07%). There was also a significant main effect of rice variety on sodium concentration ($p < 0.01$), as some rice genotypes had higher or lower sodium concentration than others, regardless of the salinity level. Moreover, there was a significant interaction effect between salinity level and rice genotype on sodium concentration ($p < 0.01$), as the difference in sodium concentration between the two salinity levels varied across the rice genotypes (Figure 2.2).

At 0 dS/m, there was no significant difference among the rice genotypes in terms of sodium concentration, as they all had similar low values (around 0.07%). However, at 12 dS/m, there was a wide variation among the rice genotypes in terms of sodium concentration, ranging from 0.4 mmol/g to 5.73 mmol/g. The highest sodium concentration was observed in IRRI 154 (5.73 mmol/g), followed by LINE 16 (4.93 mmol/g) and Kijicho (4.45 mmol/g). These three genotypes had significantly higher sodium concentration than the other genotypes at 12 dS/m. The lowest sodium concentration was observed in FL 478 (0.4 mmol/g), followed by TERIMBERE (LL29) (0.54 mmol/g) and INTSINDAGIRA BIGEGA (0.72 mmol/g). These three genotypes had significantly lower sodium concentration than the other genotypes at 12 dS/m. The remaining genotypes had intermediate values of sodium concentration at 12 dS/m, ranging from 0.76 mmol/g to 1.08 mmol/g, and they were not significantly different from each other.

The results show the mean potassium concentration in the leaves of 13 rice genotypes at two salinity levels (0 and 12 dS/m). The results indicate that there was a significant main effect of salinity level on

potassium concentration ($p < 0.01$), as the mean potassium concentration was higher at 12 dS/m (0.6 mmol/g) than at 0 dS/m (0.5 mmol/g). There was also a significant main effect of rice genotype on potassium concentration ($p < 0.01$), as some rice genotypes had higher or lower potassium concentration than others, regardless of the salinity level. Moreover, there was a significant interaction effect between salinity level and rice genotype on potassium concentration ($p < 0.01$), as the difference in potassium concentration between the two salinity levels varied across the rice genotypes.

At 0 dS/m, there was a wide variation among the rice genotypes in terms of potassium concentration, ranging from 0.34 mmol/g to 0.60 mmol/g. The highest potassium concentration was observed in FL 478 (0.6 mmol/g), followed by TERIMBERE (LL29) (0.54 mmol/g) and INTSINDAGIRA BIGEGA (0.54 mmol/g). These three genotypes had significantly higher potassium concentration than the other genotypes at 0 dS/m. The lowest potassium concentration was observed in Kijicho (0.34 mmol/g) and SATO 1 (0.34 mmol/g) followed by Nona Bokra (0.37 mmol/g). These three genotypes had significantly lower potassium concentration than the other genotypes at 0 dS/m. The remaining genotypes had intermediate values of potassium concentration at 0 dS/m, ranging from 0.39 mmol/g to 0.47 mmol/g, and they were not significantly different from each other.

At 12 dS/m, there was also a wide variation among the rice genotypes in terms of potassium concentration, ranging from 0.3 mmol/g to 0.74 mmol/g. The highest potassium concentration was observed in Pokkali (0.74 mmol/g), followed by Nona Bokra (0.71 mmol/g) and K 5 (0.65 mmol/g). These threegenotypes had significantly higher potassium concentration than the other 10 genotypes at 12 dS/m. The lowest potassium concentration was observed in Kijicho (0.30 mmol/g), which had significantly lower potassium concentration than other genotypes at 12 dS/m. The

remaining 12 genotypes had intermediate values of potassium concentration at 12 dS/m, ranging from 0.40 mmol/g to 0.62 mmol/g, and they were not significantly different from each other.

The results show the mean sodium to potassium ratio in the leaves of 13 rice genotypes at two salinity levels (0 and 12 dS/m). The results indicate that there was a significant main effect of salinity level on sodium to potassium ratio ($p < 0.01$), as the mean sodium to potassium ratio was higher at 12 dS/m (2.23) than at 0 dS/m (0.10). There was also a significant main effect of rice genotype on sodium to potassium ratio ($p < 0.01$), as some rice genotypes had higher or lower sodium to potassium ratio than others, regardless of the salinity level. Moreover, there was a significant interaction effect between salinity level and rice genotype on sodium to potassium ratio ($p < 0.01$), as the difference in sodium to potassium ratio between the two salinity levels varied across the rice genotypes.

At 0 dS/m, there was no significant difference among the rice genotypes in terms of sodium to potassium ratio, as they all had similar low values (around 0.10). However, at 12 dS/m, there was a wide variation among the rice genotypes in terms of sodium to potassium ratio, ranging from 0.39 to 8.52. The highest sodium to potassium ratio was observed in Kijicho (8.52), followed by IRRI 154 (7.67) and LINE 16 (5.78). These three genotypes had a significantly higher sodium to potassium ratio than other genotypes at 12 dS/m. The lowest sodium to potassium ratio was observed in FL 478 (0.39), followed by TERIMBERE (LL29) (0.56) and Pokkali (0.62). These three genotypes had a significantly lower sodium to potassium ratio than other genotypes at 12 dS/m. The remaining genotypes had intermediate values of sodium to potassium ratio at 12 dS/m, ranging from 0.63 to 1.13, and they were not significantly different from each other (Figure 2.2).

2.4.1.3 Response of Rice genotypes' Canopy temperature to salinity stress

The experiment aimed to screen for salinity tolerance of different rice genotypes by exposing them to salinity at 0 and 12 dS/m and recording canopy temperature (CT) data at 7, 14, and 21 days after salinization (DAS). The results showed that there was a significant effect of salinity concentration on CT at all time points (i.e., 7, 14 and 21 DAS), with higher salinity causing higher CT. There was also a significant effect of rice genotypes on CT at 21 DAS, indicating that some genotypes were more tolerant to salinity stress than others. The interaction between salinity concentration and rice genotype was also significant at 21 DAS, suggesting that the response of different genotypes to salinity was not uniform. The lowest CT values at 21 DAS were observed in FL 478 and IRRI 154 under 0 dS/m. At 12 dS/m, the highest CT values were observed in IRRI 154 and Kijicho. This implies that these genotypes were most affected genotypes to salinity stresss, while FL 478 and K5 was the least affected genotype having lower CT(Figure 2.3).

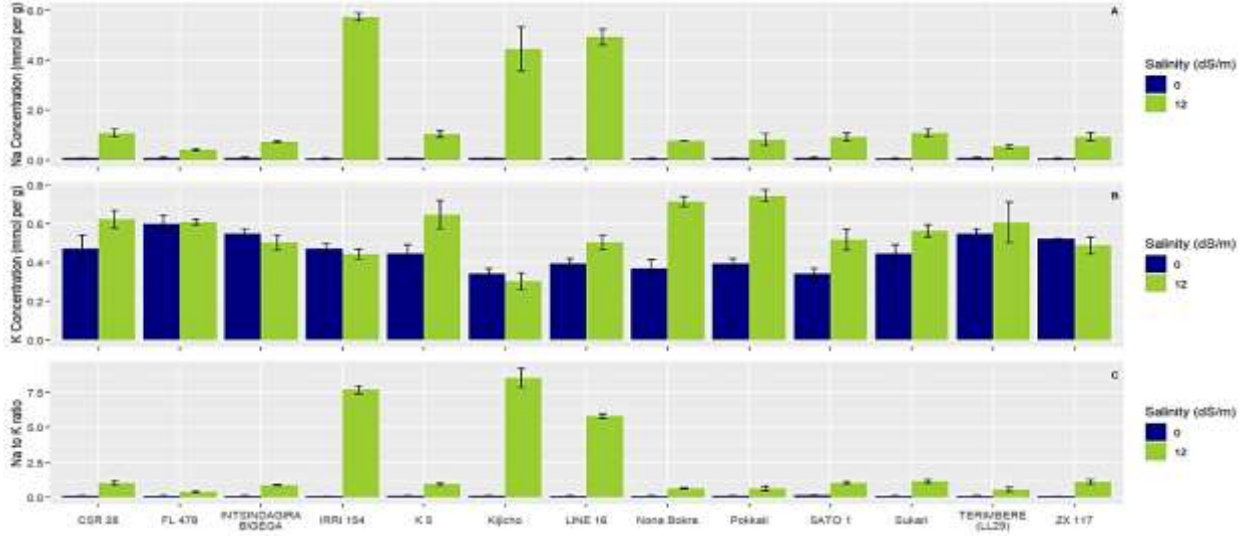

Figure 2.2: Effects of salinity levels on sodium and potassium concentrations and their ratio in the leaves of different rice *genotype*s. The bars represent the mean concentration in mmol per g or the mean Na to K ratio, and the error bars represent the standard error of the mean of three independent replications. The salinity levels are indicated by the colors navy (0 dS/m) and yellow green (12 dS/m). Panel A shows the results for sodium concentration, panel B for potassium concentration, and panel C for Na to K ratio.

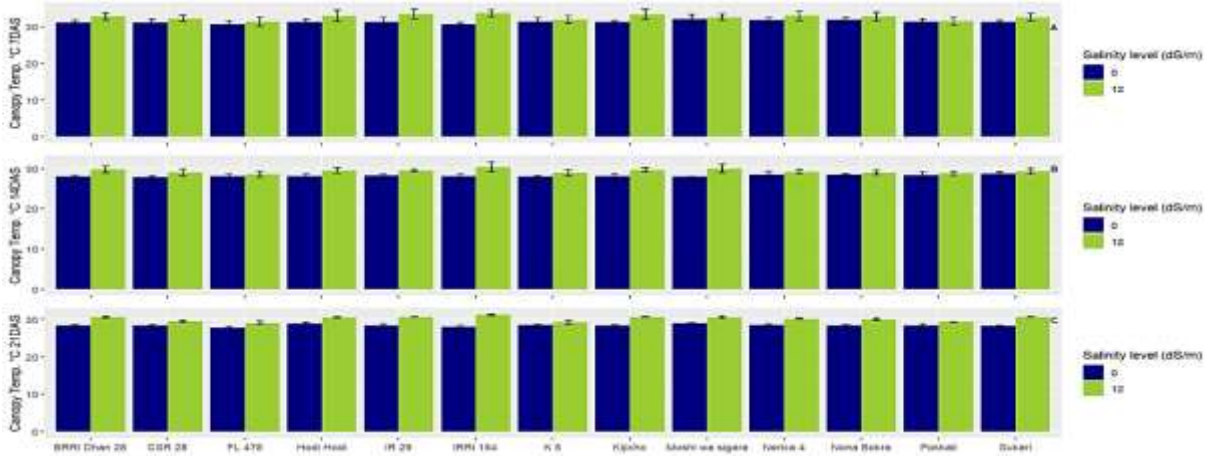

Figure 2.3: Effects of salinity levels on canopy temperature of different *genotypes* of rice at 7, 14, and 21 days after s*alinization* (DAS). The bars represent the mean canopy temperature in degrees Celsius and the error bars represent the standard error of the mean of three independent replications. The salinity levels are indicated by the *colour* navy (0 dS/m) and yellow green (*12* dS/m). Panel A shows the results for 7 DAS, panel B for 14 DAS, and panel C for 21 DAS.

2.5 Correlation Among Salinity Tolerance Parameters of Rice Genotypes

The Figure 2.4 shows that the score, which is a measure of salinity damage, is negatively correlated with most of the growth parameters, such as survival, shoot length, root length, shoot dry weight and root dry weight. This means that the higher the score, the more damage and lower growth performance under salinity stress. This suggests that salinity sensitivity in rice is associated with reduced growth and increased susceptibility to the adverse effects of salinity stress on the plant physiology.

One of the main effects of salinity stress on plants is the accumulation of sodium ions in the tissues, which can disrupt the osmotic balance and cause toxicity. The results show that the score is positively correlated with the sodium concentration and the sodium to potassium ratio, indicating that the higher the score, the more accumulation of sodium and the more imbalance of potassium in the plant. This implies that salt sensitivity in rice is related to the inability to exclude or efflux sodium from the rice genotypes, and to the intolerance or damage caused by sodium within the rice genotypes.

Another effect of salinity stress on plants is the increase in canopy temperature, which reflects the reduction in transpiration and water loss. The results show that the score is positively correlated with the canopy temperature at 14 and 21 days after salinization, suggesting that the higher the score, the higher the canopy temperature under salinity stress (Figure 2.4). This indicates that salinity sensitivity in rice is linked to the failure to maintain or enhance transpiration and water uptake, and to the disruption of water status and metabolism in response to salinity stress.

Generally, the correlation between rice growth and physiological parameters under salinity stress reveals that salinity tolerance in rice is a complex trait that involves multiple mechanisms. The variables

that are most strongly associated with salinity tolerance in rice genotypes are sodium content, sodium to potassium ratio and canopy temperature at later stages of salinity stress. These variables can be used as indicators or markers for screening and selecting salinity tolerant rice genotypes in breeding programs.

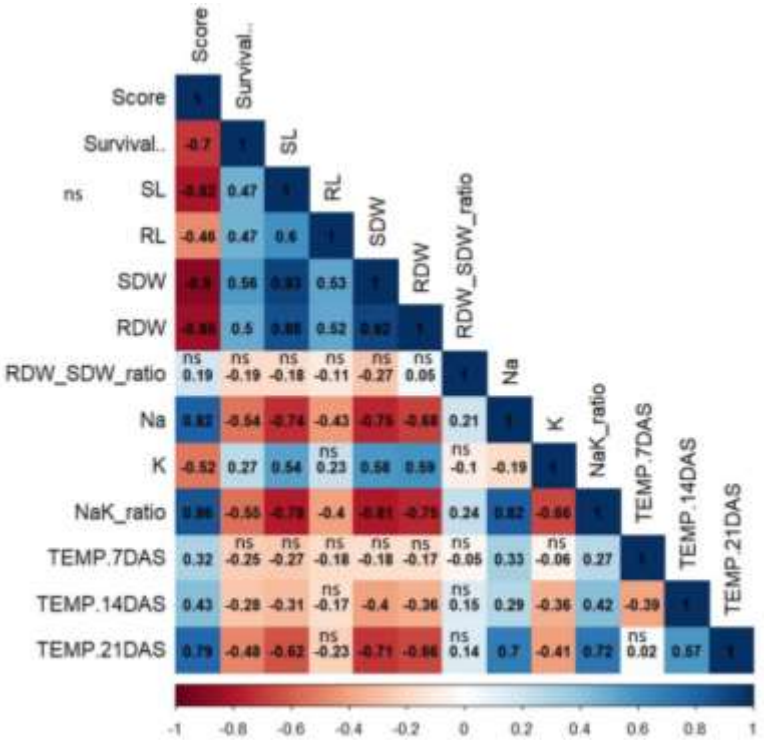

Figure 2.4: Spearman rank correlation coefficient between phenotypic variables of rice genotypes *under saline* condition (12 dS/m). Variables included in the plot are score, survival percent, shoot length (SL), root length (RL), shoot dry weight (SDW), root dry weight (RDW), root to shoot dry weight ratio (RDW_SDW_ratio temperatures at 7 (TEMP.7DAS), 14 (TEMP.14DAS), and 21 (TEMP.21DAS) days after salinization. *Correlations that are not significant are indicated by letters ns.*

2.6 Grouping Rice Genotype According to Salinity Tolerance Using Principal Component Analysis

To identify salinity-tolerant rice genotypes, included measuring ten phenotypic variables related to salinity tolerance in thirteen rice genotypes grown under saline conditions. These variables included potassium (K^+), sodium (Na^+), Na/K ratio, root dry weight (RDW), RDW/shoot dry weight (RDWSDW), root length (RL), scores, shoot dry weight (SDW), shoot length (SL) and survival. We used principal component analysis (PCA) to reduce the dimensionality of the data and identify the main sources of variation among the genotypes.

The PCA results revealed that the first four principal components (PCs) accounted for 91.31% of the total variation in the data (Figure 2.5). The first PC (PC1) explained 56.95% of the variation and was strongly associated with K^+, Na^+, Na/K, RDW, SDW, SL and survival. These variables indicated the degree of salinity tolerance of the genotypes, with higher PC1 values corresponding to higher tolerance. The second PC (PC2) explained 15.9% of the variation and was strongly associated with RDW, RDW and RDW to SDW ratio. These variables indicated the biomass allocation between roots and shoots of the genotypes, with higher PC2 values corresponding to higher root growth. The third PC (PC3) explained 10.42% of the variation and was strongly associated with RDW, RL and RDWSDW. These variables indicated the root morphology of the genotypes, with higher PC3 values corresponding to longer roots. The fourth PC (PC4) explained 8.04% of the variation and was strongly associated with RL and SDW. These variables indicated the shoot growth of the genotypes, with higher PC4 values corresponding to longer and heavier shoots.

The objective of this study was to explore the phenotypic variables that had higher contribution on salinity tolerance of rice genotypes. Based on the PCA results, we can conclude that K^+, Na^+, Na/K, RDW, SDW, SL and survival were the most important variables for salinity tolerance, as they had high loadings on PC1, which

represented a gradient of salinity tolerance among the genotypes. These variables reflected the ability of the genotypes to maintain ion homeostasis, osmotic adjustment, and biomass production under salinity stress. Therefore, these variables can be used as selection criteria for breeding salinity-tolerant rice genotypes in the future.

Figure 2.5 reveals three distinct categories, where the known tolerant check CSR 28 grouped into a moderately tolerant category alongside Intsindagira Bigega, K5, SATO 1, Sukari, Terembele (LL 29), and ZX 117. Although these genotypes did not outperform the tolerant checks (Pokkali, Nona Bokra, and FL 478) which was in the tolerant category while the sensitive category included IRRI 154, Line 16 and Kijicho.

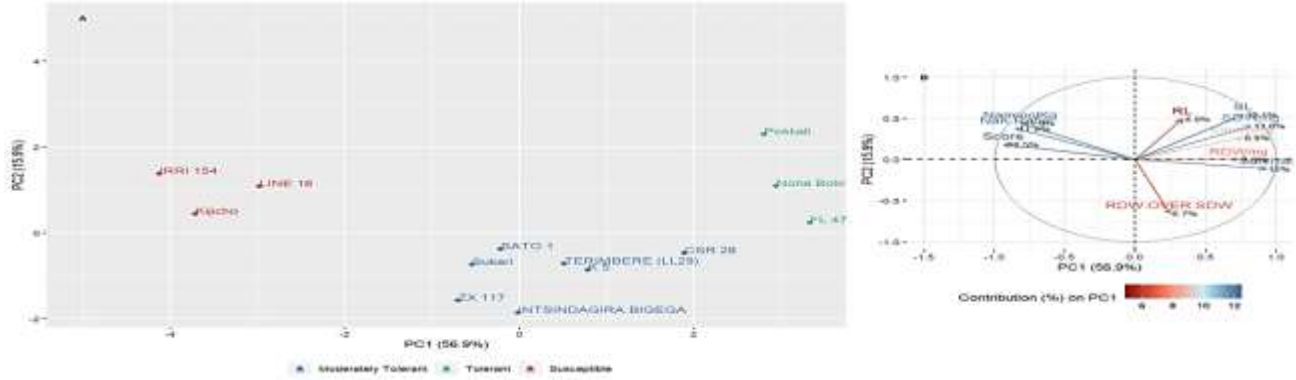

Figure 2.5: Panel A. Principal component analysis (PCA) describing the classification of rice genotypes under salinity stress. The first two principal components (PC1 and PC2) are plotted for each genotype, with PC1 on the x-axis and PC2 on the y-axis. The genotypes are color-coded by their salinity tolerance, which is determined by their PC1 scores. Panel B. Principal component analysis (PCA) for the first two principal components (PC) scores, PCA1 vs. PCA2 describing the variables associated with rice genotypes salinity tolerance under salinity stress based on PC1. Variables with *red* labels, root dry weigh (RDW), potassium *concentration* (K), shoot length (SL), shoot dry weight (SDW), root length (RL) and survival were positively correlating with salinity tolerance of rice genotypes whereas variables with *blue* labels, sodium concentration (Na), sodium to potassium ratio (Na/K), and SES *scores were* negatively correlating with salinity tolerance of rice genotypes.

2.7 Discussion

Successful screening for seedling-stage salinity tolerance requires a blend of morphological and physiological assessments that accurately represent phenotypic performance and salinity tolerance mechanisms. The current study presents a screening study designed to identify salinity-tolerant rice genotypes with promising phenotypic tolerance during the seedling stage, based on growth and physiological responses.

2.7.1 Growth response of rice genotypes to salinity stress

Salinity stress can impair the water and nutrient relations of plants, leading to reduced biomass production and allocation (Zeng and Shannon, 2000). Our results showed that salinity stress had different impacts on various growth parameters. Results showed that majority of genotypes showed greater susceptibility to salinity stress in terms of the dry weights of their roots and shoots, compared to their roots length and shoot length (Figure 2.1). This susceptibility can be attributed to the potential disruption of osmotic balance in both the roots and shoots of plants due to salinity stress, leading to a decline in root and shoot biomass accumulation among rice seedlings (Omisun *et al.,* 2018; Tahjib-UI-Arif *et al.,* 2018). These findings are consistent with previous studies on rice that reported differential effects of salinity stress on growth parameters among different genotypes (Ali et al., 2014; Kakar et al., 2019; Tahjib-UI-Arif *et al.,* 2018). The study also found genotypic variation in salinity tolerance among the screened genotypes. For tolerance checks, Nona Bokra, Pokkali, CSR 28 and FL 47, less reduction in growth parameters was observed in almost all growth parameters compared to other genotypes. Interestingly, for Pokkali there was a notable reduction in root dry weight (RDW) and RDW to SDW ratio. Possible explanation for why Pokkali has a high reduction of root dry weight in salinity stress but higher shoot dry weight is that it has a different strategy of biomass allocation under salinity stress. Pokkali may sacrifice its root growth to preserve its shoot growth, which is more important for photosynthesis and grain production (Shakri *et al.,* 2022). This may

also help Pokkali to avoid excessive accumulation of sodium ions in its roots, which can cause toxicity and damage. Other genotypes such as Intsindagira Bigega, K5, SATO 1, Sukari, Terembele (LL 29), and ZX 117 displayed a slightly higher reduction in growth parameters, resembling to the checks, suggesting a lower level of tolerance compared to checks. This study suggests that these genotypes could be tolerant at slightly lower salinity level (i.e., less than 12 dS/M). Line 16, Kijicho had much higher reduction as susceptible check (IRRI 154) suggesting that these genotypes are susceptible.

2.7.2 Physiological response of rice genotypes to salinity stress

Excess uptake of Na^+ through plants epidermal cells compete with the normal uptake of other nutrient ions, especially K^+ and causes K^+ deficiency which leads to higher Na^+/ K^+ ratio and imbalance of ionic homeostasis in rice under salinity stress condition (Assaha *et al.,* 2017; Jabeen *et al.,* 2020). In the current study, the growth parameters of most of the rice genotypes were highly reduced by salinity stress, however, some of the genotypes (Intsindagira Bigega, K5, SATO 1, Sukari, Terembele (LL 29), and ZX 117) showed salinity tolerance similar to tolerant check (CSR 28) by adjusting ion homeostasis and maintaining the lower Na^+/K^+ ratio (Figure 2.3) possibly due to Na^+ exclusion causing lower Na+ and lower Na^+/K^+ ratio in leaves (Peng *et al.,* 2016). Three tolerant checks (Nona Bokra, Pokkali, and FL 478) had much lower Na^+ and Na/K ratio suggesting their similar mechanism of salinity tolerance. Results of many previous investigations suggested that the ratios Na^+/K^+ could be utilized as an effective physiological marker for the assessment of salinity tolerance in rice (Rasel *et al.,* 2020).

The correlation between rice growth and physiological parameters under salinity stress reveals that salinity sensitivity in rice is a complex trait that involves multiple mechanisms. The variables that are most strongly associated with salinity tolerance in rice genotypes are sodium content, sodium to potassium ratio and canopy

temperature at later stages of salinity stress. There was also a significant effect of rice genotypes on CT at 21 DAS, indicating that some genotypes were more tolerant to salinity stress than others. Salinity stress affects the canopy temperature by reducing the water uptake and the stomatal conductance of the plant, leading to less transpiration and higher canopy temperature (Al-Tamimi, 2021). Therefore, canopy temperature can be used as an indicator of the salinity tolerance of different rice genotypes. Genotypes that have lower canopy temperature under salinity stress are considered more tolerant than those that have higher canopy temperature.

2.7.3 Promising genotypes

Utilizing the technique of principal component analysis (PCA), This study quantified the extent of contribution from individual components to the overall variance (Sinha & Mishra, 2013). This analytical approach affords a means to distinguish traits of substantial significance in shaping phenotypic diversity (Ray *et al.,* 2013). The PCA results revealed a prominent concentration of variation within the first four principal components (PCs), collectively accounting for a notable 91.31% of the entire dataset's variability. Notably, PC1 emerged as the dominant influence, elucidating 56.95% of the variation. This dimension exhibited a robust correlation with salinity tolerance indicators such as K^+, root and shoot dry weights, shoot length, and survival rate. These variables collectively delineated a gradient of salinity tolerance among genotypes, where higher PC1 values correlated with elevated tolerance levels.

This study findings consequently lead us to deduce that $K^{+,}$ root dry weight (RDW), shoot dry weight (SDW), shoot length (SL), and survival are the most pivotal variables influencing salinity tolerance in rice genotypes. This assertion stems from their strong loadings on PC1, which symbolizes the salinity tolerance spectrum among the genotypes. The observations align with previous studies that

similarly identified these phenotypic variables as markers of salinity tolerance in rice (Kakar *et al.,* 2019).

Notably, Figure 2.5 demonstrates three distinct categories, where the known tolerant check CSR 28 grouped into a moderately tolerant category alongside Intsindagira Bigega, K5, SATO 1, Sukari, Terembele (LL 29), and ZX 117. Although these genotypes did not outperform the tolerant checks (Pokkali, Nona Bokra, and FL 478). Moderately tolerant genotypes screened at 12 dS/m could demonstrate better performance at lower salinity levels. Consequently, the moderately tolerant category (Figure 2.5) presents promising candidates for inclusion in breeding programs aiming to develop rice varieties with enhanced salinity tolerance.

To comprehensively understand the tolerance mechanisms within the evaluated genotypes, further genotypic screening is imperative to identify the presence of QTLs, particularly the *Saltol* allele—a major QTL associated with salinity tolerance. Additionally, these materials should undergo field screening to gauge their tolerance in field conditions.

2.8 Conclusion

In conclusion, this study primarily concentrated on screening selected rice genotypes for their capacity to withstand salinity during the seedling stage. This study also encompassed screening genotypes under salinity conditions of 12 dS/m, with the aim of uncovering the physiological parameters that contribute to their adaptive tolerance to salinity stress. The overarching goal was to find genotypes could be applied to the improvement programs, specifically targeted at developing rice varieties with tolerance to salinity. The evaluation of seedling stage morpho-physiological screening revealed that the salinity-tolerant checks, namely Pokkali, Nona Bokra, and FL 47, demonstrated the most impressive morphological performances. Among various growth parameters, a significant reduction in both root and shoot dry weights was

observed in most genotypes. This reduction indicates the potential disruption of osmotic balance in both roots and shoots due to salinity stress, leading to a decline in the accumulation of biomass in rice seedlings. The physiological responses highlighted the vital role of ion homeostasis, particularly the Na+/K+ ratios, in influencing the mechanisms that confer salinity tolerance. Furthermore, through principal component analysis, key variables including K^+, Na^+, Na/K ratio, root and shoot dry weights, shoot length, and survival were identified. These variables collectively contribute to shaping the gradient of salinity tolerance. The PCA results categorized the checks into the tolerant category based on 11 parameters. Additionally, six genotypes, Intsindagira Bigega, K5, SATO 1, Sukari, Terembele (LL 29), and ZX 117—were grouped as moderately tolerant genotypes. These findings underscore the potential of these moderately tolerant genotypes for future breeding programs aimed at enhancing salinity tolerance in rice varieties. To further the understanding of the underlying mechanisms and validate these outcomes for practical applications, it is recommended to conduct additional research, including genotypic screening and field evaluations. This comprehensive approach will provide a deeper insight into the identified genotypes' salinity tolerance capabilities and pave the way for their successful integration into rice cultivation strategies.

Author's contribution

K.K.L designed the study, conducted the screening work, collected data, conducted data analysis and drafted the manuscript. A.H, M.O, O.P, S.N, and N.L.K reviewed and edited the study concept.

Conflict of interest

Authors declares no conflict of interest

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CHAPTER THREE

Genotypic Screening for Salinity Tolerance of Rice genotypes from Eastern and Southern Africa at Seedling Stage[2]

Authors

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Abstract

Salinity is among the most severe abiotic stresses leading to reduction of rice yield in many rice-growing areas of the world, including Eastern and Southern Africa. This justifies the need for developing salinity-tolerant rice varieties for improved rice productivity and yield stability under salinity-stressed environments. Since landraces can be an important source of stress tolerance, we collected a set of 120 landraces and improved cultivars from farmers' fields across Tanzania and characterized them together with other landraces and improved cultivars from Eastern and Southern Africa to comprise a set of 201 *Oryza sativa* genotypes. Genotypic analysis of the 201 genotypes was done using 1k-RiCA SNP markers to check for presence of the *Saltol* allele. The expression of salinity-tolerant traits in rice genotypes was assessed through phenotypic evaluation at seedling stage using IRRI standard

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protocols. The geographic distribution of *Saltol* possessing genotypes was analyzed for 120 genotypes collected from Tanzania. Thirty-six (36) rice genotypes possessed the tolerant *Saltol* allele. Two genotypes (K5 and Intsindagira bigega) which ranked as tolerant during the phenotypic screening were found to have *Saltol*, but other *Saltol* positive genotypes performed poorly under salinity stress. Furthermore, sixteen (16) genotypes which did not possess *Saltol* were found to be tolerant to salinity stress, suggesting the presence of salinity tolerance QTLs other than *Saltol***.** Hence, the salinity-tolerant rice genotypes with other salinity-tolerance QTLs should be further explored. The distribution of genotypes with the salinity-tolerant *Saltol* allele and phenotypic tolerance varied across Tanzanian agro-ecological zones. The Coastal Zone had a higher proportion (16.7%) of genotypes showing phenotypic tolerance compared to the Central Zone, Eastern plateaux and Mountain blocks, and other Zones (with percentages of 4.5%, 12.1%, and 0% respectively), suggesting that continuous selection pressure by farmers in the Coastal Zone might have contributed to the observed prevalence of phenotypically tolerant genotypes. These findings have the potential to be utilized in breeding for new rice varieties that possess high levels of tolerance to salinity.
Keywords: Phenotype, genotype, 1k RICA, Salinity, Salinity tolerance, *Saltol*, rice.

3.0 Introduction

Rice (*Oryza sativa L*.) is the staple food for half of the world's population (Schneider and Asch, 2020). It plays a pivotal role in improving household food security, livelihoods and national economies in Sub Saharan Africa (Nhamo *et al.,* 2014). Despite the importance of rice, its production is under threat due to a number of abiotic and biotic stresses such as salinity, drought, extreme temperature, submergence, pests and diseases (Gregorio *et al*., 2015), which are expected to worsen with the current trend of climate change. Out of many abiotic stresses, soil salinity is one of the major constraint toward global rice production (Vu *et al*., 2012).

Tian *et al*. (2020) reported that over 20% of cultivated land worldwide has high levels of salt that can lead to crop plant salt stress, and this problem is expanding at an alarming rate of 2 million hectares per year (Abbas *et al.,* 2013). Moreover, Africa has the highest proportion of saline soils, accounting for almost 63% of the total saline soils on earth (Eswar *et al.*, 2021). Rice yields can be reduced by up to 50% when grown under moderate (6 dS/m) salinity levels (Adak *et al.*, 2020). A substantial proportion of areas well-suited for rice cultivation are currently either abandoned due to salinization or experience significantly lower yields compared to the average productivity(Krishnamurthy *et al.*, 2020). In essence, the occurrence of soil salinity can be attributed to both natural and human-induced factors, and managing saline soils involves implementing techniques such as selecting crops that can tolerate salt and reducing salt levels through flushing. While there are other agronomic interventions available, growing salt-tolerant varieties is the most cost-effective solution (Akramkhanov *et al.,* 2010; Gorji *et al.,* 2015; Osman, 2018; Dar *et al.,* 2021; Omar et al., 2022).

Breeding for salinity tolerance in rice has emerged as a promising solution for mitigating the adverse effects of salinity on rice cultivation (Wani et al., 2020). Krishnamurthy et al. (2020) highlighted the need for high-yielding salt-tolerant rice varieties for commercial cultivation, which requires the introgression of salt-tolerant QTLs into high-yielding varieties. Molecular and genomic technologies have facilitated the identification and characterization of salinity tolerance genes and QTLs in rice, enabling the development of new breeding strategies (Gregorio *et al.,* 2002). However, there are still some challenges and research gaps that need to be addressed, such as the identification of suitable donors, limited understanding of the genetic mechanisms underlying salinity tolerance, and the lack of efficient screening methods for large-scale breeding programs (Zeng *et al.*, 2003). Nevertheless, the future prospects for developing high-yielding and salt-tolerant rice varieties are promising and will significantly contribute to global food security.

Selecting salt-tolerant rice varieties that can thrive in saline soils is crucial, and breeders have several approaches to identify such rice genotypes. Phenotypic screening has been one of the useful tools for identifying tolerant genotypes, however, the screening process is time-consuming and can be easily interfered by environmental factors (Reddy *et al.,* 2017). To overcome these limitations, recent advancements in biotechnology have provided breeders with tools such as marker-assisted selection that can improve the accuracy and efficiency of the screening process (Pray *et al.,* 2011). By utilizing these advanced tools, breeders can quickly identify desirable traits and introgress them into high-yielding rice varieties, producing salt-tolerant rice varieties that are commercially viable and can thrive in saline soils (Pray *et al*., 2011; Reddy *et al.,* 2017; Krishnamurthy *et al.,* 2020).

A number of genetic mapping studies in rice have located various quantitative trait loci (QTL) associated with salinity tolerance (Adak *et al*., 2020). QTLs or genes such as *qSKC1, qSNC7, Saltol, OsRR22, qSIS2, qWCSST2, qST1, qSDW2.1, qSNC5, qNaL-1.2, qKR-1, qNa/KL_1.2, qGY-2, qRSL3, qRRL3, qSH1, qNa2.1, qSTY11.1, qCDP1.1, qSLn1.1, qRLs2.1, qRFWs6.1, qST-3.1, qST-5.1, qST-6.1, qST-6.2, qSTGY2.2, qSTGF2, qRSL7, qSL7, qSIS1, qSSI1, qSL1, qSIS1.39, qChlo4, qRL6.1, qRL12.1, qRL1.2, qGLWR2, qSSIGY2.1, qSF1.4, SH12.1, qSH12.2,* and *qDSW12.1* have been identified by genomic methods (Sun *et al.,* 2019; Li *et al.,* 2022). *Saltol* is regarded as the major QTL governing salinity tolerance in rice, located on chromosome 1 (Linh *et al.,* 2012). This QTL confers salinity tolerance at the vegetative stage that governs the Na^+ /K^+ uptake ratio and explains from 64.3% to 80.2% of the phenotypic variation in salt tolerance (Arzani et al., 2008). Multiple salt-tolerant rice varieties have been developed by incorporating the *Saltol* QTL into modern high-yielding rice varieties that are otherwise sensitive to salt, using marker-assisted backcrossing and selection (Waziri *et al.,* 2016).

Most salinity-tolerance QTLs are found in landraces (such as Pokkali and Nona Bokra) which are geographically found in low-lying areas of India with soil salinity (Manohara *et al.,* 2021). These landraces have naturally adapted to salt stress over generations. However, most research on abiotic stress tolerance in plants overlooks the ecological and geographical factors of tolerant genotypes (Bin Rahman and Zhang, 2018). For instance, *Saltol*, a gene responsible for salinity tolerance, was discovered in Pokkali, a landrace grown in coastal areas of Kerala, India (Chen *et al.,* 2020). Therefore, to effectively identify donor plants for salt-tolerant QTLs, it is still essential to take into account the geographical origin of the genotypes that are being studied.

Several rice genotypes in Asia have been identified to possess the ability to withstand high levels of salt in the soil, which makes them promising candidates for breeding new rice varieties that can tolerate salinity. However, many traditional African rice varieties have not been screened for their ability to tolerate salinity. The hypothesis of this study is that African rice genotypes may harbor novel QTLs responsible for salt tolerance, which could be utilized for the development of salt-tolerant rice varieties. Furthermore, this study examined the spatial distribution of salt-tolerant rice genotypes, including those with *Saltol* genotypes, with the hypothesis that the occurrence of salt-tolerant and *Saltol*-containing genotypes would be dependent on where the genotype has been collected.

3.1 Material and Methods

3.1.1 Seed collection

To establish a panel of Tanzanian rice landraces and improved genotypes, seeds were collected from farmers' fields in 2020 by Sokoine University of Agriculture (SUA). The authorization to perform the task of rice seed collection from farmers and several Agricultural Institutes in Tanzania was granted at different levels of authorities as required by research guidelines of the country

including the SUA Deputy Vice Chancellor's office, the President's Office of Regional Administration, and Local Governments for the respective regions where seeds were collected. The researchers collected approximately 250g of seed of each rice genotype. The coordinates of these genotypes were recorded using a Garmin Emap GPS device (datum: WGS84). The zones from which the geo-referenced genotypes in Tanzania were collected include the Eastern plateaux and mountain blocks (66 genotypes; Morogoro, Kilimanjaro-Same and Tanga regions), Central Zone (22 genotypes; Tabora, Shinyanga and Mwanza regions), Southern Highlands (7 genotypes; Mbeya (Kyela and Mbeya rural) region), Northern rift zone and Volcanic highland (1 genotype; Kilimanjaro-Moshi rural), Rukwa-Ruaha rift zone (11 genotypes; Mbeya-Mbarali, Songwe, Rukwa-Sumbawanga rural and Singida regions), Ufipa plateau (1 genotype; Rukwa-Nkasi) and Coastal Zone (12 genotypes; Mtwara, Bagamoyo and Zanzibar).

Seeds of 201 rice genotypes *(Oryza sativa L.)* were collected including the panel of Tanzanian rice landraces and improved genotypes from farmers' fields across Tanzania as well as from several research institutes including the International Rice Research Institute (IRRI) stations in Tanzania, Burundi, Kenya, and the Tanzania Agricultural Research Institute (TARI). Other genotypes were acquired from Malawi, Rwanda, Ethiopia, Mozambique and Uganda. Out of the 201 genotypes, 102 were landraces and 99 were improved genotypes based on their classifications in the Tanzanian Official Seed Certification Institute (TOSCI) database (https://www.tosci.go.tz/seed-varieties?page=8). It should be noted that georeferenced data and the mapping exercise was conducted on the Tanzanian genotypes only. Five check genotypes were obtained from IRRI, Philippines, namely Pokkali, FL 478, CSR 28, and Nona Bokra, which are known for their tolerance to salinity and IRRI 154, which is a salt-sensitive genotype. The seeds were increased at SUA for conducting this study and the remaining stock

is currently stored in a cold room located within the Department of Crop Science and Horticulture Main Building.

3.1.2 Phenotypic screening

The phenotypic screening was conducted in the screen house in August 2022 at Sokoine University of Agriculture (SUA), Morogoro, Tanzania located at a latitude 6^0 49′ 27″ S, longitude 37^0 39′ 48″ E and elevation of 509 m above sea level.

Rice genotypes were screened for salt tolerance at seedling stage in a hydroponic system using the IRRI standard protocol (Gregorio *et al.,* 1997). The seeds were pre-treated at 50^0C in a convection oven for 5 days to break dormancy, and then germinated in petri dishes containing moistened filter paper for 2 days. The pre-germinated seeds were then sown on Styrofoam seedling floats established in trays filled with nutrient solution (Yoshida *et al.,* 1976) in a screen house. The experiment was conducted using a split plot design with three replications each with salinized and non-salinized treatments. The 7-day-old seedlings were initially salinized (NaCl) using an electrical conductivity (EC) of 6 dS m^{-1}, which was then increased to 12dS m^{-1} after two days to reduce immediate shock. During treatment, EC (12 dS m^{-1}) and pH (5.0-5.5) levels of the nutrient solution were checked daily and the nutrient solution was renewed weekly. The modified standard evaluation system (SES) was used in rating the visual symptoms of salt toxicity (IRRI, 1997). This scoring discriminated the susceptible from the tolerant and the moderately tolerant genotypes. Initial and final scoring was done at 14 and 21 days after salinization, respectively.

3.1.3 Genotypic screening

3.1.3.1 Sample collection

A healthy youngest fully expanded leaf of each genotype from each of the 201 rice genotypes was collected from 3-week-old plants. During sample collection, each leaf sample was rolled twice and punched to get four leaf disks of 6mm. The leaf disks were then

inserted into a specific well of 96-well plates according to sample number. The samples were kept cool on ice throughout sample collection. The sample plates were then lyophilized ready for 1k RiCA genotyping (GSL IRRI, 2021).

3.1.3.2 Genotyping

The genotypes and checks used in this study were genotyped using the 1k-Rice Custom Amplicon (1k-RiCA assay), as described by Arbelaez *et al.* (2019). Genomic DNA was obtained from leaf tissues of single plants. DNA extraction, genotyping and single nucleotide polymorphism (SNP) calling was done using the genotyping services of Agriplex Genomics (Cleveland, OH, USA). A custom SNP calling pipeline developed by Agriplex Genomics was used to assign variants on the 1k-RiCA Amplicon through alignment to the Nipponbare rice genome MSU7 version (Kawahara *et al.*, 2013). Final SNP data were merged and formatted in a single data frame with markers in rows and samples in columns providing information on the presence and absence of *Saltol*. The SNP identification, chromosome, and physical position information were also provided.

3.1.3.3 Spatial mapping of Tanzanian genotypes

The geographic origins of 120 Tanzanian genotypes with precise georeferenced information was mapped with the aim of identifying the spatial distribution of phenotypically salt-tolerant and *Saltol* QTL-possessing rice genotypes across various rice-growing regions in Tanzania. Tanzania's regional boundaries were based on shape files obtained from the National Bureau of Statistics (NBS) (2012 PHC: Shape files - level one and two), and the resulting maps were produced employing QGIS version 3.2.2.

3.2 Results

3.2.1 Identification of Rice Genotypes with Saltol QTL

Based on genotyping data, the salinity-tolerant *Saltol* allele was present in 36 genotypes (10 landraces and 26 improved genotypes) (Figure 3.1). This finding indicates that a greater proportion of

improved cultivars possess the salinity-tolerant *Saltol* allele (26.3%), compared to the landraces (9.8%) (Tables 3.1 and 3.2 found in the Supplementary materials). The chi-square test revealed a significant association between the presence or absence of the *Saltol* allele and the type of genotype (improved or landrace). The obtained p-value (p= 0.004) indicates that the observed difference in *Saltol allele* presence between the two types of cultivars is unlikely to have occurred by chance. Based on the chi-square test result, it can be concluded that the presence of the *Saltol* allele is significantly more frequently associated with the improved cultivars (26 out of 99) compared to the landraces (10 out of 102).

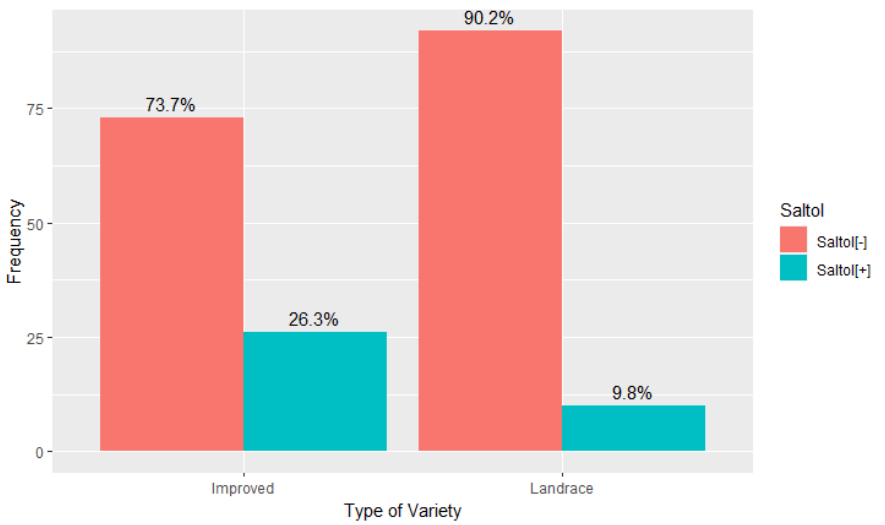

Figure 3.1: Proportion of rice genotypes from Eastern and Southern Africa (n=201) in which the salinity-tolerant *Saltol* allele is present. The collection included 102 landraces and 99 improved cultivars from Eastern and Southern Africa. The genotyping was conducted by 1k RiCA (Agriplex Genomics). Presence of *Saltol* was significantly more frequently associated with improved genotypes compared with landraces (χ^2= 8.17, df = 1, p-value = 0.004)

3.2.2 Phenotypic Screening of Salinity-tolerant Genotypes

Among 201 genotypes that were subjected to phenotypic screening using IRRI standard protocol 19 genotypes (7 landraces and 12 improved cultivars) were tolerant (SES<6) at EC of 12 dS m^{-1} under Yoshida hydroponic culture (Table 3.1 and Table 3.2 found in the Supplementary materials). The rice genotypes tested showed a range of phenotypic responses to salinity stress at the seedling stage. Three (1.5% of 201) genotypes (K5, Intsindagira bigega, ZX 117) were classified as tolerant with an SES score of 3–4.3 while fifteen (7.5%) genotypes (Jaribu, Kijicho, Nerica 4, SATO 1, TXD 88 Improved, Moshi wa sigara, Mpaka wa bibi, Sukari, BR, Rumbuka, Nemeyubutaka, Terimbere, Chupa, Line 16 and Rumbuka bug 2013A) were moderately tolerant with SES scores of 5–5.7. One hundred and twenty-one (60.2%) genotypes were susceptible (SES score 6-8.3) and the remaining 62 genotypes (30.8%) were highly susceptible to salinity (SES score 9). However, only the tolerant checks (Pokkali, FL 478 and Nona Bokra) qualified to be highly tolerant with scores ranging from 1-1.7. In overall, a small proportion (6.9%) of the landraces and improved cultivars (12.1 %) that were screened showed tolerance to salt stress with SES scores less than 6 (Figure 3.2). The chi-square test was conducted and the results showed no statistically significant difference in the distribution of phenotypic tolerance between the landrace and improved genotypes (X^2= 1.06, df = 1, p-value = 0.30). The calculated chi-square value of 1.06 with 1 degree of freedom indicates that the observed distribution of phenotypic tolerance is not significantly different between the two types of genotypes. The associated p-value of 0.30 suggests that the observed association between cultivar type and phenotypic tolerance is likely to have occurred by chance.

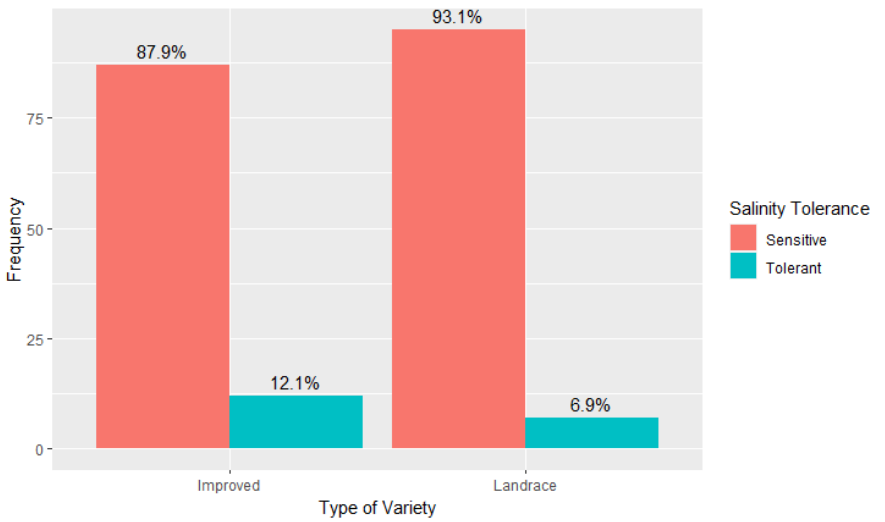

Figure 3.2: **Proportion of phenotypically salt-tolerant (SES Score <6) rice genotypes from Eastern South African segregated into landraces and improved cultivars (n =201). The collection included 102 landraces and 99 improved genotypes from Eastern and Southern Africa. Phenotypic tolerance is not significantly different between the two types of genotypes (X^2= 1.06, df = 1, p-value = 0.30).**

3.2.3 Comparison of Genotypic and Phenotypic Screening Results

The study revealed not all genotypes that phenotypically showed tolerance had the *Saltol* allele. We identified two genotypes, K5 from Uganda and Intsindagira bigega from Rwanda, that were both phenotypically salinity tolerant and in which the salinity-tolerant *Saltol* allele is present. This suggests that phenotypic screening is necessary to confirm the salinity tolerance of genotypes that possess the *Saltol* allele. Moreover, the salinity-tolerant *Saltol* allele was absent in some of the genotypes (16) which were considered phenotypically tolerant; of these, one genotype (ZX 117) was considered as tolerant while 15 genotypes were moderately tolerant (Jaribu, Kijicho, Nerica 4, SATO 1, TXD 88 Improved, Moshi wa

sigara, Mpaka wa bibi, Sukari, BR, Rumbuka, Nemeyubutaka, Terimbere, Chupa, Line 16 and Rumbuka bug 2013A) (Figure 3.3). This result highlights the need for further genotypic analysis to understand their mode of salt-tolerance. Interestingly, the study also found that some of the *Saltol*-possessing genotypes (34 genotypes) were phenotypically susceptible to salt (Figure 3.3). This result suggests that *Saltol* alone may not provide sufficient salinity tolerance and that perhaps there are other QTLs and/or factors that may be contributing to their level of salinity tolerance.

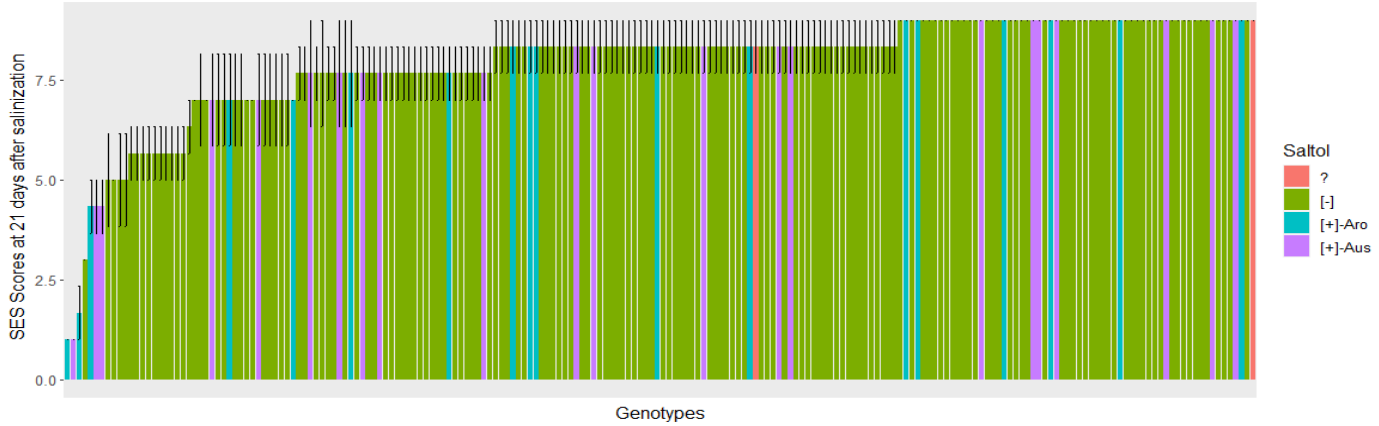

Figure 3.3: ***Saltol*** **alleles and visual scores for the genotypes selected from rice growing areas of Eastern and Southern Africa, screened for 21 days at 12 dS m^{-1} salt concentration. The scores are the average of three replication of which 1 represents (highly tolerant), 3-4.3 (tolerant), 5-5.7 (moderate tolerant), 6-8.3 (susceptible) and 9 (highly susceptible).** ***Saltol*** **alleles were determined by 1K-RiCA Single nucleotide polymorphism (SNP) assay and the bar colors indicate the** ***Saltol*** **allele. + and - indicate presence and absence of the** ***Saltol*** **allele respectively; ? indicates genotypes that were not called. Aro refers to aromatic rice and Aus refers aus rice subgroups**

3.2.4 Geographic distribution of Tanzanian genotypes in relation to Saltol alleles and SES scores

Geographical maps (Figure 3.4 and Figure 3.6) were produced to study the spatial distribution of the Tanzanian rice genotypes that have undergone phenotypic and genotypic screening for salinity tolerance. The spatial coverage of sampling locations included seven agro-climatic zones of the country, namely Central plateau, Coastal Zone, Eastern plateaux and Mountain blocks, Northern rift zone and volcanic highland, Rukwa-Ruaha rift zone, Southern highland and Ufipa plateau.

The salinity-tolerant *Saltol* allele was present in nine genotypes (7.5%) out of 120 genotypes from the sampled Tanzanian rice growing areas across eight Agroecological Zones. One out of 12 (8%) *Saltol* possessing genotypes was found in the Coastal Zone. The salinity tolerant *Saltol* allele was present in six out of 66 genotypes (9%) from the Eastern plateaux and Mountain blocks, in one of the 1 genotype (100 %) from the Northern rift zone and volcanic highlands, and in one out of 11 genotypes (9) from Rukwa-Ruaha rift zone. The salinity-tolerant *Saltol* allele was absent in the 22 genotypes, 7 genotypes and 1 genotype from Central plateau, Southern highlands and Ufipa plateau, respectively (Figure 3.4 and Figure 3.5).

Phenotypically, 11 genotypes (9.2%) out of 120 genotypes from the sampled Tanzanian rice growing areas across eight Agroecological Zones showed phenotypic salinity tolerance (SES scores less than 6). Out of 66 genotypes in the Eastern plateaux and Mountain blocks, eight genotypes (12.1 %) showed SES scores less than 6. Two out of 12 genotypes (16.7 %) were from the Coastal Zone, and one of the 22 genotypes (4.5 %) was from the Central plateau showed phenotypic salinity tolerance (SES scores less than 6). None of the genotypes from the Southern Highlands, Northern rift zone Volcanic highlands, Rukwa-Ruaha rift zone and Ufipa plateau

showed phenotypic salinity tolerance despite some of them possessing the *Saltol* allele (Figure 3.6 and Figure 3.7).

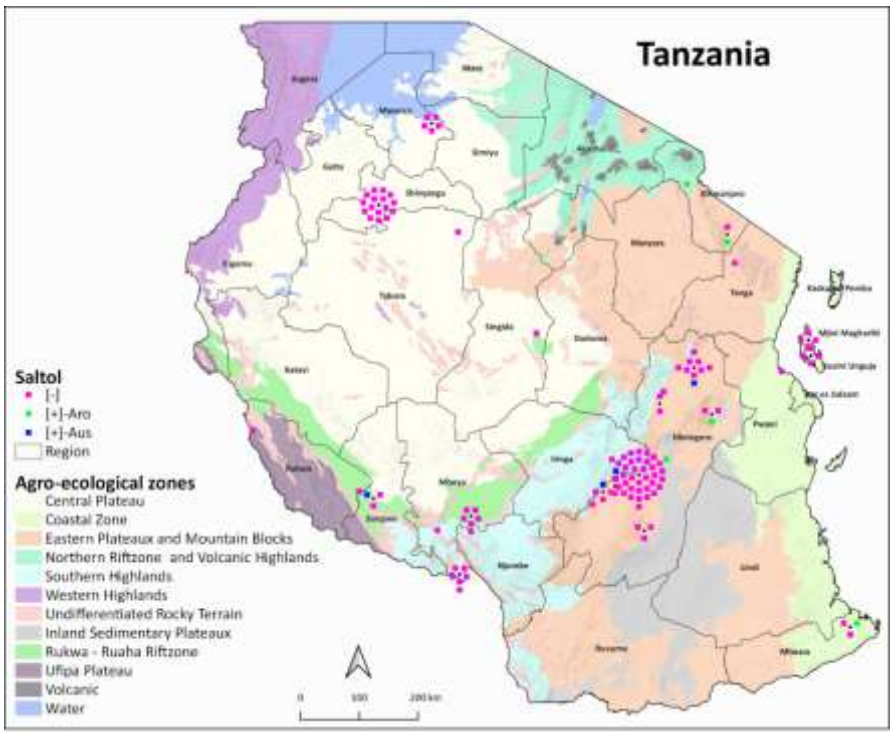

Figure 3.4: **Spatial distribution of rice genotypes showing the presence and absence of *Saltol* in the genotypes collected from Tanzania. The *Saltol* allele was identified after genotyping through 1K-Rice Custom Amplicon (1K-RiCA assay), as indicated by the symbol color. Aro refers to aromatic rice and Aus refers aus rice subgroups**

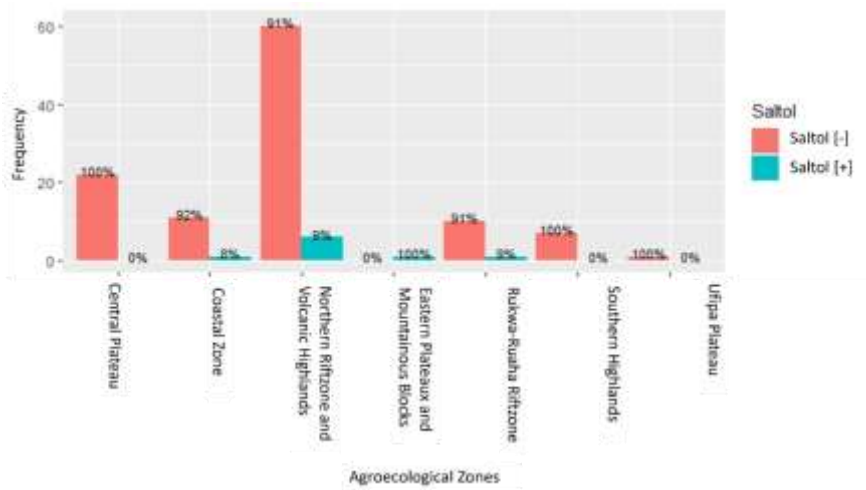

Figure 3.5: **The percentages of rice genotypes possessing the salinity-tolerant *Saltol* allele in different agro-climatic zones of Tanzania. The percentages are calculated based on the number of genotypes in which the *Saltol* allele was present out of the total number of genotypes studied from each agro-ecological zone.**

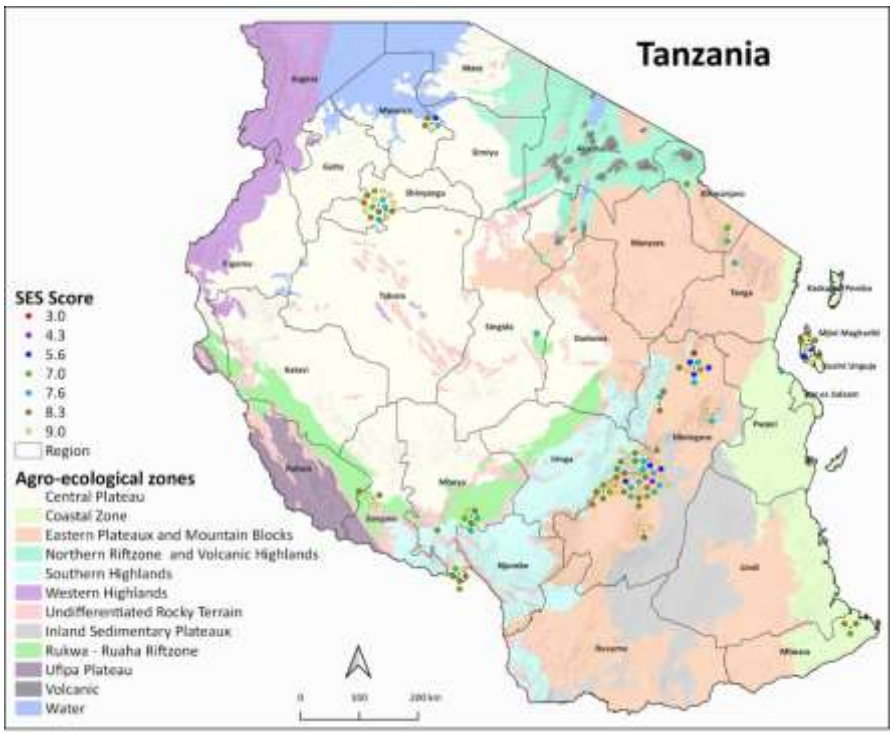

Figure 3.6: **The spatial distribution of the screened rice genotypes indicating the lowest to highest Standard evaluation system (SES) scores from rice growing areas of Tanzania screened for 21 days at 12 dS m^{-1} salt concentration. The red, purple and blue colored dots highlight the genotypes with low visual scores indicating tolerance while green, grey and yellow highlight genotypes with high visual scores indicating susceptibility (s 1: highly tolerant, 3-4.3: tolerant, 5-5.7: moderate tolerant, 6-8.3: susceptible, 9: highly susceptible.**

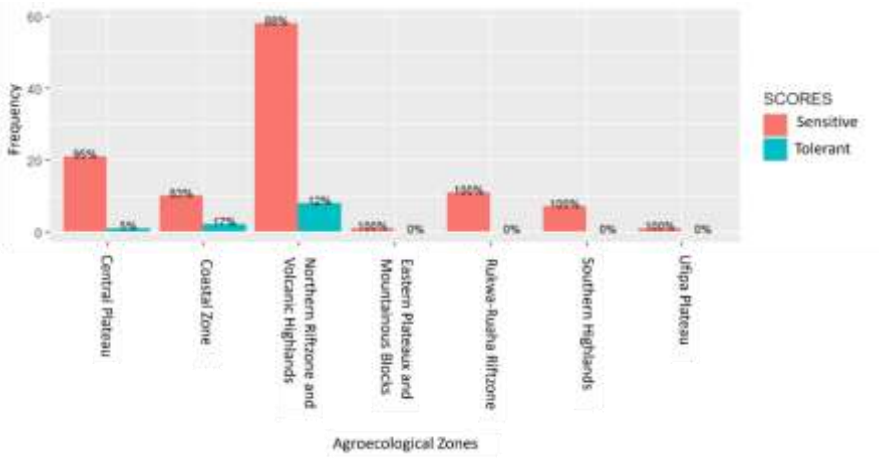

Figure 3.7: **The distribution of rice genotypes categorized as tolerant (scoring <6 under phenotypic screening) in various agro climatic zones of Tanzania. The number of genotypes studied varied across different zones.**

3.3 Discussion

The screening of rice genotypes at the seedling stage for salinity tolerance has gained widespread acceptance as a method for selecting rice genotypes that exhibit tolerance to salt stress (Tahjib-Ul- Arif *et al.,* 2018; Tabassum *et al.,* 2021). This study employed both phenotypic and genotypic screening methods to assess the salinity tolerance of a collection of landraces and improved cultivars from Eastern and Southern Africa. Genotypic screening using 1K-Rica SNP markers checked for the presence of the *Saltol* allele, a major allele responsible for salinity tolerance at seedling stage (Marè *et al.,* 2023). The Standard Evaluation System (SES) was used to evaluate genotypes for phenotypic tolerance to salinity.

Since the results indicated that the salinity tolerant *Saltol* allele was significantly more frequently present in improved cultivars than in the landraces we screened, we suggest that the *Saltol* allele may have been selectively bred or introduced in the improved genotypes to

confer certain desirable traits. We attribute the observed variability to either intentional or unintentional introgression of salinity tolerant *Saltol* allele during the breeding process. While genotypic screening indicated that improved varieties are more likely to possess *Saltol* allele, the phenotypic screening indicated non-significant difference in phenotypic tolerance between the landrace and improved genotypes. This suggests that the cultivar type may not be a major factor influencing phenotypic tolerance in this study. Other genetic or environmental factors might play a more significant role in determining the phenotypic tolerance of Eastern and Southern African rice genotypes.

The genotypes K5 and Intsindagira bigega were identified as salinity-tolerant at seedling stage exhibiting both phenotypic tolerance to salinity and the presence of the salinity-tolerant *Saltol* allele. In these genotypes, the observed tolerance may be due to low Na^+ absorption, high K^+ absorption, and a low Na^+/K^+ ratio in rice shoots under salinity stress as reported by Krishnamurthy *et al.* (2020). The *Saltol* allele functions by controlling the rate of sodium ion exclusion from the roots and their subsequent transport to the shoots. It helps to maintain a low sodium concentration in the leaves, which is vital for preventing cellular damage and maintaining proper physiological processes (Tabassum *et al.,* 202: Singh *et al.,* 2021). However, exceptions were observed in a few genotypes, such as ZX 117, SATO 1, Terimbere, Nemeyebutaka, and Rumbuka which were tolerant in the phenotypic screening but were categorized as not having *Saltol* (Figure 3.1). These results suggest that perhaps other QTLs apart from *Saltol* may be affecting the salinity tolerance at seedling stage in these genotypes. Studies have indicated that mechanisms for salt tolerance are complex since many genes are involved in salt tolerance (Singh *et al.,* 2021). A study conducted by Nguyen *et al.* (2022) on Mekong River Delta landrace “Doc Phung” indicated its tolerance to be independent of the *Saltol* allele as opposed to other varieties such as Pokkali. Therefore, these genotypes could represent new sources of salinity

tolerance and be used to develop new breeding lines with high levels of salinity tolerance at the seedling stage.

Understanding the distribution of salt-tolerant genotypes in different zones provides insights into rice plants' adaptive capabilities under varying environmental conditions. This study analyzed a panel of 120 georeferenced Tanzanian genotypes and highlighted the presence and distribution of the salinity-tolerant *Saltol* allele in various genotypes across different agro-ecological zones in Tanzania. The results revealed that the *Saltol* allele was present in some genotypes from the sampled rice growing areas, with varying frequencies in different agro-ecological zones. Despite a low number of sampled genotypes in certain areas, a high percentage of genotypes with the *Saltol* gene was observed. Additionally, the study ranked the agro-climatic zones based on phenotypic salinity tolerance, with the Coastal Zone exhibiting the highest proportion of tolerant genotypes. Among the 12 genotypes analyzed from the Coastal Zone, two (16.7%) exhibited the salinity tolerance trait, which was the highest observed phenotypic tolerance among the sampled genotypes. The observed tolerance in genotypes from the Coastal Zone may be due to the fact that local farmers and breeders historically prioritized the cultivation of rice varieties with known or observed salinity tolerance.

Some genotypes with lower SES scores under salinity stress and those having the *Saltol* allele were found in regions that are known for their salt-prone environment (Meliyo *et al.,* 2016; Kashenge-Killenga *et al.,* 2016; Omar *et al.,* 2022). Emphasizing the impact of the environment on salinity tolerance as elaborated by Manohara *et al.* (2021), who described several genotypes including Pokkali that are geographically found in low-lying areas with soil salinity. According to Bin Rahman and Zhang (2018) the tolerance could have been acquired through recurrent exposure to the salt stress in a specific geographic area and directional selection by rice farmers in these areas. Studies have indicated that adaptive selection can be

among of the major reason for varieties with tolerance to stress to be found in places where that particular stress is found. Nguyen *et al.* (2022) proposed that adaptive selection for salinity tolerance might have influenced the salinity-tolerant rice accessions originating from the salinity affected Ca Mau coastal region, similar to the indigenous varieties Nona Bokra and Pokkali, which are known for their salinity tolerance and originated from Bangladesh and coastal India where salinity stress is common, respectively. Given that certain genotypes with the *Saltol allele* and lower SES scores under salinity stress were found in regions known for their salinity-prone environments, future selection efforts should prioritize these specific geographic areas. These regions are more likely to harbor genotypes that have adapted to salinity stress.

3.4 Conclusion and Recommendations

This evaluated 201 rice genotypes from Eastern and Southern Africa to assess their phenotypic tolerance to salinity (12dS m^{-1}) and the presence of the *Saltol* allele. Findings indicate that the presence of the *Saltol* allele does not guarantee salinity tolerance during phenotypic screening. Interestingly, observed that certain genotypes exhibited salinity tolerance or moderate tolerance despite not possessing the *Saltol* allele, suggesting the presence of other novel salinity tolerance QTLs. Furthermore, the study examined the spatial distribution of phenotypically salinity-tolerant genotypes and the presence of the *Saltol* allele across Tanzania. The variations in the distribution of *Saltol* allele-possessing genotypes suggest that specific regions may hold greater potential for selection of salinity-tolerant rice genotypes. In conclusion, this study establishes an important foundation for future research aimed at improving the breeding of salinity-tolerant rice genotypes in Tanzania and Africa as a whole. The findings suggest that African rice genotypes may possess novel QTLs responsible for salinity tolerance, which can be harnessed to develop new salinity-tolerant rice varieties in Africa. To enhance future research in this area, several recommendations should be considered. Firstly, it would be beneficial to increase the

number of accessions tested and ensure a homogeneous representation across different agro-ecological zones. Additionally, underrepresented areas should be carefully analyzed to ensure a comprehensive understanding of the distribution and prevalence of salinity-tolerant genotypes. It is also important to assess the salinity tolerance of these genotypes during reproductive stages to assess their potential for enriching the gene pool of salinity-tolerant rice by addressing the recommendations outlined above, so as to advance the understanding and application of salinity tolerance traits in rice breeding programs, ultimately contributing to increased resilience and productivity in salinity-affected rice growing areas across Africa.

Author's contribution

K.K.L designed the study, conducted the screening work, collected data, conducted data analysis and drafted the manuscript. A.H, M.O, O.P, S.N, and N.L.K reviewed and edited the study concept.

Conflict of interest

Authors declares no conflict of interest

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Supplementary Materials

Table 3.1: Genotyping and phenotyping results of 120 genotypes collected from Tanzania which includes landraces, improved genotypes and advanced lines. + and - indicate presence and absence of the Saltol gene respectively. Aro refers to aromatic rice and Aus refers aus rice subgroups. The Standard Evaluation System (SES) scores (which are the average of three replications) are organized according to decreasing tolerance: 1 (highly tolerant), 3-4.3 (tolerant), 5-5.7 (moderate tolerant), 6-8.3 (susceptible) and 9 (highly susceptible).

Name	Type of Genotype	Saltol	SES Scores	Location of seed collection	Country	Latitude	Longitude
ZX 117	Improved, Released 2020	[-]	3.00	IRRI Dakawa (Gsr)	Tanzania	-6.415561	37.53627
JARIBU	Improved	[-]	5.67	TARI Ifakara	Tanzania	-8.044306	36.67619
Kijicho	Landrace	[-]	5.67	Ifakara	Tanzania	-8.044306	36.67619
NERICA 4	Improved, Released 2009	[-]	5.67	TARI Ifakara	Tanzania	-8.044306	36.67619
SATO 1	Improved, Released 2015	[-]	5.67	TARI Dakawa	Tanzania	-6.415561	37.53627
TXD 88 IMPROVED	Improved, Released 2001	[-]	5.67	IRRI Dakawa	Tanzania	-6.415561	37.53627
Moshi wa sigara	Landrace	[-]	5.67	Cheju Zanzibar	Tanzania	-6.214111	39.36561
Mpaka wa bibi	Landrace	[-]	5.67	Cheju Zanzibar	Tanzania	-6.214111	39.36561
Sukari	Landrace	[-]	5.67	Magu Mwanza	Tanzania	-2.585894	33.43631
Mwasungo	Landrace	[-]	7.00	Kyela Mbeya	Tanzania	-9.619433	33.87901
HODI HODI	Landrace	[-]	7.00	Ifakara	Tanzania	-8.132239	36.67331
Kisegese	Landrace	[-]	7.00	Mngeta Kilombero	Tanzania	-9.495553	33.84521
FAYA DUME 2	Landrace	[-]	7.00	Kapunga Mbeya	Tanzania	-8.697658	34.05161
Mbega	Landrace	[-]	7.00	Mngeta Kilombero	Tanzania	-8.323833	36.11591
Msonga	Landrace	[+]-Aus	7.00	Mngeta Kilombero	Tanzania	-8.323833	36.11591

Limota	Landrace	[-]	7.00	Ifakara	Tanzania	-8.044306	36.67619
SATO 9	Improved, Released 2015	[-]	7.00	TARI Dakawa	Tanzania	-6.415561	37.53627
Magereza	Landrace	[-]	7.00	Maore	Tanzania	-4.270058	38.0566
Kalundi	Landrace	[-]	7.00	Kahama Shinyanga	Tanzania	-3.865486	32.62878
Themanini	Landrace	[-]	7.00	Kahama Shinyanga	Tanzania	-3.859744	32.60695
Kubwa jinga	Landrace	[+]-Aro	7.00	Mawala Moshi	Tanzania	-3.535942	37.42853
Mbawa ya njiwa	Landrace	[-]	7.00	Mtwara	Tanzania	-10.4119°	39.97984
FAYA DUME 3	Landrace	[-]	7.67	Kapunga Mbeya	Tanzania	-8.702578	34.04738
Angola star	Landrace	[-]	7.67	Kapunga Mbeya	Tanzania	-8.696039	34.04946
Mbawambili	Landrace	[-]	7.67	Ifakara	Tanzania	-8.155972	36.69724
Gamti	Landrace	[-]	7.67	Ifakara	Tanzania	-8.151517	36.67718
Basmati	Landrace	[-]	7.67	TARI Ifakara	Tanzania	-8.044306	36.67619
Jaribu 220	Improved	[-]	7.67	TARI Ifakara	Tanzania	-8.044306	36.67619
NERICA 2	Improved, Released 2009	[-]	7.67	TARI Ifakara	Tanzania	-8.044306	36.67619
Loya	Improved	[-]	7.67	TARI Ifakara	Tanzania	-8.044306	36.67619
Mwangaza	Improved, Released 2006	[-]	7.67	TARI Ifakara	Tanzania	-8.044306	36.67619
TEMERIN -381	Improved	[-]	7.67	TARI Ifakara	Tanzania	-8.044306	36.67619
Gombe	Landrace	[+]-Aro	7.67	Matombo Morogoro	Tanzania	-7.122122	37.81476
Masantula	Landrace	[-]	7.67	Kilangali Kilosa	Tanzania	-6.950383	37.08395
Mbuyu	Landrace	[-]	7.67	Bagamoyo	Tanzania	-6.455283	38.90534
SUPA BC IMPROVED	Improved, Released 2020	[-]	7.67	IRRI Dakawa	Tanzania	-6.415561	37.53627
TXD 85 IMPROVED	Improved, Released 2001	[+]-Aus	7.67	IRRI Dakawa	Tanzania	-6.415561	37.53627
Faya (Chikuyu manyoni)	Landrace	[-]	7.67	Chikuyu Manyoni	Tanzania	-5.862356	35.07482
Wahiwahi	Landrace	[-]	7.67	Mkumbara Korogwe	Tanzania	-4.766081	38.17423
Moshi	Landrace	[+]-Aro	7.67	Ndungu	Tanzania	-4.375072	38.0634°
Magongo ya Wayungu	Landrace	[-]	7.67	Kahama Shinyanga	Tanzania	-3.865889	32.62803

Mdomo wa fisi	Landrace	[-]	7.67	Kahama Shinyanga	Tanzania	-3.865889	32.62803
Katumahi	Landrace	[-]	7.67	Kahama Shinyanga	Tanzania	-3.865486	32.62878
MWANZA	Landrace	[-]	7.67	Mwanza	Tanzania	-2.585894	33.43631
Kilombero	Landrace	[-]	8.33	Kyela Mbeya	Tanzania	-9.619433	33.87901
Mbawambili kyela	Landrace	[-]	8.33	Kyela Mbeya	Tanzania	-9.619433	33.87901
Kyela	Landrace	[-]	8.33	Kyela Mbeya	Tanzania	-9.616756	33.87633
Kalivumbula	Landrace	[-]	8.33	Chilombola Mahenge	Tanzania	-8.929561	36.76084
URO-01	Improved	[-]	8.33	TARI Uyole Mbeya	Tanzania	-8.919308	33.52423
FAYA DUME 4	Landrace	[-]	8.33	Kapunga Mbeya	Tanzania	-8.706922	34.05784
FAYA DUME 5	Landrace	[-]	8.33	Kapunga Mbeya	Tanzania	-8.700636	34.05103
Afaa melela	Landrace	[-]	8.33	Chita Kilombero	Tanzania	-8.519819	35.95276
Mbawambili nyeupe	Landrace	[-]	8.33	Momba	Tanzania	-8.426361	32.52823
Jambo twende	Landrace	[-]	8.33	Mngeta Kilombero	Tanzania	-8.324103	36.1149
Mzinga	Landrace	[-]	8.33	Mngeta Kilombero	Tanzania	-8.323833	36.11591
Itumbula 2	Landrace	[-]	8.33	Kamsamba	Tanzania	-8.315061	32.30243
Mbawambili rangimbili	Landrace	[-]	8.33	Ifakara	Tanzania	-8.155972	36.69724
Chambena	Landrace	[-]	8.33	Ifakara	Tanzania	-8.142942	36.6971
Kihogo	Landrace	[-]	8.33	Ifakara	Tanzania	-8.044306	36.67619
Kihogo Red Morogoro	Improved	[-]	8.33	TARI Ifakara	Tanzania	-8.044306	36.67619
Komboka	Improved, Released 2012	[-]	8.33	TARI Ifakara	Tanzania	-8.044306	36.67619
Ringa	Landrace	[-]	8.33	Ifakara	Tanzania	-8.044306	36.67619
Supa	Improved, Released 1950s	[-]	8.33	Ifakara	Tanzania	-8.044306	36.67619
Supa India	Improved, Released 50s	[-]	8.33	Ifakara	Tanzania	-8.044306	36.67619
Supa Katrin	Landrace	[-]	8.33	TARI Ifakara	Tanzania	-8.044306	36.67619
NERICA 7	Improved, Released 2009	[-]	8.33	TARI Ifakara	Tanzania	-8.044306	36.67619
Tunduru	Improved	[-]	8.33	TARI Ifakara	Tanzania	-8.044306	36.67619
WABS 450	Improved, Released 2009	[-]	8.33	TARI Ifakara	Tanzania	-8.044306	36.67619

SUPA KIJIVU	Landrace	[-]	8.33	Zombo Kilosa	Tanzania	-6.967089	36.92234
Nawa tule na Bwana	Landrace	[-]	8.33	Chanzuru	Tanzania	-6.770942	37.06261
Cherehani	Landrace	[-]	8.33	Mkindo Mvomero	Tanzania	-6.243672	37.55516
Dhahabu	Landrace	[-]	8.33	Cheju Zanzibar	Tanzania	-6.214111	39.36561
Kaniki	Landrace	[-]	8.33	Kibokwa Zanzibar	Tanzania	-5.964414	39.32434
Kia la ngawa	Landrace	[-]	8.33	Kibokwa Zanzibar	Tanzania	-5.964414	39.32434
Maua mekundu	Landrace	[-]	8.33	Kibokwa Zanzibar	Tanzania	-5.964414	39.32434
Nondo	Landrace	[-]	8.33	Kahama Shinyanga	Tanzania	-3.866103	32.62794
Faya mafuta	Landrace	[-]	8.33	Kahama Shinyanga	Tanzania	-3.862506	32.58774
Tondogoso	Landrace	[-]	8.33	Kahama Shinyanga	Tanzania	-3.859744	32.60695
Baramata	Landrace	[-]	8.33	Kahama Shinyanga	Tanzania	-3.846706	32.57981
Supa ukerewe	Landrace	[-]	8.33	Mwanza	Tanzania	-2.585894	33.43631
Afaa mwanza 1/159	Improved	[-]	8.33	Mwanza	Tanzania	-2.585333	33.43882
Mkia wa nyumbu	Landrace	[+]-Aro	8.33	Tunduru	Tanzania	-10.4119°	39.97984
Tunduru Dihimba	Landrace	[-]	8.33	Dihimba Mtwara	Tanzania	-10.4119°	39.97984
Kagiha	Landrace	[-]	8.33	Kahama Shinyanga	Tanzania	-3.8615°	32.58554
TXD 306(SARO5) IMRPOVED	Improved, Released 2002	[-]	8.33	IRRI Dakawa	Tanzania	-6.415561	37.53627
Mwarabu	Landrace	[-]	9.00	Kyela Mbeya	Tanzania	-9.619433	33.87901
Lingwelingweli	Landrace	[-]	9.00	Chilombola Mahenge	Tanzania	-8.924731	36.75892
Tosa	Landrace	[-]	9.00	Chilombola Mahenge	Tanzania	-8.924731	36.75892
FAYA DUME 1	Landrace	[-]	9.00	Kapunga Mbeya	Tanzania	-8.700403	34.05197
Kalamata	Landrace	[-]	9.00	Momba	Tanzania	-8.426361	32.52823
Serena	Landrace	[+]-Aus	9.00	Ivuna Momba	Tanzania	-8.426361	32.52823
Shingo ya mwali	Landrace	[-]	9.00	Mofu Kilombero	Tanzania	-8.292008	36.34307
Mbawa mbili mwekundu	Landrace	[-]	9.00	Mbingu, Kilombero	Tanzania	-8.176903	36.25584
Afaa kikangaga	Landrace	[-]	9.00	Ifakara	Tanzania	-8.148869	36.66468
Kalalu	Improved, Released 2006	[-]	9.00	TARI Ifakara	Tanzania	-8.143217	36.69702

Kaling'anaula	Landrace	[-]	9.00	Ifakara	Tanzania	-8.143217	36.69702
Kihogo red	Improved	[-]	9.00	Ifakara	Tanzania	-8.044306	36.67619
NERICA 1	Improved, Released 2009	[-]	9.00	TARI Ifakara	Tanzania	-8.044306	36.67619
Pishori(brown)	Improved	[-]	9.00	TARI Ifakara	Tanzania	-8.044306	36.67619
Rangi mbili	Landrace	[-]	9.00	Ifakara	Tanzania	-8.044306	36.67619
Rangimbili nyekundu	Landrace	[-]	9.00	Ifakara	Tanzania	-8.044306	36.67619
Sotea	Improved	[-]	9.00	TARI Ifakara	Tanzania	-8.044306	36.67619
Supa kijicho	Landrace	[+]-Aus	9.00	Ifakara	Tanzania	-8.044306	36.67619
Usiniguse	Landrace	[-]	9.00	Ifakara	Tanzania	-8.044306	36.67619
WITA 9	Improved	[+]-Aro	9.00	TARI Ifakara	Tanzania	-8.044306	36.67619
Zambia	Landrace	[-]	9.00	Ifakara	Tanzania	-8.044306	36.67619
Sumbawanga	Improved	[-]	9.00	Kirando Sumbawanga	Tanzania	-7.375347	30.6375
Lunyuki	Landrace	[-]	9.00	Matombo Morogoro	Tanzania	-7.121289	37.81294
Mleke alongole	Landrace	[-]	9.00	Matombo Morogoro	Tanzania	-7.121289	37.81294
TXD 307	Improved, Released 2022	[-]	9.00	TARI Dakawa	Tanzania	-6.415561	37.53627
BKN/SUPA	Improved	[-]	9.00	Cheju Zanzibar	Tanzania	-6.214111	39.36561
Niwahi	Landrace	[-]	9.00	Upenja Zanzibar	Tanzania	-5.985122	39.32899
Mzungu	Landrace	[-]	9.00	Igunga Tabora	Tanzania	-4.282944	33.84996
Mabula	Landrace	[-]	9.00	Shinyanga	Tanzania	-3.865725	32.62935
Sifara	Landrace	[-]	9.00	Kahama Shinyanga	Tanzania	-3.865486	32.62871
Sindano kubwa	Landrace	[-]	9.00	Kahama Shinyanga	Tanzania	-3.862419	32.60319
Sindano nyeupe	Landrace	[-]	9.00	Kahama Shinyanga	Tanzania	-3.862419	32.60319
Simzito	Landrace	[-]	9.00	Kahama Shinyanga	Tanzania	-3.862031	32.60544
Domo la fisi	Landrace	[-]	9.00	Kahama Shinyanga	Tanzania	-3.844381	32.58185
AFAA MWANZA	Landrace	[-]	9.00	Mwanza	Tanzania	-2.585894	33.43631

Table 3.2: Genotyping and Phenotyping results of 86 genotypes not from Tanzania but from other countries in Africa, which includes landraces, improved varieties, breeding lines, advanced lines and sensitive and tolerant checks for salinity). + and - indicates presence and absence of the Saltol gene respectively. Aro refers to aromatic rice and Aus refers aus rice subgroups. The Standard Evaluation System (SES) scores are organized according to decreasing tolerance: 1 (highly tolerant), 3-4.3 (tolerant), 5-5.7 (moderate tolerant), 6-8.3 (susceptible) and 9 (highly susceptible).

Name	Genotype Type	Saltol	SES Scores (Average of three replications)	Country
Pokkali	Tolerant check	[+]-Aro	1.00	Philippines
FL 478	Tolerant check	[+]-Aus	1.00	Philippines
Nona Bokra	Tolerant check	[+]-Aro	1.67	Philippines
K 5	Improved	[+]-Aro	4.33	Uganda
INTSINDAGIRA BIGEGA	Improved	[+]-Aus	4.33	Rwanda
CSR 28	Tolerant check	[+]-Aus	4.33	Philippines
BR	Improved	[-]	5.00	Rwanda
RUMBUKA	Improved	[-]	5.00	Rwanda
Nemeyubutaka	Improved	[-]	5.00	Rwanda
TERIMBERE (LL29)	Landrace	[-]	5.00	Rwanda
Chupa	Landrace	[-]	5.67	Mozambique
LINE 16	Improved	[-]	5.67	Kenya
RUMBUKA bug 2013A	Improved	[-]	5.67	Rwanda
Duorado precose	Improved	[-]	7.00	Kenya
Intsinzi	Improved	[+]-Aus	7.00	Rwanda
Ndamirabahinzi	Improved	[-]	7.00	Rwanda
IR14D121	Improved	[-]	7.00	Burundi
BRRI Dhan 28	Improved	[+]-Aro	7.00	Philippines
BG 90-2	Improved	[+]-Aus	7.67	Kenya

FRX 92-14	**Improved**	**[-]**	**7.67**	**Malawi**
FASHINGABO (Bug2013A)	**Improved**	**[-]**	**7.67**	**Rwanda**
Gakire	**Improved**	**[+]-Aus**	**7.67**	**Rwanda**
IB 126 (BUG 2013A)	**Improved**	**[-]**	**7.67**	**Rwanda**
IRRI 213	**Improved**	**[+]-Aus**	**7.67**	**Unknown**
IRRI 79511 (GWIZUMWIMBU)	**Improved**	**[-]**	**7.67**	**Burundi**
JYAMBERE (Bug2013A)	**Improved**	**[+]-Aus**	**7.67**	**Rwanda**
Kachambo	**Landrace**	**[-]**	**7.67**	**Malawi**
FRX 78-12	**Improved**	**[-]**	**7.67**	**Malawi**
LINE-18-NIWUR 1	**Improved**	**[-]**	**7.67**	**Kenya**
NERICA 10	**Improved**	**[-]**	**7.67**	**Unknown**
Basmati 370	**Improved**	**[+]-Aro**	**8.33**	**India**
BR 153	**Improved**	**[-]**	**8.33**	**Kenya**
Salinas 27	**Improved**	**[+]-Aro**	**8.33**	**Burundi**
Chamoto	**Landrace**	**[+]-Aro**	**8.33**	**Unknown**
FAYA 14M69	**Improved**	**[-]**	**8.33**	**Unknown**
HUA 565	**Improved**	**[+]-Aus**	**8.33**	**Mozambique**
INGWIZABUKUNGU UL 26	**Improved**	**[-]**	**8.33**	**Rwanda**
IR 16T1067	**Improved**	**[-]**	**8.33**	**Burundi**
IR 16T1339	**Improved**	**[+]-Aus**	**8.33**	**Burundi**
Ediget (wab 189-b-b-b hb)	**Improved**	**[-]**	**8.33**	**Ethopia**
IRRI 214 (TAI)	**Improved**	**[-]**	**8.33**	**Unknown**
ITA 304	**Improved**	**[-]**	**8.33**	**Kenya**
Kanamalia	**Landrace**	**[-]**	**8.33**	**Malawi**
KIGEGA	**Improved**	**[+]-Aro**	**8.33**	**Rwanda**
KUNGAHARA (Bug 2011A)	**Improved**	**[-]**	**8.33**	**Rwanda**
Lifumba	**Landrace**	**[-]**	**8.33**	**Malawi**
Lifuwu	**Landrace**	**[+]-Aus**	**8.33**	**Malawi**
LINE 11 WARDA	**Improved**	**[-]**	**8.33**	**Kenya**
LINE-8A-2	**Improved**	**[-]**	**8.33**	**Kenya**
IR 127793-849-1-1-1-3	**Improved**	**[-]**	**8.33**	**Burundi**
IR 15T1302	**Improved**	**?**	**8.33**	**Burundi**
Nzahara	**Improved**	**[+]-Aus**	**8.33**	**Rwanda**

ROJOMENA 271/10	**Improved**	**[+]-Aus**	**8.33**	**Ethopia**
FRX 472	**Improved**	**[-]**	**8.33**	**Malawi**
IR 13240-108-2-2-3	**Improved**	**[-]**	**8.33**	**Kenya**
Tarabinzona	**Improved**	**[-]**	**8.33**	**Rwanda**
Umanho	**Improved**	**[-]**	**8.33**	**Unknown**
Waya	**Landrace**	**[-]**	**8.33**	**Unknown**
Yunyin	**Improved**	**[-]**	**8.33**	**Rwanda**
Basmati 217	**Improved**	**[+]-Aro**	**9.00**	**India**
BW 196	**Improved**	**[+]-Aro**	**9.00**	**Kenya**
Chimdima	**Landrace**	**[-]**	**9.00**	**Malawi**
Cyicaro	**Improved**	**[-]**	**9.00**	**Rwanda**
FAC 56	**Improved**	**[-]**	**9.00**	**Rwanda**
Farcago 906	**Improved**	**[-]**	**9.00**	**Rwanda**
Fashingabo	**Improved**	**[-]**	**9.00**	**Rwanda**
Faya karonga	**Landrace**	**[-]**	**9.00**	**Malawi**
Gigante	**Improved**	**[-]**	**9.00**	**Unknown**
IR 16T1348	**Improved**	**[-]**	**9.00**	**Burundi**
IR 18T1015	**Improved**	**[+]-Aus**	**9.00**	**Burundi**
IR 2793-80-1	**Improved**	**[-]**	**9.00**	**Burundi**
Iron	**Improved**	**[-]**	**9.00**	**Rwanda**
IRRI 77713 (VYUNINZARA)	**Improved**	**[-]**	**9.00**	**Burundi**
ITA 310	**Improved**	**[+]-Aro**	**9.00**	**Kenya**
Kachikope	**Landrace**	**[-]**	**9.00**	**Malawi**
IR 121183-5-2-1-1-B	**Improved**	**[+]-Aus**	**9.00**	**Burundi**
IR 117834-12-1 RGA-1 RGA-1 RGA-2	**Improved**	**[+]-Aus**	**9.00**	**Burundi**
IR 127795-1121-1-1-2-1	**Improved**	**[+]-Aro**	**9.00**	**Burundi**
Kivuli	**Landrace**	**[+]-Aus**	**9.00**	**Unknown**
WAT 317-WAS-B-55-11-3-5-1	**Improved**	**[-]**	**9.00**	**Kenya**
Mpembuke	**Landrace**	**[-]**	**9.00**	**Rwanda**
Mwana matongo 2	**Landrace**	**[-]**	**9.00**	**Malawi**
IR 117831-11-1 RGA-1 RGA-1 RGA-1	**Improved**	**[+]-Aro**	**9.00**	**Burundi**
IR 117842-11-1 RGA-1 RGA-1 RGA-2	**Improved**	**[-]**	**9.00**	**Burundi**
V 18	**Improved**	**[+]-Aus**	**9.00**	**Burundi**
IRRI 154	**Sensitive check**	**?**	**9.00**	**Philippines**

CHAPTER FOUR

4.0 GENERAL DISCUSSION

Salinity stress has adverse effects on plant water and nutrient relations, leading to decreased biomass production. Various growth parameters respond diversely to salinity stress, the majority of genotypes exhibit higher vulnerability in terms of root and shoot dry weights. This susceptibility can be attributed to disturbances in osmotic equilibrium, resulting in diminished biomass accumulation. Among genotypes, there is variability in salinity tolerance, with some demonstrating lesser reduction in growth parameters.

Physiological responses highlight that excessive Na^+ intake disrupts K^+ uptake, causing an imbalanced ionic state. Certain genotypes, such as Intsindagira Bigega and K5, maintain lower Na^+/K^+ ratios, indicating their tolerance. Canopy temperature also relates to tolerance, lower temperatures signify higher tolerance to salinity stress, signifying genotype's high ability to stomata conductance. Principal Component Analysis identifies critical factors influencing salinity tolerance, including K^+ levels, root and shoot dry weights, shoot length, and survival rate. Genotypes with moderate tolerance, like K5, are recognized and recommended for breeding initiatives.

Both genotypic and phenotypic screenings reveal that there are some genotypes that possess the salinity-tolerant *Saltol* allele and also exhibitic phenotypic tolerance to salinity stress. Genotypes like K5 and Intsindagira bigega exhibit tolerance due to limited Na^+ absorption and elevated K^+ absorption. The mechanisms are complex, as some genotypes remain tolerant despite lacking the *Saltol* allele, suggesting other factors or QTL may be responsible for observed tolerance. Geographical adaptation also plays a role, with tolerant genotypes often located in areas prone to salinity. This study underscores the significance of considering multiple factors, such as genetic markers and environmental adaptation, when selecting rice genotypes tolerant to salinity

CHAPTER FIVE

5.0 GENERAL CONCLUSION AND RECOMMENDATIONS

5.1 General Conclusion

In conclusion, the study has effectively achieved its main objective of identifying salt-tolerant rice genotypes with potential applications in breeding programs targeted at addressing salinity challenges within rice-growing areas of Eastern and Southern Africa. By conducting assessments of selected rice genotypes, particularly focusing on their performance under salt stress during the seedling stage, the research outcomes have illuminated crucial insights into enhancing the salinity tolerance of rice varieties. Manuscript 1 provided a detailed evaluation of morpho-physiological parameters, revealing significant differences in performance among genotypes. The use of principal component analysis highlighted key variables offering a valuable perspective on salt tolerance. Notably, several moderately tolerant genotypes emerged, showcasing their promise for future breeding endeavors. Building on this foundation, Manuscript 2 extended the investigation to encompass genotypic assessments and geographical distribution analyses. The finding that the presence of the *Saltol* allele does not solely dictate phenotypic salinity tolerance underscores the complexity of tolerance mechanisms and the potential influence of novel QTLs. The variations in allele presence across different regions further emphasized the importance of tailored breeding strategies based on geographic considerations. Collectively, these findings underscore the significance of adopting a comprehensive research approach, merging genetic insights with practical screening techniques, to unlock the full potential of rice genotypes for enhanced salinity resilience. By contributing to the advancement of rice breeding programs, this study offers prospects for supporting food security in regions where salinity-induced stresses threaten rice cultivation.

5.2 General Recommendations

Based on the findings from both manuscripts, several recommendations can be proposed to guide future research and rice breeding efforts focused on enhancing salinity tolerance.

i. To further advance the understanding of salinity tolerance mechanisms, it is crucial to conduct extensive genotypic screening encompassing a broader range of landrace rice accessions. This would contribute to the identification of additional tolerant genotypes and novel mechanisms that underpin salinity tolerance.
ii. The study recommends more equal representation across various agro-ecological zones to capture the spatial heterogeneity of salinity stress conditions.
iii. In parallel, detailed evaluations during reproductive stages are essential to ascertain the genotypes' performance under more complex physiological scenarios.
iv. The of tolerant to moderately tolerant promising genotypes lacking the *Saltol* allele highlights the need for comprehensive genetic studies to unveil these alternative tolerance mechanisms.

APPENDICES

Appendix 1: Mean ± standard errors of phenotypic parameters for different rice varieties under salinity (12 dS/m) and non-saline condition (Experiment 1)

VARIETY	Salinity	Score	Survival	SL	RL	SDW	RDW	RDWOVERSDW
AFAA MWANZA	0	1 ± 0	100 ± 0	54.43 ± 0.35	21.03 ± 0.2	343.33 ± 23.33	123.33 ± 6.67	0.36 ± 0.04
	12	9 ± 0	0 ± 0	20.93 ± 0.78	14.4 ± 0.26	53.33 ± 3.33	10 ± 0	0.19 ± 0.01
Afaa kikangaga	0	1 ± 0	100 ± 0	45.78 ± 0.88	22.12 ± 1.84	210 ± 43.59	90 ± 20	0.42 ± 0.04
	12	9 ± 0	0 ± 0	18.73 ± 1.03	17.4 ± 0.67	36.67 ± 3.33	13.33 ± 3.33	0.36 ± 0.07
Afaa melela	0	1 ± 0	100 ± 0	40.52 ± 0.66	25.41 ± 1.18	210 ± 15.28	106.67 ± 6.67	0.52 ± 0.06
	12	8.33 ± 0.67	8.33 ± 8.33	21.32 ± 0.27	19.17 ± 0.73	36.67 ± 3.33	10 ± 0	0.28 ± 0.03
Afaa mwanza 1/159	0	1 ± 0	100 ± 0	41.07 ± 1.01	20.73 ± 1.04	353.33 ± 32.83	120 ± 5.77	0.35 ± 0.04
	12	8.33 ± 0.67	10 ± 10	17.53 ± 0.52	16.16 ± 1.01	43.33 ± 3.33	10 ± 0	0.23 ± 0.02
Angola star	0	1 ± 0	100 ± 0	45.2 ± 0.7	21.44 ± 1.16	340 ± 11.55	136.67 ± 3.33	0.4 ± 0.01
	12	7.67 ± 0.67	16.67 ± 8.82	21.39 ± 0.57	14.3 ± 1.29	40 ± 0	13.33 ± 3.33	0.33 ± 0.08
BG 90-2	0	1 ± 0	100 ± 0	30.71 ± 0.6	22.12 ± 0.88	283.33 ± 12.02	106.67 ± 3.33	0.38 ± 0
	12	7.67 ± 1.33	13.33 ± 13.33	14.13 ± 0.59	13.87 ± 0.32	30 ± 0	10 ± 0	0.33 ± 0
BKN/SUPA	0	1 ± 0	100 ± 0	46.97 ± 0.72	22.84 ± 0.68	283.33 ± 8.82	116.67 ± 3.33	0.41 ± 0.02
	12	9 ± 0	0 ± 0	17.98 ± 0.65	14.3 ± 0.51	23.33 ± 3.33	40 ± 30	1.44 ± 0.94
BR	0	1 ± 0	100 ± 0	50.24 ± 0.57	25.94 ± 0.97	303.33 ± 12.02	110 ± 0	0.36 ± 0.02
	12	5 ± 1.15	58.33 ± 6.01	31.93 ± 2.43	22.16 ± 0.35	83.33 ± 24.04	20 ± 0	0.28 ± 0.07
BR 153	0	1 ± 0	100 ± 0	32.37 ± 0.71	23.86 ± 0.33	246.67 ± 8.82	106.67 ± 3.33	0.43 ± 0.03

BR 153	12	8.33 ± 0.67	10 ± 10	16.6 ± 0.45	18.2 ± 0.61	33.33 ± 3.33	16.67 ± 3.33	0.5 ± 0.1
BRRI Dhan 28	0	1 ± 0	100 ± 0	32.87 ± 0.7	21.74 ± 0.78	203.33 ± 18.56	106.67 ± 3.33	0.54 ± 0.06
	12	7 ± 0	35 ± 8.66	18.79 ± 0.79	17.33 ± 1	30 ± 5.77	10 ± 0	0.36 ± 0.07
BW 196	0	1 ± 0	100 ± 0	31.24 ± 0.23	22.68 ± 0.89	176.67 ± 14.53	100 ± 10	0.56 ± 0.02
	12	9 ± 0	0 ± 0	17 ± 0.76	20.37 ± 0.57	26.67 ± 3.33	13.33 ± 3.33	0.55 ± 0.22
Baramata	0	1 ± 0	100 ± 0	48.06 ± 1.16	25.1 ± 0.38	230 ± 15.28	126.67 ± 6.67	0.55 ± 0.03
	12	8.33 ± 0.67	6.67 ± 6.67	21.89 ± 0.85	15.8 ± 0.49	36.67 ± 3.33	10 ± 0	0.28 ± 0.03
Basmati	0	1 ± 0	100 ± 0	30.68 ± 0.42	21.1 ± 1.05	293.33 ± 6.67	116.67 ± 3.33	0.4 ± 0.02
	12	7.67 ± 0.67	23.33 ± 12.02	19.59 ± 0.55	17.2 ± 0.47	40 ± 0	10 ± 0	0.25 ± 0
Basmati 217	0	1 ± 0	100 ± 0	40.07 ± 0.66	18.47 ± 0.85	203.33 ± 8.82	93.33 ± 6.67	0.46 ± 0.02
	12	9 ± 0	0 ± 0	17.52 ± 0.56	16.14 ± 0.96	20 ± 0	10 ± 0	0.5 ± 0
Basmati 370	0	1 ± 0	100 ± 0	37.21 ± 0.78	17.97 ± 0.48	183.33 ± 12.02	106.67 ± 8.82	0.59 ± 0.09
	12	8.33 ± 0.67	10 ± 10	17.06 ± 0.24	14.68 ± 0.19	20 ± 5.77	10 ± 0	0.61 ± 0.2
CSR 28	0	1 ± 0	100 ± 0	37.9 ± 0.49	18.43 ± 0.34	283.33 ± 27.28	120 ± 0	0.43 ± 0.04
	12	4.33 ± 0.67	78.33 ± 4.41	27.18 ± 0.98	16.87 ± 0.19	116.67 ± 21.86	30 ± 0	0.27 ± 0.04
Chambena	0	1 ± 0	100 ± 0	51.48 ± 0.67	27.38 ± 1.21	273.33 ± 6.67	110 ± 0	0.4 ± 0.01
	12	8.33 ± 0.67	11.67 ± 11.67	24.17 ± 0.88	15.49 ± 0.16	50 ± 5.77	10 ± 0	0.21 ± 0.02
Chamoto	0	1 ± 0	100 ± 0	36.44 ± 0.35	19.78 ± 1.52	163.33 ± 8.82	96.67 ± 13.33	0.59 ± 0.06
	12	8.33 ± 0.67	11.67 ± 11.67	14.93 ± 0.23	13.7 ± 0.47	30 ± 0	13.33 ± 3.33	0.44 ± 0.11
Cherehani	0	1 ± 0	100 ± 0	47.86 ± 0.68	20.07 ± 0.23	263.33 ± 8.82	120 ± 0	0.46 ± 0.01
	12	8.33 ± 0.67	10 ± 10	21.82 ± 0.8	15 ± 0.4	43.33 ± 3.33	10 ± 0	0.23 ± 0.02

Chimdima	0	1 ± 0	100 ± 0	45.26 ± 0.7	19.46 ± 0.51	256.67 ± 8.82	103.33 ± 8.82	0.4 ± 0.05
	12	9 ± 0	0 ± 0	21.67 ± 0.71	15.47 ± 0.5	43.33 ± 6.67	10 ± 0	0.24 ± 0.04
Chupa	0	1 ± 0	100 ± 0	48.37 ± 0.37	23.8 ± 1.67	240 ± 30.55	103.33 ± 6.67	0.44 ± 0.05
	12	5.67 ± 0.67	53.33 ± 7.26	24.84 ± 2	17.5 ± 1.15	90 ± 5.77	13.33 ± 3.33	0.15 ± 0.03
Cyicaro	0	1 ± 0	100 ± 0	40.86 ± 0.28	23.23 ± 1.07	306.67 ± 17.64	133.33 ± 6.67	0.44 ± 0.05
	12	9 ± 0	0 ± 0	18.24 ± 0.6	16.68 ± 1.45	30 ± 0	10 ± 0	0.33 ± 0
Dhahabu	0	1 ± 0	100 ± 0	52.93 ± 0.55	23.38 ± 0.53	283.33 ± 14.53	113.33 ± 3.33	0.4 ± 0.01
	12	8.33 ± 0.67	8.33 ± 8.33	21.38 ± 0.58	15.52 ± 1.52	40 ± 0	13.33 ± 3.33	0.33 ± 0.08
Domo la fisi	0	1 ± 0	100 ± 0	47.01 ± 1.02	21.98 ± 0.94	313.33 ± 6.67	106.67 ± 8.82	0.34 ± 0.03
	12	9 ± 0	0 ± 0	22.32 ± 0.55	15.48 ± 1.25	46.67 ± 3.33	10 ± 0	0.22 ± 0.02
Duorado precose	0	1 ± 0	100 ± 0	47.03 ± 0.43	24.67 ± 1	253.33 ± 3.33	113.33 ± 3.33	0.45 ± 0.01
	12	7 ± 0	23.33 ± 3.33	25.06 ± 0.74	21.31 ± 0.87	43.33 ± 3.33	10 ± 0	0.23 ± 0.02
Ediget (wab 189-b-b-b hb)	0	1 ± 0	100 ± 0	43.66 ± 0.95	19.73 ± 0.43	306.67 ± 17.64	123.33 ± 8.82	0.4 ± 0.02
	12	8.33 ± 0.67	6.67 ± 6.67	22.88 ± 1.44	16.21 ± 0.32	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
FAC 56	0	1 ± 0	100 ± 0	36.49 ± 0.47	28.56 ± 1.2	320 ± 15.28	116.67 ± 3.33	0.36 ± 0.03
	12	9 ± 0	0 ± 0	15.14 ± 0.19	16.62 ± 0.7	23.33 ± 3.33	10 ± 0	0.44 ± 0.06
FASHINGABO (Bug2013A)	0	1 ± 0	100 ± 0	32.73 ± 1.05	21.97 ± 0.75	346.67 ± 3.33	126.67 ± 3.33	0.36 ± 0.01
	12	7.67 ± 1.33	15 ± 15	14.93 ± 0.18	13.1 ± 0.55	23.33 ± 3.33	10 ± 0	0.44 ± 0.06
FAYA 14M69	0	1 ± 0	100 ± 0	48.77 ± 3.07	25.79 ± 0.21	356.67 ± 12.02	130 ± 11.55	0.36 ± 0.03
	12	8.33 ± 0.67	13.33 ± 13.33	21.62 ± 1.21	15.68 ± 1.47	36.67 ± 3.33	11 ± 1	0.3 ± 0.03
FAYA DUME 1	0	1 ± 0	100 ± 0	49.86 ± 0.78	21.93 ± 0.83	206.67 ± 6.67	116.67 ± 3.33	0.57 ± 0.03

	12	9 ± 0	0 ± 0	18.98 ± 0.75	17.22 ± 0.33	30 ± 0	10 ± 0	0.33 ± 0
FAYA DUME 2	0	1 ± 0	100 ± 0	49.47 ± 0.44	20.41 ± 0.63	343.33 ± 12.02	130 ± 5.77	0.38 ± 0.02
	12	7 ± 1.15	16.67 ± 8.82	25.66 ± 1.18	16.24 ± 0.93	30 ± 0	10 ± 0	0.33 ± 0
FAYA DUME 3	0	1 ± 0	100 ± 0	50.47 ± 1.18	22.89 ± 1.16	343.33 ± 8.82	126.67 ± 8.82	0.37 ± 0.02
	12	7.67 ± 0.67	16.67 ± 8.82	22.42 ± 1.28	15.21 ± 1.16	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
FAYA DUME 4	0	1 ± 0	100 ± 0	32.21 ± 0.74	28.02 ± 1.2	246.67 ± 3.33	110 ± 0	0.45 ± 0.01
	12	8.33 ± 0.67	11.67 ± 11.67	18.46 ± 0.36	16.18 ± 0.34	46.67 ± 3.33	10 ± 0	0.22 ± 0.02
FAYA DUME 5	0	1 ± 0	100 ± 0	34.34 ± 0.55	26.31 ± 0.4	210 ± 23.09	106.67 ± 8.82	0.51 ± 0.02
	12	8.33 ± 0.67	8.33 ± 8.33	16.28 ± 0.43	16.7 ± 0.59	43.33 ± 3.33	13.33 ± 3.33	0.3 ± 0.05
FL 478	0	1 ± 0	100 ± 0	39.93 ± 0.64	20.59 ± 0.69	293.33 ± 43.33	110 ± 5.77	0.38 ± 0.04
	12	1 ± 0	100 ± 0	28.7 ± 0.9	16.09 ± 0.39	180 ± 30	43.33 ± 3.33	0.27 ± 0.08
FRX 472	0	1 ± 0	100 ± 0	36.17 ± 1.32	21.29 ± 0.76	230 ± 11.55	100 ± 5.77	0.44 ± 0.03
	12	8.33 ± 0.67	8.33 ± 8.33	16.38 ± 0.44	15.87 ± 0.93	46.67 ± 3.33	13.33 ± 3.33	0.28 ± 0.06
FRX 78-12	0	1 ± 0	100 ± 0	30.76 ± 0.58	24.7 ± 0.96	220 ± 15.28	100 ± 5.77	0.46 ± 0.05
	12	7.67 ± 0.67	10 ± 5.77	19.89 ± 1.07	16.99 ± 0.91	53.33 ± 3.33	10 ± 0	0.19 ± 0.01
FRX 92-14	0	1 ± 0	100 ± 0	32.19 ± 0.76	26.19 ± 0.35	313.33 ± 8.82	113.33 ± 3.33	0.36 ± 0.02
	12	7.67 ± 0.67	15 ± 7.64	17.27 ± 0.79	15.61 ± 0.62	43.33 ± 3.33	10 ± 0	0.23 ± 0.02
Farcago 906	0	1 ± 0	100 ± 0	37.36 ± 0.82	30.11 ± 1.98	313.33 ± 8.82	130 ± 0	0.41 ± 0.01
	12	9 ± 0	0 ± 0	17.76 ± 0.22	13.67 ± 0.41	40 ± 0	10 ± 0	0.25 ± 0
Fashingabo	0	1 ± 0	100 ± 0	40.58 ± 0.81	22.63 ± 2.11	350 ± 17.32	113.33 ± 3.33	0.32 ± 0.01
	12	9 ± 0	0 ± 0	17.89 ± 0.7	15.58 ± 0.65	43.33 ± 3.33	10 ± 0	0.23 ± 0.02
Faya (Chikuyu manyoni)	0	1 ± 0	100 ± 0	50.54 ± 1.05	23.57 ± 0.23	336.67 ± 8.82	113.33 ± 3.33	0.33 ± 0.01

	12	7.67 ± 0.67	13.33 ± 7.26	23.03 ± 0.78	16.08 ± 0.78	46.67 ± 3.33	20 ± 0	0.43 ± 0.03
Faya karonga	0	1 ± 0	100 ± 0	45.61 ± 1.02	27.42 ± 0.42	306.67 ± 12.02	133.33 ± 3.33	0.43 ± 0.01
	12	9 ± 0	0 ± 0	21.31 ± 1	14.27 ± 0.92	40 ± 0	13.33 ± 3.33	0.33 ± 0.08
Faya mafuta	0	1 ± 0	100 ± 0	42.43 ± 0.96	17.77 ± 0.23	300 ± 17.32	120 ± 11.55	0.4 ± 0.03
	12	8.33 ± 0.67	8.33 ± 8.33	21.06 ± 0.28	15.58 ± 0.37	46.67 ± 3.33	20 ± 0	0.43 ± 0.03
Gakire	0	1 ± 0	100 ± 0	31.26 ± 0.92	27.87 ± 1.04	246.67 ± 6.67	120 ± 17.32	0.49 ± 0.06
	12	7.67 ± 1.33	10 ± 10	16.61 ± 0.58	16.09 ± 0.31	50 ± 0	13.33 ± 3.33	0.27 ± 0.07
Gamti	0	1 ± 0	100 ± 0	47.61 ± 1.02	19.07 ± 0.29	256.67 ± 12.02	116.67 ± 3.33	0.46 ± 0.01
	12	7.67 ± 1.33	8.33 ± 8.33	23.94 ± 0.75	16.96 ± 0.15	46.67 ± 3.33	13.33 ± 3.33	0.28 ± 0.06
Gigante	0	1 ± 0	100 ± 0	45 ± 0.4	26.77 ± 1.18	326.67 ± 12.02	123.33 ± 8.82	0.38 ± 0.04
	12	9 ± 0	0 ± 0	21.87 ± 0.59	20.54 ± 2.03	116.67 ± 86.67	20 ± 0	0.47 ± 0.2
Gombe	0	1 ± 0	100 ± 0	44.18 ± 0.7	19.51 ± 1.14	236.67 ± 6.67	106.67 ± 8.82	0.45 ± 0.04
	12	7.67 ± 1.33	11.67 ± 11.67	23.56 ± 0.34	16.47 ± 0.75	33.33 ± 3.33	13.33 ± 3.33	0.39 ± 0.06
HODI HODI	0	1 ± 0	100 ± 0	32.9 ± 1.03	21.19 ± 1.89	233.33 ± 17.64	110 ± 5.77	0.47 ± 0.01
	12	7 ± 0	50 ± 5.77	21.2 ± 0.96	17.8 ± 0.7	26.67 ± 3.33	16.67 ± 3.33	0.67 ± 0.19
HUA 565	0	1 ± 0	100 ± 0	32.22 ± 0.89	18.36 ± 0.95	280 ± 10	110 ± 5.77	0.39 ± 0.02
	12	8.33 ± 0.67	5 ± 5	18.06 ± 0.73	15.8 ± 0.91	23.33 ± 3.33	10.67 ± 0.67	0.47 ± 0.03
IB 126 (BUG 2013A)	0	1 ± 0	100 ± 0	37.49 ± 0.36	27.93 ± 0.07	253.33 ± 14.53	193.33 ± 58.4	0.75 ± 0.18
	12	7.67 ± 0.67	15 ± 7.64	18.93 ± 0.23	16.4 ± 0.7	46.67 ± 3.33	13.33 ± 3.33	0.28 ± 0.06
INGWIZABUKUNGUUL 26	0	1 ± 0	100 ± 0	41.58 ± 0.53	24.07 ± 1.83	233.33 ± 8.82	110 ± 5.77	0.47 ± 0.01
	12	8.33 ± 0.67	8.33 ± 8.33	21.57 ± 0.76	18.79 ± 0.81	46.67 ± 3.33	13.33 ± 3.33	0.28 ± 0.06
INTSINDAGIRA	0	1 ± 0	100 ± 0	39.73 ± 1.22	22.38 ± 1.94	240 ± 23.09	123.33 ±	0.52 ± 0.03

BIGEGA							13.33	
	12	4.33 ± 0.67	70 ± 5.77	21.06 ± 2.75	17.6 ± 1.08	110 ± 5.77	23.33 ± 3.33	0.21 ± 0.02
IR 117831-11-1 RGA-1 RGA-1 RGA-1	0	1 ± 0	100 ± 0	34 ± 0.81	21.31 ± 0.33	276.67 ± 14.53	106.67 ± 3.33	0.39 ± 0.03
	12	9 ± 0	0 ± 0	14.7 ± 0.61	13.57 ± 0.52	13.33 ± 3.33	10 ± 0	0.83 ± 0.17
IR 117834-12-1 RGA-1 RGA-1 RGA-2	0	1 ± 0	100 ± 0	27.02 ± 0.85	23.47 ± 0.57	143.33 ± 8.82	100 ± 5.77	0.71 ± 0.07
	12	9 ± 0	0 ± 0	14.53 ± 0.73	13.1 ± 0.82	26.67 ± 3.33	10 ± 0	0.39 ± 0.06
IR 117842-11-1 RGA-1 RGA-1 RGA-2	0	1 ± 0	100 ± 0	34.24 ± 0.75	19.79 ± 1.55	180 ± 11.55	93.33 ± 6.67	0.52 ± 0.02
	12	9 ± 0	0 ± 0	15.33 ± 0.68	13.37 ± 0.43	23.33 ± 3.33	10 ± 0	0.44 ± 0.06
IR 121183-5-2-1-1-B	0	1 ± 0	100 ± 0	28.43 ± 0.54	22.28 ± 0.78	196.67 ± 8.82	106.67 ± 3.33	0.54 ± 0.01
	12	9 ± 0	0 ± 0	16.17 ± 0.44	14 ± 0.35	30 ± 0	10 ± 0	0.33 ± 0
IR 127793-849-1-1-1-3	0	1 ± 0	100 ± 0	29.83 ± 0.96	17.8 ± 0.9	216.67 ± 12.02	103.33 ± 3.33	0.48 ± 0.04
	12	8.33 ± 0.67	8.33 ± 8.33	16.21 ± 0.32	15.7 ± 0.75	43.33 ± 3.33	16.67 ± 3.33	0.38 ± 0.07
IR 127795-1121-1-1-2-1	0	1 ± 0	100 ± 0	28.22 ± 0.54	16.63 ± 0.68	146.67 ± 21.86	90 ± 5.77	0.65 ± 0.12
	12	9 ± 0	0 ± 0	15.39 ± 1.08	13.1 ± 0.72	16.67 ± 6.67	10 ± 0	0.78 ± 0.22
IR 13240-108-2-2-3	0	1 ± 0	100 ± 0	31.93 ± 0.98	23.13 ± 1.69	216.67 ± 14.53	100 ± 5.77	0.47 ± 0.05
	12	8.33 ± 0.67	13.33 ± 13.33	16.52 ± 0.49	16.97 ± 0.93	46.67 ± 3.33	13.33 ± 3.33	0.28 ± 0.06
IR 15T1302	0	1 ± 0	100 ± 0	35.33 ± 0.18	17.01 ± 1.04	210 ± 15.28	106.67 ± 3.33	0.51 ± 0.03
	12	8.33 ± 0.67	10 ± 10	18.17 ± 0.17	13.47 ± 0.2	50 ± 0	16.67 ± 3.33	0.33 ± 0.07
IR 16T1067	0	1 ± 0	100 ± 0	27.01 ± 1.07	23.34 ± 0.38	220 ± 15.28	103.33 ± 8.82	0.48 ± 0.07
	12	8.33 ± 0.67	6.67 ± 6.67	15.13 ± 0.27	14.1 ± 0.66	20 ± 0	20 ± 0	1 ± 0
IR 16T1339	0	1 ± 0	100 ± 0	30.99 ± 0.8	28.39 ± 0.84	153.33 ± 13.33	100 ± 10	0.66 ± 0.07

	12	8.33 ± 0.67	10 ± 10	15.57 ± 0.35	14.67 ± 0.47	33.33 ± 3.33	16.67 ± 3.33	0.5 ± 0.1
IR 16T1348	0	1 ± 0	100 ± 0	25.41 ± 0.55	19.5 ± 0.36	140 ± 15.28	93.33 ± 8.82	0.68 ± 0.1
	12	9 ± 0	0 ± 0	14.67 ± 0.61	14 ± 0.51	13.33 ± 3.33	10 ± 0	0.83 ± 0.17
IR 18T1015	0	1 ± 0	100 ± 0	26.68 ± 0.77	21.97 ± 0.9	146.67 ± 8.82	96.67 ± 8.82	0.66 ± 0.02
	12	9 ± 0	0 ± 0	14.7 ± 0.67	13.4 ± 0.31	26.67 ± 3.33	10 ± 0	0.39 ± 0.06
IR 2793-80-1	0	1 ± 0	100 ± 0	27.51 ± 1.04	24.48 ± 0.55	183.33 ± 12.02	106.67 ± 8.82	0.58 ± 0.03
	12	9 ± 0	0 ± 0	15.14 ± 0.23	20.69 ± 0.49	30 ± 0	10 ± 0	0.33 ± 0
IR 29	0	1 ± 0	100 ± 0	31.34 ± 0.7	18.48 ± 1.42	196.67 ± 8.82	100 ± 0	0.51 ± 0.02
	12	8.33 ± 0.67	0 ± 0	15.47 ± 0.27	13.47 ± 0.43	20 ± 5.77	10 ± 0	0.61 ± 0.2
IR14D121	0	1 ± 0	100 ± 0	33.2 ± 0.42	25.73 ± 1.16	256.67 ± 17.64	100 ± 5.77	0.4 ± 0.05
	12	7 ± 1.15	18.33 ± 10.14	17.94 ± 0.4	14.77 ± 0.12	46.67 ± 3.33	13.33 ± 3.33	0.28 ± 0.06
IRRI 154	0	1 ± 0	100 ± 0	32.94 ± 2.19	19.14 ± 0.17	186.67 ± 18.56	96.67 ± 3.33	0.53 ± 0.07
	12	9 ± 0	0 ± 0	13.84 ± 0.26	12.44 ± 0.82	20 ± 0	10 ± 0	0.5 ± 0
IRRI 213	0	1 ± 0	100 ± 0	35.59 ± 1.18	23.27 ± 0.37	256.67 ± 12.02	116.67 ± 6.67	0.45 ± 0.01
	12	7.67 ± 0.67	18.33 ± 9.28	22.19 ± 0.58	15.72 ± 0.61	50 ± 0	16.67 ± 3.33	0.33 ± 0.07
IRRI 214 (TAI)	0	1 ± 0	100 ± 0	35.18 ± 0.7	22.76 ± 0.83	246.67 ± 17.64	96.67 ± 8.82	0.4 ± 0.05
	12	8.33 ± 0.67	10 ± 10	20.56 ± 0.47	17.7 ± 0.45	60 ± 5.77	20 ± 0	0.34 ± 0.03
IRRI 77713 (VYUNINZARA)	0	1 ± 0	100 ± 0	36.29 ± 0.3	24.47 ± 0.39	270 ± 11.55	103.33 ± 3.33	0.38 ± 0.02
	12	9 ± 0	0 ± 0	17.28 ± 0.15	18.43 ± 1.01	40 ± 0	13.33 ± 3.33	0.33 ± 0.08
IRRI 79511 (GWIZUMWIMBU)	0	1 ± 0	100 ± 0	36.81 ± 1.38	20.63 ± 1.09	203.33 ± 8.82	103.33 ± 6.67	0.51 ± 0.05
	12	7.67 ± 0.67	18.33 ± 10.14	16.4 ± 0.32	15.57 ± 0.5	36.67 ± 3.33	10 ± 0	0.28 ± 0.03

ITA 304	0	1 ± 0	100 ± 0	30.84 ± 0.79	22.28 ± 0.49	233.33 ± 17.64	110 ± 5.77	0.48 ± 0.04
	12	8.33 ± 0.67	10 ± 10	15.48 ± 0.33	16.71 ± 0.66	30 ± 0	13.33 ± 3.33	0.44 ± 0.11
ITA 310	0	1 ± 0	100 ± 0	31.87 ± 1.29	32.89 ± 1.51	266.67 ± 20.28	106.67 ± 8.82	0.41 ± 0.06
	12	9 ± 0	0 ± 0	16.29 ± 0.26	20.84 ± 0.21	36.67 ± 3.33	10.33 ± 0.33	0.29 ± 0.04
Intsinzi	0	1 ± 0	100 ± 0	32.86 ± 0.98	22.36 ± 0.53	210 ± 15.28	106.67 ± 8.82	0.51 ± 0.05
	12	7 ± 1.15	21.67 ± 10.93	16.47 ± 0.55	18.2 ± 0.17	46.67 ± 3.33	13.33 ± 3.33	0.28 ± 0.06
Iron	0	1 ± 0	100 ± 0	34.43 ± 0.96	17.93 ± 0.52	223.33 ± 14.53	120 ± 20.82	0.53 ± 0.08
	12	9 ± 0	0 ± 0	20.58 ± 0.23	16.47 ± 0.33	30 ± 0	13.33 ± 3.33	0.44 ± 0.11
Itumbula 2	0	1 ± 0	100 ± 0	47.68 ± 1.01	21.44 ± 0.53	326.67 ± 12.02	123.33 ± 8.82	0.38 ± 0.01
	12	8.33 ± 0.67	13.33 ± 13.33	17.83 ± 0.49	16.13 ± 1.45	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
JARIBU	0	1 ± 0	100 ± 0	42.97 ± 0.82	21.97 ± 0.55	256.67 ± 18.56	106.67 ± 3.33	0.42 ± 0.02
	12	5.67 ± 0.67	46.67 ± 4.41	26.52 ± 1.06	17.31 ± 0.58	116.67 ± 3.33	20 ± 0	0.17 ± 0
JYAMBERE (Bug2013A)	0	1 ± 0	100 ± 0	37.8 ± 0.72	22.2 ± 0.61	236.67 ± 8.82	106.67 ± 3.33	0.45 ± 0.03
	12	7.67 ± 0.67	26.67 ± 13.64	21.3 ± 0.61	14.02 ± 0.18	43.33 ± 3.33	10 ± 0	0.23 ± 0.02
Jambo twende	0	1 ± 0	100 ± 0	46.36 ± 0.65	25.14 ± 0.9	230 ± 11.55	106.67 ± 8.82	0.46 ± 0.03
	12	8.33 ± 0.67	13.33 ± 13.33	22.01 ± 0.85	18.19 ± 0.81	43.33 ± 3.33	13.33 ± 3.33	0.3 ± 0.05
Jaribu 220	0	1 ± 0	100 ± 0	41.52 ± 0.57	21.3 ± 1.19	243.33 ± 3.33	106.67 ± 3.33	0.44 ± 0.02
	12	7.67 ± 0.67	21.67 ± 10.93	21.13 ± 0.81	16.67 ± 0.73	43.33 ± 3.33	10 ± 0	0.23 ± 0.02
K 5	0	1 ± 0	100 ± 0	40.59 ± 1.01	23.01 ± 2.92	273.33 ± 28.48	113.33 ± 8.82	0.42 ± 0.01
	12	4.33 ± 0.67	58.33 ± 7.26	24.04 ± 1.71	18.67 ± 1.41	140 ± 25.17	23.33 ± 3.33	0.18 ± 0.05
KIGEGA	0	1 ± 0	100 ± 0	32.82 ± 1.21	21.59 ± 0.55	280 ± 11.55	110 ± 0	0.39 ± 0.01

	12	8.33 ± 0.67	8.33 ± 8.33	14.43 ± 0.49	14.96 ± 0.51	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
KUNGAHARA (Bug 2011A)	0	1 ± 0	100 ± 0	32.61 ± 1.08	31.41 ± 0.95	180 ± 11.55	100 ± 5.77	0.56 ± 0.04
	12	8.33 ± 0.67	13.33 ± 13.33	15.71 ± 0.38	15.9 ± 0.42	40 ± 5.77	13.33 ± 3.33	0.33 ± 0.04
Kachambo	0	1 ± 0	100 ± 0	43.41 ± 0.56	25.01 ± 0.18	306.67 ± 17.64	110 ± 0	0.36 ± 0.02
	12	7.67 ± 0.67	15 ± 7.64	24.13 ± 0.9	18.31 ± 1.09	73.33 ± 6.67	13.33 ± 3.33	0.18 ± 0.04
Kachikope	0	1 ± 0	100 ± 0	45.87 ± 2.89	23.43 ± 1.95	270 ± 10	90 ± 5.77	0.34 ± 0.03
	12	9 ± 0	0 ± 0	20.63 ± 0.98	14.32 ± 0.19	26.67 ± 3.33	16.67 ± 3.33	0.61 ± 0.06
Kagiha	0	1 ± 0	100 ± 0	29.91 ± 0.37	23.44 ± 0.56	236.67 ± 23.33	100 ± 5.77	0.43 ± 0.06
	12	8.33 ± 0.67	10 ± 10	16.8 ± 0.15	14.72 ± 0.65	50 ± 0	20 ± 0	0.4 ± 0
Kalalu	0	1 ± 0	100 ± 0	32.72 ± 0.72	18.56 ± 0.5	206.67 ± 17.64	103.33 ± 6.67	0.51 ± 0.07
	12	9 ± 0	0 ± 0	17.96 ± 0.62	15.81 ± 0.54	23.33 ± 3.33	10 ± 0	0.44 ± 0.06
Kalamata	0	1 ± 0	100 ± 0	50.1 ± 1.02	21.62 ± 0.6	253.33 ± 14.53	110 ± 0	0.44 ± 0.03
	12	9 ± 0	0 ± 0	23.06 ± 0.17	17.57 ± 0.81	53.33 ± 3.33	13.33 ± 3.33	0.26 ± 0.07
Kaling'anaula	0	1 ± 0	100 ± 0	46.41 ± 0.5	21.07 ± 1.44	253.33 ± 12.02	106.67 ± 3.33	0.42 ± 0.03
	12	9 ± 0	0 ± 0	19.31 ± 0.24	14.48 ± 0.89	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
Kalivumbula	0	1 ± 0	100 ± 0	40.96 ± 0.92	20.43 ± 0.59	190 ± 5.77	100 ± 5.77	0.53 ± 0.03
	12	8.33 ± 0.67	11.67 ± 11.67	16.23 ± 0.28	15.5 ± 0.81	16.67 ± 3.33	13.33 ± 3.33	0.83 ± 0.17
Kalundi	0	1 ± 0	100 ± 0	51.08 ± 0.64	30.53 ± 1.24	230 ± 15.28	110 ± 0	0.48 ± 0.03
	12	7 ± 1.15	15 ± 7.64	22.64 ± 0.67	18.52 ± 0.43	30 ± 5.77	13.33 ± 3.33	0.44 ± 0.06
Kanamalia	0	1 ± 0	100 ± 0	41.91 ± 0.85	23.68 ± 0.52	266.67 ± 8.82	106.67 ± 3.33	0.4 ± 0.01
	12	8.33 ± 0.67	8.33 ± 8.33	22.59 ± 1.19	15.44 ± 0.85	46.67 ± 3.33	10 ± 0	0.22 ± 0.02

Kaniki	0	1 ± 0	100 ± 0	45.02 ± 1.08	21.46 ± 0.9	306.67 ± 6.67	110 ± 0	0.36 ± 0.01
	12	8.33 ± 0.67	21.67 ± 4.41	22.13 ± 0.82	15.5 ± 0.36	46.67 ± 3.33	16.67 ± 3.33	0.35 ± 0.05
Katumahi	0	1 ± 0	100 ± 0	52.74 ± 1.4	23.42 ± 1.46	313.33 ± 23.33	120 ± 0	0.39 ± 0.03
	12	7.67 ± 0.67	11.67 ± 6.01	18.63 ± 0.61	17.29 ± 0.61	53.33 ± 3.33	13.33 ± 3.33	0.26 ± 0.07
Kia la ngawa	0	1 ± 0	100 ± 0	35.42 ± 0.99	21.94 ± 0.24	173.33 ± 14.53	96.67 ± 8.82	0.57 ± 0.08
	12	8.33 ± 0.67	8.33 ± 8.33	23 ± 0.62	18.24 ± 0.38	36.67 ± 3.33	13.33 ± 3.33	0.36 ± 0.07
Kihogo	0	1 ± 0	100 ± 0	50.52 ± 0.44	27.28 ± 1.41	363.33 ± 29.63	133.33 ± 3.33	0.37 ± 0.02
	12	8.33 ± 0.67	6.67 ± 6.67	15.24 ± 0.17	14.84 ± 0.63	33.33 ± 3.33	13.33 ± 3.33	0.39 ± 0.06
Kihogo Red Morogoro	0	1 ± 0	100 ± 0	52.68 ± 0.83	22.04 ± 0.15	290 ± 20.82	113.33 ± 3.33	0.4 ± 0.02
	12	8.33 ± 0.67	6.67 ± 6.67	24.3 ± 2.06	16.38 ± 0.56	36.67 ± 3.33	13.33 ± 3.33	0.36 ± 0.07
Kihogo red	0	1 ± 0	100 ± 0	51.41 ± 0.56	24.3 ± 1.14	226.67 ± 14.53	116.67 ± 3.33	0.52 ± 0.05
	12	9 ± 0	0 ± 0	17.81 ± 0.8	15.26 ± 0.79	40 ± 0	10 ± 0	0.25 ± 0
Kijicho	0	1 ± 0	100 ± 0	46.63 ± 0.88	21.3 ± 1.9	223.33 ± 20.28	106.67 ± 3.33	0.48 ± 0.05
	12	5.67 ± 0.67	33.33 ± 4.41	23.88 ± 2.13	17.53 ± 0.81	90 ± 5.77	20 ± 0	0.22 ± 0.01
Kilombero	0	1 ± 0	100 ± 0	46.3 ± 1.35	18.67 ± 0.48	230 ± 11.55	106.67 ± 3.33	0.47 ± 0.04
	12	8.33 ± 0.67	10 ± 10	22.04 ± 0.92	15.37 ± 0.69	50 ± 0	10 ± 0	0.2 ± 0
Kisegese	0	1 ± 0	100 ± 0	50.79 ± 0.21	23.24 ± 2.31	280 ± 15.28	123.33 ± 3.33	0.44 ± 0.02
	12	7 ± 1.15	11.67 ± 6.01	17.39 ± 0.2	18.56 ± 0.8	40 ± 0	10 ± 0	0.25 ± 0
Kivuli	0	1 ± 0	100 ± 0	43.71 ± 0.77	24.2 ± 0.42	196.67 ± 8.82	96.67 ± 8.82	0.5 ± 0.07
	12	9 ± 0	0 ± 0	17.94 ± 0.81	15.32 ± 0.24	50 ± 0	13.33 ± 3.33	0.27 ± 0.07
Komboka	0	1 ± 0	100 ± 0	42.3 ± 1.02	23.56 ± 0.69	293.33 ± 17.64	113.33 ± 3.33	0.39 ± 0.02
	12	8.33 ± 0.67	10 ± 10	18.97 ± 0.73	19.16 ± 0.99	50 ± 5.77	20 ± 0	0.41 ± 0.05

Kubwa jinga	0	1 ± 0	100 ± 0	38.81 ± 0.5	24.17 ± 3.92	256.67 ± 16.67	103.33 ± 3.33	0.41 ± 0.01
	12	7 ± 1.15	21.67 ± 10.93	24.83 ± 1.17	18.28 ± 2.67	80 ± 15.28	23.33 ± 3.33	0.3 ± 0.02
Kyela	0	1 ± 0	100 ± 0	53.31 ± 0.46	25.48 ± 0.27	320 ± 11.55	126.67 ± 3.33	0.4 ± 0.01
	12	8.33 ± 0.67	8.33 ± 8.33	22.33 ± 0.97	15.94 ± 0.54	23.33 ± 3.33	10 ± 0	0.44 ± 0.06
LINE 11 WARDA	0	1 ± 0	100 ± 0	37.1 ± 0.78	21.92 ± 0.83	236.67 ± 8.82	110 ± 0	0.47 ± 0.02
	12	8.33 ± 0.67	11.67 ± 11.67	22.19 ± 0.87	18.78 ± 1.43	46.67 ± 3.33	13.33 ± 3.33	0.28 ± 0.06
LINE 16	0	1 ± 0	100 ± 0	45.88 ± 1.27	25 ± 0.23	230 ± 35.12	96.67 ± 8.82	0.43 ± 0.04
	12	5.67 ± 0.67	46.67 ± 7.26	27.09 ± 1.41	20.39 ± 0.86	76.67 ± 8.82	20 ± 0	0.27 ± 0.03
LINE-18-NIWUR 1	0	1 ± 0	100 ± 0	46.63 ± 0.84	24.07 ± 0.35	253.33 ± 14.53	116.67 ± 3.33	0.46 ± 0.03
	12	7.67 ± 0.67	11.67 ± 7.26	24.66 ± 2.06	18.8 ± 0.35	36.67 ± 3.33	10 ± 0	0.28 ± 0.03
LINE-8A-2	0	1 ± 0	100 ± 0	40.86 ± 0.85	23.3 ± 0.7	203.33 ± 8.82	103.33 ± 6.67	0.51 ± 0.02
	12	8.33 ± 0.67	8.33 ± 8.33	15.71 ± 0.55	15.91 ± 0.88	30 ± 0	13.33 ± 3.33	0.44 ± 0.11
Lifumba	0	1 ± 0	100 ± 0	54.07 ± 0.75	21.08 ± 0.19	300 ± 5.77	113.33 ± 3.33	0.38 ± 0.01
	12	8.33 ± 0.67	6.67 ± 6.67	20.47 ± 0.55	18.47 ± 0.23	36.67 ± 3.33	10 ± 0	0.28 ± 0.03
Lifuwu	0	1 ± 0	100 ± 0	28.98 ± 0.77	19.81 ± 1.43	196.67 ± 8.82	103.33 ± 3.33	0.53 ± 0.04
	12	8.33 ± 0.67	8.33 ± 8.33	15.36 ± 0.86	15.26 ± 0.55	30 ± 0	10 ± 0	0.33 ± 0
Limota	0	1 ± 0	100 ± 0	37.46 ± 0.56	22.08 ± 0.91	223.33 ± 14.53	106.67 ± 3.33	0.48 ± 0.04
	12	7 ± 1.15	21.67 ± 10.93	15.71 ± 0.62	13.7 ± 0.45	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
Lingwelingweli	0	1 ± 0	100 ± 0	43.76 ± 0.61	18.77 ± 0.77	216.67 ± 8.82	130 ± 25.17	0.6 ± 0.12
	12	9 ± 0	0 ± 0	21.04 ± 0.82	16.47 ± 0.58	39 ± 1	13.33 ± 3.33	0.34 ± 0.08
Loya	0	1 ± 0	100 ± 0	51.9 ± 0.78	23.42 ± 0.21	223.33 ± 17.64	103.33 ± 3.33	0.47 ± 0.06

	12	7.67 ± 0.67	11.67 ± 6.01	22.8 ± 0.15	14.53 ± 0.75	56.67 ± 3.33	16.67 ± 3.33	0.29 ± 0.04
Lunyuki	0	1 ± 0	100 ± 0	42.89 ± 0.56	21.64 ± 0.49	226.67 ± 3.33	103.33 ± 6.67	0.46 ± 0.02
	12	9 ± 0	0 ± 0	17.66 ± 0.25	16.89 ± 1.05	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
MWANZA	0	1 ± 0	100 ± 0	40 ± 0.23	25.97 ± 1.18	306.67 ± 12.02	130 ± 5.77	0.42 ± 0.03
	12	7.67 ± 0.67	13.33 ± 7.26	23.8 ± 0.72	18.72 ± 0.96	46.67 ± 3.33	10 ± 0	0.22 ± 0.02
Mabula	0	1 ± 0	100 ± 0	37.93 ± 0.99	28.62 ± 0.64	193.33 ± 12.02	103.33 ± 6.67	0.54 ± 0.06
	12	9 ± 0	0 ± 0	17.07 ± 0.23	17.17 ± 0.69	36.67 ± 3.33	10 ± 0	0.28 ± 0.03
Magongo ya Wayungu	0	1 ± 0	100 ± 0	50.97 ± 0.26	22.21 ± 0.98	340 ± 15.28	133.33 ± 3.33	0.39 ± 0.03
	12	7.67 ± 0.67	15 ± 7.64	21.34 ± 1.72	15.46 ± 0.71	56.67 ± 6.67	16.67 ± 3.33	0.3 ± 0.06
Masantula	0	1 ± 0	100 ± 0	50.59 ± 1.13	21.07 ± 0.87	233.33 ± 20.28	106.67 ± 3.33	0.46 ± 0.03
	12	7.67 ± 0.67	13.33 ± 7.26	21.58 ± 0.47	15.36 ± 0.89	36.67 ± 3.33	10 ± 0	0.28 ± 0.03
Maua mekundu	0	1 ± 0	100 ± 0	50.89 ± 0.39	23.63 ± 0.38	240 ± 26.46	106.67 ± 3.33	0.46 ± 0.06
	12	8.33 ± 0.67	6.67 ± 6.67	22.46 ± 0.23	17.23 ± 0.91	23.33 ± 3.33	13.33 ± 3.33	0.56 ± 0.06
Mbawa mbili mwekundu	0	1 ± 0	100 ± 0	47.54 ± 1.05	23.28 ± 1.36	196.67 ± 17.64	100 ± 10	0.53 ± 0.09
	12	9 ± 0	0 ± 0	20.99 ± 0.16	17.57 ± 0.3	46.67 ± 3.33	16.67 ± 3.33	0.37 ± 0.09
Mbawa ya njiwa	0	1 ± 0	100 ± 0	47.32 ± 0.91	28.52 ± 0.27	223.33 ± 6.67	106.67 ± 8.82	0.48 ± 0.05
	12	7 ± 0	18.33 ± 3.33	20.99 ± 1.18	21.73 ± 0.15	43.33 ± 3.33	13.33 ± 3.33	0.32 ± 0.09
Mbawambili	0	1 ± 0	100 ± 0	48.46 ± 1.13	19.68 ± 0.58	246.67 ± 17.64	126.67 ± 3.33	0.52 ± 0.04
	12	7.67 ± 0.67	15 ± 7.64	23.91 ± 0.95	14.12 ± 0.79	50 ± 5.77	13.33 ± 3.33	0.26 ± 0.04
Mbawambili kyela	0	1 ± 0	100 ± 0	47.14 ± 2.05	21.78 ± 1.13	233.33 ± 3.33	120 ± 5.77	0.52 ± 0.03
	12	8.33 ± 0.67	6.67 ± 6.67	20.2 ± 0.3	14.96 ± 0.81	33.33 ± 3.33	13.33 ± 3.33	0.39 ± 0.06
Mbawambili nyeupe	0	1 ± 0	100 ± 0	47.78 ± 1.12	19.7 ± 1.35	213.33 ± 23.33	110 ± 5.77	0.54 ± 0.09

	12	8.33 ± 0.67	8.33 ± 8.33	21.07 ± 0.18	15 ± 0.4	43.33 ± 6.67	10 ± 0	0.24 ± 0.04
Mbawambili rangimbili	0	1 ± 0	100 ± 0	45 ± 0.81	21.42 ± 0.42	230 ± 17.32	106.67 ± 3.33	0.47 ± 0.05
	12	8.33 ± 0.67	5 ± 5	23.26 ± 0.41	16.91 ± 0.55	36.67 ± 3.33	16.67 ± 3.33	0.44 ± 0.06
Mbega	0	1 ± 0	100 ± 0	45.91 ± 0.61	21.22 ± 0.28	313.33 ± 17.64	106.67 ± 3.33	0.34 ± 0.03
	12	7 ± 0	26.67 ± 3.33	20.56 ± 1.03	16.79 ± 0.14	40 ± 0	16.67 ± 3.33	0.42 ± 0.08
Mbuyu	0	1 ± 0	100 ± 0	46.83 ± 0.78	23.08 ± 0.13	313.33 ± 20.28	113.33 ± 3.33	0.36 ± 0.02
	12	7.67 ± 0.67	16.67 ± 8.33	22.26 ± 0.98	15.1 ± 0.15	36.67 ± 3.33	16 ± 3.06	0.46 ± 0.12
Mdomo wa fisi	0	1 ± 0	100 ± 0	45.78 ± 0.41	18.17 ± 0.84	220 ± 20.82	116.67 ± 3.33	0.54 ± 0.05
	12	7.67 ± 0.67	15 ± 7.64	22.91 ± 1.3	15.07 ± 0.9	50 ± 0	13.33 ± 3.33	0.27 ± 0.07
Mkia wa nyumbu	0	1 ± 0	100 ± 0	42.04 ± 0.82	26.72 ± 0.6	280 ± 17.32	136.67 ± 8.82	0.49 ± 0.04
	12	8.33 ± 0.67	13.33 ± 1.67	21.42 ± 0.42	18.32 ± 1.17	43.33 ± 3.33	13.33 ± 3.33	0.3 ± 0.05
Mleke alongole	0	1 ± 0	100 ± 0	41.81 ± 0.82	23.53 ± 0.58	296.67 ± 14.53	123.33 ± 3.33	0.42 ± 0.03
	12	9 ± 0	0 ± 0	20.48 ± 1.19	18.12 ± 1	30 ± 0	10 ± 0	0.33 ± 0
Moshi	0	1 ± 0	100 ± 0	51.32 ± 0.54	27.67 ± 0.62	323.33 ± 14.53	123.33 ± 3.33	0.38 ± 0.02
	12	7.67 ± 0.67	15 ± 7.64	22.6 ± 1.48	14.2 ± 0.89	53.33 ± 3.33	10 ± 0	0.19 ± 0.01
Moshi wa sigara	0	1 ± 0	100 ± 0	46.23 ± 1.41	20.03 ± 0.58	293.33 ± 16.67	103.33 ± 3.33	0.35 ± 0.02
	12	5.67 ± 0.67	40 ± 5.77	23.84 ± 2.01	14.56 ± 0.71	90 ± 5.77	20 ± 0	0.22 ± 0.01
Mpaka wa bibi	0	1 ± 0	100 ± 0	44.73 ± 0.67	27.78 ± 1.13	256.67 ± 42.56	123.33 ± 8.82	0.5 ± 0.06
	12	5.67 ± 0.67	43.33 ± 8.33	24.62 ± 2.01	18.34 ± 0.53	90 ± 5.77	23.33 ± 3.33	0.26 ± 0.02
Mpembuke	0	1 ± 0	100 ± 0	43.98 ± 0.21	21.69 ± 1.16	253.33 ± 14.53	106.67 ± 3.33	0.43 ± 0.04
	12	9 ± 0	0 ± 0	20.72 ± 1.73	15.87 ± 0.52	50 ± 0	10 ± 0	0.2 ± 0
Msonga	0	1 ± 0	100 ± 0	35.98 ± 0.6	20.79 ± 1.13	293.33 ± 12.02	126.67 ± 3.33	0.43 ± 0.02

	12	7 ± 1.15	16.67 ± 8.82	20.7 ± 1.51	16.53 ± 0.42	53.33 ± 3.33	10 ± 0	0.19 ± 0.01
Mwana matongo 2	0	1 ± 0	100 ± 0	47.82 ± 0.97	23.04 ± 0.18	303.33 ± 14.53	120 ± 0	0.4 ± 0.02
	12	9 ± 0	0 ± 0	21.12 ± 0.92	17 ± 1.04	46.67 ± 3.33	10 ± 0	0.22 ± 0.02
Mwangaza	0	1 ± 0	100 ± 0	47.28 ± 2.4	22.97 ± 0.03	333.33 ± 31.8	130 ± 0	0.4 ± 0.04
	12	7.67 ± 0.67	15 ± 7.64	24.84 ± 0.8	19.8 ± 0.91	50 ± 0	13.33 ± 3.33	0.27 ± 0.07
Mwarabu	0	1 ± 0	100 ± 0	44.37 ± 0.49	19.64 ± 1.59	270 ± 15.28	103.33 ± 3.33	0.38 ± 0.03
	12	9 ± 0	0 ± 0	17.88 ± 0.36	13.73 ± 0.55	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
Mwasungo	0	1 ± 0	100 ± 0	48.09 ± 1.17	23.36 ± 0.36	286.67 ± 20.28	110 ± 0	0.39 ± 0.03
	12	7 ± 1.15	11.67 ± 6.01	19.04 ± 0.75	15.17 ± 0.82	36.67 ± 3.33	13.33 ± 3.33	0.36 ± 0.07
Mzinga	0	1 ± 0	100 ± 0	44.61 ± 0.86	22.68 ± 2.56	246.67 ± 14.53	96.67 ± 3.33	0.39 ± 0.03
	12	8.33 ± 0.67	8.33 ± 8.33	24.91 ± 0.67	18.73 ± 1	50 ± 0	13.33 ± 3.33	0.27 ± 0.07
Mzungu	0	1 ± 0	100 ± 0	51.1 ± 0.46	23.12 ± 0.34	273.33 ± 20.28	106.67 ± 3.33	0.4 ± 0.04
	12	9 ± 0	0 ± 0	20.39 ± 0.5	13.2 ± 0.69	46.67 ± 3.33	16.67 ± 3.33	0.37 ± 0.09
NERICA 1	0	1 ± 0	100 ± 0	34.18 ± 0.78	23.09 ± 0.31	220 ± 20.82	103.33 ± 3.33	0.48 ± 0.05
	12	9 ± 0	0 ± 0	17.73 ± 0.5	16.52 ± 1.17	13.33 ± 3.33	10 ± 0	0.83 ± 0.17
NERICA 10	0	1 ± 0	100 ± 0	33.18 ± 1.33	17.86 ± 0.56	186.67 ± 8.82	96.67 ± 3.33	0.52 ± 0.01
	12	7.67 ± 0.67	8.33 ± 4.41	15.17 ± 0.37	14.7 ± 1.01	20 ± 0	16.67 ± 3.33	0.83 ± 0.17
NERICA 2	0	1 ± 0	100 ± 0	37.82 ± 0.87	20.53 ± 0.29	196.67 ± 8.82	106.67 ± 3.33	0.54 ± 0.01
	12	7.67 ± 0.67	13.33 ± 7.26	21.56 ± 0.08	16 ± 0.42	50 ± 0	10 ± 0	0.2 ± 0
NERICA 4	0	1 ± 0	100 ± 0	41.06 ± 3.83	20.24 ± 0.99	180 ± 15.28	96.67 ± 3.33	0.55 ± 0.06
	12	5.67 ± 0.67	45 ± 5.77	20.74 ± 1.51	18.33 ± 0.52	60 ± 25.17	23.33 ± 3.33	0.48 ± 0.12
NERICA 7	0	1 ± 0	100 ± 0	35.83 ± 0.09	23.8 ± 0.95	230 ± 11.55	113.33 ± 3.33	0.49 ± 0.01

	12	8.33 ± 0.67	11.67 ± 11.67	17.13 ± 0.93	15.84 ± 0.49	20 ± 0	10 ± 0	0.5 ± 0
Nawa tule na Bwana	0	1 ± 0	100 ± 0	35.11 ± 0.41	29.01 ± 0.4	296.67 ± 14.53	123.33 ± 3.33	0.42 ± 0.01
	12	8.33 ± 0.67	6.67 ± 6.67	15.89 ± 0.2	13.83 ± 0.38	30 ± 0	13.33 ± 3.33	0.44 ± 0.11
Ndamirabahinzi	0	1 ± 0	100 ± 0	44.59 ± 0.63	20.67 ± 0.57	250 ± 26.46	100 ± 5.77	0.41 ± 0.04
	12	7 ± 1.15	16.67 ± 8.82	24.23 ± 0.39	17.47 ± 0.26	53.33 ± 3.33	16.67 ± 3.33	0.31 ± 0.06
Nemeyubutaka	0	1 ± 0	100 ± 0	38.92 ± 0.3	22.13 ± 0.87	223.33 ± 12.02	103.33 ± 3.33	0.46 ± 0.02
	12	5 ± 1.15	53.33 ± 7.26	27.64 ± 4.36	16.69 ± 0.72	106.67 ± 3.33	16.67 ± 3.33	0.15 ± 0.03
Niwahi	0	1 ± 0	100 ± 0	46.22 ± 0.97	20.44 ± 0.48	240 ± 17.32	106.67 ± 3.33	0.45 ± 0.02
	12	9 ± 0	0 ± 0	20 ± 0.58	13.63 ± 0.35	20 ± 0	16.67 ± 3.33	0.83 ± 0.17
Nona Bokra	0	1 ± 0	100 ± 0	54.37 ± 1.68	23.16 ± 1.52	316.67 ± 53.33	116.67 ± 3.33	0.4 ± 0.09
	12	1.67 ± 0.67	100 ± 0	45.17 ± 2.35	19 ± 0.72	220 ± 15.28	36.67 ± 3.33	0.17 ± 0.02
Nondo	0	1 ± 0	100 ± 0	48.24 ± 0.71	32.41 ± 0.54	326.67 ± 6.67	110 ± 0	0.33 ± 0.01
	12	8.33 ± 0.67	6.67 ± 6.67	21.62 ± 0.92	16.1 ± 1.34	43.33 ± 3.33	13.33 ± 3.33	0.3 ± 0.05
Nzahara	0	1 ± 0	100 ± 0	33.38 ± 1.15	28.52 ± 0.74	243.33 ± 8.82	110 ± 0	0.45 ± 0.02
	12	8.33 ± 0.67	8.33 ± 8.33	18.48 ± 0.34	18.23 ± 0.5	30 ± 0	10 ± 0	0.33 ± 0
Pishori(brown)	0	1 ± 0	100 ± 0	51.72 ± 0.98	27.94 ± 0.81	240 ± 17.32	100 ± 0	0.42 ± 0.03
	12	9 ± 0	0 ± 0	18.01 ± 0.52	14.37 ± 0.64	36.67 ± 3.33	10 ± 0	0.28 ± 0.03
Pokkali	0	1 ± 0	100 ± 0	55.68 ± 1.49	25.71 ± 1.31	326.67 ± 16.67	120 ± 0	0.37 ± 0.02
	12	1 ± 0	100 ± 0	50.17 ± 2.7	21.62 ± 1.93	176.67 ± 33.83	38.33 ± 4.18	0.25 ± 0.07
ROJOMENA 271/10	0	1 ± 0	100 ± 0	42.73 ± 1.03	25.09 ± 0.31	260 ± 15.28	120 ± 0	0.46 ± 0.03
	12	8.33 ± 0.67	8.33 ± 8.33	18.17 ± 0.33	17.44 ± 0.53	26.67 ± 3.33	10 ± 0	0.39 ± 0.06
RUMBUKA	0	1 ± 0	100 ± 0	40.07 ± 0.99	22.31 ± 1.42	200 ± 5.77	110 ± 5.77	0.55 ± 0.04

	12	5 ± 0	55 ± 5.77	23.07 ± 0.64	18.38 ± 0.23	93.33 ± 6.67	13.33 ± 3.33	0.15 ± 0.05
RUMBUKA bug 2013A	0	1 ± 0	100 ± 0	40.46 ± 0.39	20.2 ± 0.95	263.33 ± 12.02	103.33 ± 3.33	0.4 ± 0.02
	12	5.67 ± 0.67	40 ± 5.77	23.76 ± 2.28	16.47 ± 0.48	73.33 ± 3.33	20 ± 0	0.28 ± 0.01
Rangi mbili	0	1 ± 0	100 ± 0	48.8 ± 0.15	27.04 ± 0.46	300 ± 5.77	123.33 ± 6.67	0.41 ± 0.03
	12	9 ± 0	0 ± 0	17.97 ± 0.29	13.47 ± 0.67	20 ± 0	10 ± 0	0.5 ± 0
Rangimbili nyekundu	0	1 ± 0	100 ± 0	47.72 ± 0.15	25.72 ± 1.19	273.33 ± 17.64	120 ± 0	0.44 ± 0.03
	12	9 ± 0	0 ± 0	19.19 ± 0.87	13.77 ± 0.73	30 ± 0	13.33 ± 3.33	0.44 ± 0.11
Ringa	0	1 ± 0	100 ± 0	34.03 ± 0.9	21.8 ± 0.89	290 ± 20.82	110 ± 0	0.38 ± 0.03
	12	8.33 ± 0.67	6.67 ± 6.67	23.8 ± 0.25	16.57 ± 0.98	43.33 ± 3.33	13.33 ± 3.33	0.3 ± 0.05
SATO 1	0	1 ± 0	100 ± 0	35.2 ± 1.29	25.19 ± 0.56	220 ± 17.32	116.67 ± 3.33	0.54 ± 0.05
	12	6.33 ± 0.67	70 ± 5.77	20.32 ± 1.01	17.09 ± 0.64	90 ± 5.77	20 ± 0	0.22 ± 0.01
SATO 9	0	1 ± 0	100 ± 0	35.7 ± 0.85	23.87 ± 0.52	226.67 ± 14.53	113.33 ± 3.33	0.51 ± 0.05
	12	7 ± 1.15	45 ± 22.55	18.49 ± 0.4	15.58 ± 0.45	53.33 ± 3.33	10 ± 0	0.19 ± 0.01
SUPA BC IMPROVED	0	1 ± 0	100 ± 0	41.78 ± 0.84	20.69 ± 1.14	210 ± 15.28	103.33 ± 3.33	0.5 ± 0.03
	12	7.67 ± 0.67	16.67 ± 8.82	22.06 ± 0.28	15.47 ± 0.62	60 ± 0	16.67 ± 3.33	0.28 ± 0.05
SUPA KIJIVU	0	1 ± 0	100 ± 0	45.32 ± 0.33	20.17 ± 1.27	220 ± 15.28	106.67 ± 3.33	0.49 ± 0.05
	12	8.33 ± 0.67	11.67 ± 11.67	16.7 ± 0.96	14.23 ± 0.84	23.33 ± 3.33	13.33 ± 3.33	0.56 ± 0.06
Salinas 27	0	1 ± 0	100 ± 0	27.04 ± 0.65	22.93 ± 1.5	193.33 ± 3.33	103.33 ± 17.64	0.53 ± 0.08
	12	8.33 ± 0.67	6.67 ± 6.67	15.46 ± 0.47	15.53 ± 0.58	46.67 ± 3.33	14 ± 3.06	0.3 ± 0.05
Serena	0	1 ± 0	100 ± 0	30.96 ± 0.82	25.21 ± 1.76	210 ± 15.28	106.67 ± 6.67	0.52 ± 0.06
	12	9 ± 0	0 ± 0	15.66 ± 0.25	14.17 ± 0.72	30 ± 0	10 ± 0	0.33 ± 0

Shingo ya mwali	0	1 ± 0	100 ± 0	51.86 ± 0.68	23.64 ± 2.11	296.67 ± 29.63	123.33 ± 3.33	0.42 ± 0.04
	12	9 ± 0	0 ± 0	22.27 ± 0.67	14.93 ± 0.9	31.33 ± 1.33	10 ± 0	0.32 ± 0.01
Sifara	0	1 ± 0	100 ± 0	52.16 ± 0.9	22.06 ± 0.86	240 ± 15.28	113.33 ± 3.33	0.48 ± 0.03
	12	9 ± 0	0 ± 0	21.86 ± 0.26	15.93 ± 1.4	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
Simzito	0	1 ± 0	100 ± 0	51.53 ± 0.85	23.34 ± 1.83	236.67 ± 17.64	110 ± 5.77	0.47 ± 0.05
	12	9 ± 0	0 ± 0	18.8 ± 0.44	14.61 ± 0.56	13.33 ± 3.33	13.33 ± 3.33	1.17 ± 0.44
Sindano kubwa	0	1 ± 0	100 ± 0	47.57 ± 0.59	22.88 ± 0.38	236.67 ± 6.67	106.67 ± 3.33	0.45 ± 0.02
	12	9 ± 0	0 ± 0	18.21 ± 0.71	18.08 ± 0.75	23.33 ± 3.33	10 ± 0	0.44 ± 0.06
Sindano nyeupe	0	1 ± 0	100 ± 0	47.67 ± 0.33	21.01 ± 1.83	233.33 ± 17.64	83.33 ± 16.67	0.35 ± 0.05
	12	9 ± 0	0 ± 0	20.32 ± 0.96	16.32 ± 0.38	33.33 ± 3.33	13.33 ± 3.33	0.42 ± 0.13
Sotea	0	1 ± 0	100 ± 0	46.1 ± 0.46	24.41 ± 0.26	213.33 ± 8.82	103.33 ± 6.67	0.48 ± 0.02
	12	9 ± 0	0 ± 0	19.84 ± 1.37	13.77 ± 0.55	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
Sukari	0	1 ± 0	100 ± 0	46.23 ± 0.91	21.62 ± 2.58	270 ± 17.32	113.33 ± 3.33	0.43 ± 0.04
	12	5.67 ± 0.67	56.67 ± 9.28	25.79 ± 1.54	15.71 ± 0.68	96.67 ± 8.82	20 ± 0	0.21 ± 0.02
Sumbawanga	0	1 ± 0	100 ± 0	50.89 ± 0.39	23.49 ± 1.08	280 ± 28.87	113.33 ± 3.33	0.41 ± 0.06
	12	9 ± 0	0 ± 0	18.89 ± 1.07	15.97 ± 1.25	33.33 ± 3.33	13.33 ± 3.33	0.39 ± 0.06
Supa	0	1 ± 0	100 ± 0	45.57 ± 1.5	22.72 ± 0.54	266.67 ± 8.82	130 ± 5.77	0.49 ± 0.04
	12	8.33 ± 0.67	8.33 ± 8.33	15.8 ± 0.59	13.81 ± 0.22	43.33 ± 3.33	10 ± 0	0.23 ± 0.02
Supa India	0	1 ± 0	100 ± 0	38.5 ± 0.36	26.02 ± 0.93	250 ± 11.55	113.33 ± 3.33	0.46 ± 0.03
	12	8.33 ± 0.67	11.67 ± 11.67	20.71 ± 1.22	14.84 ± 0.09	33.33 ± 3.33	16.67 ± 3.33	0.5 ± 0.1
Supa Katrin	0	1 ± 0	100 ± 0	45.46 ± 3.48	25.17 ± 0.8	340 ± 11.55	123.33 ± 3.33	0.36 ± 0.02
	12	8.33 ± 0.67	8.33 ± 8.33	23.44 ± 0.71	15.26 ± 0.81	46.67 ± 3.33	16.67 ± 3.33	0.35 ± 0.05

Supa kijicho	0	1 ± 0	100 ± 0	47.7 ± 0.15	24.21 ± 0.99	346.67 ± 12.02	116.67 ± 3.33	0.33 ± 0.01
	12	9 ± 0	0 ± 0	21.13 ± 1.62	20.41 ± 1.18	50 ± 5.77	20 ± 0	0.41 ± 0.05
Supa ukerewe	0	1 ± 0	100 ± 0	50.42 ± 0.82	24.12 ± 0.3	230 ± 10	103.33 ± 3.33	0.45 ± 0.03
	12	8.33 ± 0.67	8.33 ± 8.33	19.7 ± 0.4	17.89 ± 1.02	26.67 ± 3.33	10 ± 0	0.39 ± 0.06
TEMERIN -381	0	1 ± 0	100 ± 0	49.42 ± 0.62	24.26 ± 0.83	286.67 ± 8.82	113.33 ± 6.67	0.39 ± 0.01
	12	7.67 ± 0.67	18.33 ± 9.28	25.2 ± 1.07	18.34 ± 0.58	53.33 ± 3.33	16.67 ± 3.33	0.31 ± 0.06
TERIMBERE (LL29)	0	1 ± 0	100 ± 0	29.9 ± 0.59	20 ± 0.4	253.33 ± 43.33	103.33 ± 3.33	0.43 ± 0.08
	12	5 ± 1.15	78.33 ± 10.14	20.76 ± 1.58	17.63 ± 0.26	80 ± 35.12	23.33 ± 3.33	1.12 ± 0.94
TXD 306(SARO5) IMRPOVED	0	1 ± 0	100 ± 0	34.42 ± 0.64	21.77 ± 1.94	240 ± 20.82	103.33 ± 3.33	0.43 ± 0.03
	12	8.33 ± 0.67	11.67 ± 11.67	22.7 ± 1.97	17.76 ± 1.25	20 ± 5.77	13.33 ± 3.33	0.94 ± 0.53
TXD 307	0	1 ± 0	100 ± 0	35.07 ± 0.29	22.33 ± 0.9	243.33 ± 6.67	103.33 ± 3.33	0.43 ± 0.03
	12	9 ± 0	0 ± 0	15.49 ± 0.71	13.93 ± 0.79	36.67 ± 3.33	10 ± 0	0.28 ± 0.03
TXD 85 IMPROVED	0	1 ± 0	100 ± 0	28.37 ± 0.68	19.53 ± 1.99	200 ± 23.09	100 ± 0	0.52 ± 0.06
	12	7.67 ± 0.67	16.67 ± 8.33	16.32 ± 0.37	13.57 ± 0.66	50 ± 0	13.33 ± 3.33	0.27 ± 0.07
TXD 88 IMPROVED	0	1 ± 0	100 ± 0	35.67 ± 1.2	24.67 ± 1.86	240 ± 25.17	110 ± 5.77	0.46 ± 0.03
	12	5.67 ± 0.67	71.67 ± 6.01	20.3 ± 0.87	17.72 ± 0.3	83.33 ± 8.82	26.67 ± 3.33	0.34 ± 0.07
Tarabinzona	0	1 ± 0	100 ± 0	45.61 ± 1.46	23.34 ± 0.51	293.33 ± 26.67	106.67 ± 3.33	0.37 ± 0.03
	12	8.33 ± 0.67	6.67 ± 6.67	21.92 ± 0.17	18.91 ± 0.95	46.67 ± 3.33	13.33 ± 3.33	0.3 ± 0.1
Themanini	0	1 ± 0	100 ± 0	48.56 ± 0.08	32.02 ± 0.94	286.67 ± 6.67	103.33 ± 3.33	0.36 ± 0.02
	12	7 ± 1.15	18.33 ± 9.28	22.19 ± 0.35	15.8 ± 1.04	43.33 ± 3.33	13.33 ± 3.33	0.32 ± 0.09
Tondogoso	0	1 ± 0	100 ± 0	45.66 ± 1.7	25.61 ± 0.69	240 ± 20.82	100 ± 5.77	0.42 ± 0.03

	12	8.33 ± 0.67	8.33 ± 8.33	18.17 ± 0.84	13.7 ± 0.75	30 ± 0	13.33 ± 3.33	0.44 ± 0.11
Tosa	0	1 ± 0	100 ± 0	41.34 ± 0.71	18.61 ± 1.27	223.33 ± 23.33	103.33 ± 3.33	0.47 ± 0.05
	12	9 ± 0	0 ± 0	15 ± 0.36	13.43 ± 0.72	20 ± 0	10 ± 0	0.5 ± 0
Tunduru	0	1 ± 0	100 ± 0	43.57 ± 1.11	24.36 ± 1.2	263.33 ± 6.67	113.33 ± 3.33	0.43 ± 0.01
	12	8.33 ± 0.67	5 ± 5	21.02 ± 0.33	19.64 ± 1.09	53.33 ± 3.33	16.67 ± 3.33	0.31 ± 0.06
Tunduru Dihimba	0	1 ± 0	100 ± 0	49.24 ± 0.75	25.08 ± 0.92	240 ± 5.77	113.33 ± 3.33	0.47 ± 0.02
	12	8.33 ± 0.67	11.67 ± 11.67	21.49 ± 0.57	17.84 ± 0.98	26.67 ± 3.33	10 ± 0	0.39 ± 0.06
URO-01	12	9 ± NA	0 ± NA	21.5 ± NA	13.9 ± NA	40 ± NA	10 ± NA	0.25 ± NA
UROO 1	0	1 ± 0	100 ± 0	51 ± 0.87	22.98 ± 1.48	353.33 ± 8.82	123.33 ± 3.33	0.35 ± 0.01
	12	8 ± 1	15 ± 15	21.2 ± 2.4	14.7 ± 0.1	45 ± 5	10 ± 0	0.22 ± 0.02
Umanho	0	1 ± 0	100 ± 0	52.77 ± 0.62	30.59 ± 0.43	290 ± 20.82	123.33 ± 3.33	0.43 ± 0.04
	12	8.33 ± 0.67	6.67 ± 6.67	24.47 ± 1.02	16.6 ± 0.95	53.33 ± 3.33	10 ± 0	0.19 ± 0.01
Usiniguse	0	1 ± 0	100 ± 0	42.7 ± 0.7	20.28 ± 1.85	296.67 ± 14.53	103.33 ± 6.67	0.35 ± 0.03
	12	9 ± 0	0 ± 0	22.66 ± 1.02	14.67 ± 0.27	46.67 ± 3.33	10 ± 0	0.22 ± 0.02
V 18	0	1 ± 0	100 ± 0	32.49 ± 1.05	23.29 ± 1.14	263.33 ± 18.56	103.33 ± 3.33	0.4 ± 0.01
	12	9 ± 0	0 ± 0	15.82 ± 0.1	16.67 ± 0.46	40 ± 5.77	10 ± 0	0.26 ± 0.04
WABS 450	0	1 ± 0	100 ± 0	42.56 ± 1.03	28.53 ± 0.64	236.67 ± 12.02	110 ± 0	0.47 ± 0.02
	12	8.33 ± 0.67	8.33 ± 8.33	20.09 ± 1.37	17.19 ± 0.46	26.67 ± 3.33	10 ± 0	0.39 ± 0.06
WAT 317-WAS-B-55-11-3-5-1	0	1 ± 0	100 ± 0	35.58 ± 0.47	30.12 ± 0.29	233.33 ± 3.33	103.33 ± 6.67	0.44 ± 0.03
	12	9 ± 0	0 ± 0	18.2 ± 0.81	17.5 ± 0.57	33.33 ± 3.33	10 ± 0	0.3 ± 0.03
WITA 9	0	1 ± 0	100 ± 0	28.59 ± 0.61	22.8 ± 1.65	253.33 ± 13.33	103.33 ± 3.33	0.41 ± 0.01
	12	9 ± 0	0 ± 0	17.43 ± 0.54	17.11 ± 0.2	50 ± 0	10 ± 0	0.2 ± 0

Wahiwahi	0	1 ± 0	100 ± 0	51.61 ± 1.4	24.07 ± 1.31	323.33 ± 18.56	106.67 ± 3.33	0.33 ± 0.02
	12	7.67 ± 0.67	18.33 ± 10.14	25.92 ± 1.13	15.78 ± 0.43	73.33 ± 8.82	23.33 ± 3.33	0.32 ± 0.01
Waya	0	1 ± 0	100 ± 0	38.18 ± 0.3	21.41 ± 0.61	213.33 ± 27.28	100 ± 5.77	0.49 ± 0.07
	12	8.33 ± 0.67	8.33 ± 8.33	17.56 ± 0.44	17.63 ± 0.9	40 ± 0	10 ± 0	0.25 ± 0
Yunyin	0	1 ± 0	100 ± 0	31.27 ± 0.92	22.2 ± 0.7	260 ± 15.28	103.33 ± 6.67	0.4 ± 0.04
	12	8.33 ± 0.67	5 ± 5	15.07 ± 0.37	13.4 ± 0.7	33.33 ± 3.33	13.33 ± 3.33	0.39 ± 0.06
ZX 117	0	1 ± 0	100 ± 0	34.74 ± 0.81	20.12 ± 1.15	203.33 ± 43.33	113.33 ± 8.82	0.6 ± 0.12
	12	3 ± 0	88.33 ± 6.01	21.46 ± 1.21	16.67 ± 1.2	106.67 ± 3.33	20 ± 0	0.19 ± 0.01
Zambia	0	1 ± 0	100 ± 0	46.93 ± 1.06	23.04 ± 0.15	316.67 ± 12.02	116.67 ± 3.33	0.37 ± 0.01
	12	9 ± 0	0 ± 0	21.62 ± 0.98	13.4 ± 0.49	20 ± 0	13.33 ± 3.33	0.67 ± 0.17
magereza	0	1 ± 0	100 ± 0	32.6 ± 1.42	20.02 ± 1.7	276.67 ± 16.67	110 ± 0	0.4 ± 0.02
	12	7 ± 1.15	10 ± 5.77	20.42 ± 0.87	15.14 ± 0.87	60 ± 5.77	20 ± 0	0.34 ± 0.03

Appendix 2: Mean ± standard errors of phenotypic parameters for different rice varieties under salinity (12 dS/m) and non-saline condition (Experiment 2)

VARIETY	Salinity	Score	Survival	SL cm	RL cm	SDW mg	RDW mg	RDWOVERSDW	Nammolg	K mmolKg	NaK.Ratio
CSR 28	0	1 ± 0	100 ± 0	38.28 ± 0.82	22.17 ± 1.29	283.33 ± 28.48	136.67 ± 3.33	0.49 ± 0.04	0.08 ± 0	470.9 ± 68.59	0.11 ± 0.01
	12	4.33 ± 0.67	86.67 ± 13.33	28.67 ± 2.17	15.94 ± 1.65	233.33 ± 14.53	86.67 ± 3.33	0.39 ± 0.02	1.08 ± 0.16	622.51 ± 46.37	1.03 ± 0.14
FL 478	0	1 ± 0	100 ± 0	37.94 ± 0.2	20.55 ± 0.78	306.67 ± 14.53	116.67 ± 3.33	0.37 ± 0.01	0.08 ± 0.01	598.83 ± 43.44	0.08 ± 0.02
	12	2.33 ± 0.67	100 ± 0	34.63 ± 0.7	16.73 ± 0.44	300 ± 36.06	123.33 ± 13.33	0.3 ± 0.04	0.4 ± 0.04	607.39 ± 15.12	0.39 ± 0.04
INTSINDAGIRA BIGEGA	0	1 ± 0	100 ± 0	41.3 ± 0.39	26.44 ± 0.29	303.33 ± 14.53	146.67 ± 24.04	0.48 ± 0.06	0.08 ± 0.01	548.67 ± 25.92	0.09 ± 0.02
	12	4.33 ± 0.67	83.33 ± 10.14	17.67 ± 1.33	13.44 ± 0.8	93.33 ± 8.82	30 ± 0	0.33 ± 0.03	0.72 ± 0.04	501.53 ± 40.01	0.85 ± 0.04
IR 29	0	1 ± 0	100 ± 0	36 ± 1.07	22.89 ± 1.24	223.33 ± 3.33	100 ± 5.77	0.45 ± 0.03	0.07 ± 0.01	522.75 ± 44.9	0.09 ± 0.01
	12	9 ± 0	0 ± 0	13.61 ± 1.45	11.56 ± 1.06	76.67 ± 6.67	13.33 ± 3.33	0.18 ± 0.06	6.21 ± 0.16	531.77 ± 0	6.87 ± 0.18
IRRI 154	0	1 ± 0	100 ± 0	39.83 ± 2.42	25.17 ± 1.23	250 ± 15.28	116.67 ± 3.33	0.47 ± 0.04	0.06 ± 0.01	470.9 ± 25.92	0.08 ± 0.02
	12	9 ± 0	0 ± 0	17.67 ± 0.58	13.11 ± 0.78	100 ± 5.77	10 ± 0	0.1 ± 0.01	5.73 ± 0.16	441.04 ± 26.19	7.67 ± 0.3
K 5	0	1 ± 0	100 ± 0	38.99 ± 0.2	26.78 ± 1.09	243.33 ± 20.28	110 ± 5.77	0.46 ± 0.03	0.07 ± 0.01	444.98 ± 44.9	0.1 ± 0.02
	12	4.33 ± 0.67	63.33 ± 1.67	24.44 ± 0.89	17.56 ± 0.48	110 ± 11.55	43.33 ± 3.33	0.41 ± 0.08	1.04 ± 0.14	645.43 ± 73.14	0.95 ± 0.11
Kijicho	0	1 ± 0	100 ± 0	46.28 ± 1.31	23.72 ± 0.66	213.33 ± 17.64	110 ± 10	0.52 ± 0.02	0.07 ± 0.01	341.29 ± 25.92	0.13 ± 0
	12	8.33 ± 0.67	15 ± 15	18.28 ± 0.89	16.78 ± 1.54	56.67 ± 8.82	16.67 ± 3.33	0.29 ± 0.02	4.45 ± 0.89	301.22 ± 43.63	8.52 ± 0.66
LINE 16	0	1 ± 0	100 ± 0	46.28 ± 0.15	33.27 ± 0.83	226.67 ± 8.82	110 ± 5.77	0.49 ± 0.02	0.06 ± 0.02	393.13 ± 25.92	0.09 ± 0.04
	12	8.33 ± 0.67	10 ± 10	19.89 ± 0.8	18.11 ± 1.1	53.33 ± 8.82	13.33 ± 3.33	0.25 ± 0.03	4.93 ± 0.32	502.84 ± 39.03	5.78 ± 0.16
Nona Bokra	0	1 ± 0	100 ± 0	55.56 ± 2.79	26.06 ± 1.59	296.67 ± 3.33	113.33 ± 8.82	0.38 ± 0.03	0.06 ± 0.01	367.21 ± 44.9	0.09 ± 0.02
	12	3 ± 0	100 ± 0	42.4 ± 3.61	17.61 ± 0.15	260 ± 15.28	66.67 ± 13.33	0.26 ± 0.06	0.76 ± 0	713.24 ± 26.19	0.63 ± 0.02
Pokkali	0	1 ± 0	100 ± 0	51.7 ± 1.21	22.83 ± 0.42	313.33 ± 13.33	116.67 ± 6.67	0.37 ± 0	0.07 ± 0.01	393.13 ± 25.92	0.11 ± 0.02
	12	3 ± 0	100 ± 0	46.52 ± 3.48	19.11 ± 1.28	263.33 ± 8.82	33.33 ± 3.33	0.13 ± 0.01	0.8 ± 0.24	743.48 ± 30.24	0.62 ± 0.17
SATO 1	0	1 ± 0	100 ± 0	36.44 ± 0.25	25.83 ± 0.35	270 ± 5.77	126.67 ± 8.82	0.47 ± 0.03	0.09 ± 0.01	341.29 ± 25.92	0.16 ± 0.01
	12	5 ± 0	56.67 ± 3.33	19.78 ± 1.5	16.89 ± 1.85	116.67 ± 6.67	26.67 ± 3.33	0.23 ± 0.03	0.92 ± 0.16	516.65 ± 54.52	1.04 ± 0.07
Sukari	0	1 ± 0	100 ± 0	51.35 ± 1.81	23.05 ± 0.49	280 ± 11.55	126.67 ± 3.33	0.45 ± 0.02	0.07 ± 0.01	444.98 ± 44.9	0.09 ± 0.01
	12	5.67 ± 0.67	43.33 ± 4.41	22.11 ± 1.06	15.33 ± 0.51	83.33 ± 3.33	23.33 ± 3.33	0.28 ± 0.03	1.08 ± 0.16	662.02 ± 30.25	1.13 ± 0.15
TERIMBERE (LL29)	0	1 ± 0	100 ± 0	33.13 ± 3.1	23.5 ± 3.03	230 ± 10	103.33 ± 3.33	0.45 ± 0	0.08 ± 0.01	548.67 ± 25.92	0.09 ± 0.02
	12	4.33 ± 0.67	66.67 ± 6.01	21.56 ± 1.44	16.45 ± 0.91	116.67 ± 6.67	33.33 ± 6.67	0.28 ± 0.05	0.54 ± 0.08	605.42 ± 104.04	0.56 ± 0.15
ZK 117	0	1 ± 0	100 ± 0	34.89 ± 0.4	22.17 ± 0.44	206.67 ± 12.02	116.67 ± 12.02	0.56 ± 0.03	0.07 ± 0.01	522.75 ± 0	0.08 ± 0.01
	12	5 ± 0	63.33 ± 10.93	18 ± 1.15	14.22 ± 0.62	56.67 ± 12.02	16.67 ± 3.33	0.3 ± 0.05	0.92 ± 0.16	486.4 ± 45.37	1.11 ± 0.15