MOLECULAR AND MORPHOLOGICAL CHARACTERIZATION OF GRAINYIELD AND ROOT ARCHITECTURE OF SELECTED FAYA RICEGENOTYPES

ELIAS JEKE

A DISSERTATION SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE IN CROP SCIENCE OF SOKOINE UNIVERSITY OF AGRICULTURE. MOROGORO, TANZANIA.

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ABSTRACT

The screen house and field experiments were conducted during the 2017 /2018 rainy season in order to characterize grain yield and root architecture of fifteen(15) selected Faya rice genotypes namely; Faya 14 M 69, Faya Zambia, Faya Mafuta 1, Faya Mafuta 2, Faya Makanjira, Acc 5934, Mw 1685, Acc 9290, Acc 9293, Acc 18037, Acc 18028, Acc 17323, Acc 17344, Acc 5933, and Faya Kalonga, at both molecular and morphological levels for further utilization in crop breeding programmes. The fifteen (15) selected Faya rice genotypes were obtained from Lifuwu Agricultural Research Station (LARS). The molecular work was conducted at the Molecular Biology Laboratory of Sokoine University of Agriculture (Tanzania) using ten (10) Simple Sequence Repeat (SSR) markers. The morphological study was done at Lifuwu Research Station (Malawi) on twelve (12) qualitative and twelve (12) quantitative morphological traits, five (5) root architectural traits and seven (7)grain quality traits in screen house (using PVC pipes) and field conditions. The present study illustrated rich genetic divergence for different quantitative and qualitative traits among the Faya rice genotypes. The quantitative traits such as grain yield, 1000 grain weight, spikelet fertility, number of panicles per plant, number of tillers per plant, panicle length, leaf length, leaf width, flag leaf length, flag leaf width and number of spikelets per panicle illustrated most variation. The studied root architectural traits such as fresh root mass, root number, maximum root length, fresh shoot mass, dry root mass and dry shoot mass showed great variation among the studied genotypes. All the grain quality traits in the present study showed no variation except translucency, chalkiness, gelatinization temperature and gel consistency. The eleven qualitative traits studied depicted great variation. Grain yield trait correlated positively with root

number, root thickness (root volume), 1000 grain weight, number of spikelets per panicle, spikelet fertility and plant height and negatively with the other associated traits that were analyzed. The agglomerative hierarchical clustering using twenty five (25) quantitative morphological, grain quality, and root architectural traits grouped the fifteen (15) Faya rice genotypes into four (4) clusters and five Principal Components while the same genotypes were categorized into three clusters when ten (10) SSR markers were used for clustering. All the ten (10) SSR (Microsatellite) markers that were used in studying the 15 Faya rice genotypes turned out to be polymorphic for the target traits and amplified 142 bands and 63 alleles. The least genetic similarity index magnitude detected for and among the genotypes implies that some of the genotypes studied have closely similar genetic constitution while others are distantly similar. The highest Polymerase Information Content (PIC) value was recorded for primer RM215 and all the markers used in this study were neutral, convenient and co-dominant in nature. The screening of the genotypes using both morphological and molecular (SSR) markers for the fifteen (15) rice genotypes has revealed that the genotypes are diverse and would produce significant transgressive segregants if used in general and hybridization breeding work. All the SSR markers used in this study have proven to be a success in studying the land races of rice as evidenced in the current work where all markers turned out to be polymorphic.

DECLARATION

I, Elias Jeke, do hereby declare to the Senate of Sokoine University of Agriculture that this Dissertation is my own original work done within the period of Master Study and that it has never been submitted to any university for an award of any degree.

_____ _____

Elias Jeke Date

(MSc. Candidate)

The above declaration is confirmed by:

_____ _____

Dr. Ashura Luzi Kihupi. Date

(Supervisor)

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DEDICATION

I dedicate this work to my daughters; Ellen and Christina, you are a delight in this journey. To my wife Kester; thank you for being there for me even when times could be hard. To my parents, brothers and sisters, for your encouragement and patience during my study.

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LIST OF ABBREVIATIONS

°C	Degree Celsius
%	Percentage
AFLP	Amplified Fragment Length Polymorphism
AGE	Agarose Gel Electrophoresis
AHC	Agglomerative Hierarchical Clustering
APPSA	Agricultural Productivity Program for Southern Africa
Bp	Base Pairs
CTAB	Cetyl Trimethyl Ammonium Bromide
DARS	Department of Agricultural Research Services
DNA	Deoxyribonucleic Acid
ESA	East and Southern Africa
IRRI	International Rice Research Institute
L	Ladder
LARS	Lifuwu Agricultural Research Station
MOAIWD	Ministry of Agriculture, Irrigation and Water Development
NILs	Near Isogenic Lines
µl	Microliter
PCR	Polymerase Chain Reaction
PIC	Polymorphism Information Content
QTL	Quantitative Traits Loci
PVC	Polyvinyl Chloride
RCBD	Randomized Complete Block Design

SCAR	Sequence Cleaved Amplified Region
RAPD	Randomly Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
Rpm	Revolutions per minute
SES	Standard Evaluation System
SNP	Single Nucleotide Polymorphism
SSRs	Simple Sequence Repeats
STMs	Sequence Tagged Microsatellites
T	Treatment
SUA	Sokoine University of Agriculture
UV	Ultraviolet
UPGMA	Unweighted Paired Group Mathematical Average

CHAPTER ONE

1.0 INTRODUCTION

Rice *(Oryza sativa L)* is one of the most important staple food crops of the world. Rice is a nutritious cereal crop, providing 15 per cent of protein consumed by the world's population. It is believed that rice originated in south - eastern Asia from where it spread eastward into China. Eventually it spread west - wards into Asia Minor, Southern Europe and Africa. In some African countries such as Malawi and Tanzania, it is ranked second to maize (Mzengeza, 2010) and (FAOSTAT, 2015), and first in some Asian countries like India and china in feeding the increasing population (Zhang, 2007). Malawi has an estimated annual rice production of 99,272 tons from a total of 50,146 hectares of rice paddy area (Kanyika, *et al* 2007) grown as rain fed lowland, rainfed upland and irrigated lowland.

Rice taxonomical aspect illustrates that it belongs to the kingdom: Plantae, subkingdom: Tracheobionta, superdivision: Spermatophyta, division: Magnoliophyta, class: Lilliopsida, subclass: Commelinidae, order: Cyperales, family: Poaceae or Gramineae, genus: Oryza L, species: *Oryza sativa L* (Acquaah, 2007; Ballan, 2013) and is a monocot. The genus Oryza is distributed throughout the tropics and subtropics of the world. The genus consists of 23 wild and weedy species and two cultivated species, namely; *O. sativa L*. and *O. glaberrima.* L for Asia and Africa respectively (Joachim, 2015).There are three (3) geographical races of *Oryza sativa* rice worldwide, namely; Indica group, consisting of the cultivated rices of the tropical regions in India, Indo – China, and the Philippines, Japonica group and javanica group, which are highly or partially sterile. The basic chromosome number of the

genus is n=12. The species are either diploid with 2n=24 chromosomes or tetraploids with 2n=48 chromosomes. The genotypes studied in this investigation are diploids with 2n=24 chromosomes and are landraces suitable for lowland rainfed conditions.

Oryza sativa L. is basically an autogamous plant propagating through seeds produced by self pollination. Generally *O. sativa* as a self-pollinated species can only permit a 0.5% natural out crossing. The rice inflorescence is a panicle which bears single – flowered spikelets. Fertilization occurs in spikelets, which have six anthers with more than one thousand (1,000) pollen grains in each, and an ovule with a branched stigma. The flower is surrounded by a lemma and palea, structures which form the hull that encloses the threshed grain. The outer glumes are usually obscure, being only about one – fourth the length of the lemma and palea, despite that in some varieties they approach the lemma and palea in length. The blooming of rice normally takes place between 8 A.M and 4 P.M., with the largest number of flowers opening around or before noon. The mean blooming duration of a flower in a single panicle ranges from seven to ten days and this varies depending on the varieties and rice growing environment.

In this study, the main focus was to characterize grain yield, grain quality, other plant growth parameters, and root architectural diversity of the selected Faya rice genotypes using both molecular and morphological markers. Grain yield in rice is generally determined from yield components namely; number of panicles / sq m, 1000 grain weight, spikelet fertility, and number of spikelets/panicle. The yield of rice also depends on grain quality characteristics (Mzengeza, 2010). Examples of such grain quality characteristics include nutritional and milling qualities, appearance, and grain

size. The size of the rice grain is very fundamental for its contribution to both yield and marketing of the grain as consumer preferences differ. Determination of the grain size considers such characters as grain length, width and shape.

According to Abade *et al*., (2016), Kilombero and Faya 14M 69 are the most aromatic landraces that are produced and have high marketability value in Malawi. However, there is a lack of information on grain quality characteristics for most Faya rice genotypes.

The rice grain quality can be described in two distinguishing categories, namely; the consumers' basis and the millers' basis. The consumer describes rice quality basing on grain size and shape, cooking behaviour, grain colour, taste, tenderness, flavor when cooked, and nutritional value (Abdallah *et al.,* 2016). On the other hand, the millers' description of quality is based on total milling recovery and the proportion of head and broken rice on milling. Grain quality is a crucial character to study not only because of its contribution to yield, but also due to its influence in rice marketing and trade (Abdallah *et al.,* 2016). Grain length, width and shape are positively correlated characters (Anandakumar and Utharasu, 2013). Studies on grain quality characters have shown different results concerning its genetic control. It is from these great attributes of grain quality in rice that made this study consider characterizing the Faya genotypes quality.

Furthermore, it is appreciated that much work in rice has been done on the upper part of the plant namely; tillering ability, number of panicles, flag leaf length, leaf area grain yield and spikelet fertility, among others, and little on the lower part (root

architecture). Rice has a fibrous root system which is divided into three categories namely; seminal roots, mesocotyl roots and nodal roots. It is the latter root type (nodal root) which was studied in this paper. The root system plays an important role under both normal and drought conditions. The nature and extent of root characteristics are considered to be major factors affecting plant response to water stress. The root diameter (thickness) and root length density (RLD) are used to characterize root system development of rice cultivars (Henry et al., 2011). Roots offer anchorage to the rice plant. The absorption of nutrients and water from the soil which is eventually translated into grain is accomplished by roots. Roots are responsible for determination of the tillering ability of some rice cultivars. It was important therefore to conduct more studies on rice cultivar differences in terms of root system developments and their correlations with other plant growth parameters.

The process of studying the aforementioned traits demands a combination of both morphological and molecular markers, as morphological markers alone have tended to be limited and not associated with important economic traits (for example; grain yield and quality).Some examples of morphological markers include leaf shape, flower colour and ligule length. Molecular marker technique is a tool for selecting such complex traits as root and yield, and permit molecular breeders to detect genetic loci controlling traits for drought tolerance / resistance, grain yield, aroma, and grain recovery among others without having to measure the phenotype. Examples of such molecular markers include Simple Sequence Repeats (SSRs) Markers. These studies are vital for molecular breeders and variety developers as they help to identify traits and genotypes that can be utilized in further rice genetic improvement and / or introduced as cultivars.

1.1 Overall objective.

The overall objective was therefore to characterize grain yield and root architecture of selected Faya rice genotypes in order to identify superior genotypes that can be used in breeding programmes.

1.2 Specific Objectives

The specific objectives of the study were to;

(1) Phenotype the root traits and other growth parameters using morphological markers.

(2) Evaluate grain quality, grain yield components and some growth parameters of the genotypes.

(3) Determine diversity of grain yield and some root traits of the genotypes using Simple Sequence Repeats (SSR) molecular markers.

CHAPTER TWO

2.0 LITELATURE REVIEW

2.1 Rice production

Rice (*Oryza sativa. L*) is one of the most important staple food crops (Khush,2005) feeding more than half of the world's population (Veeresha *et al.*,2015). It is estimated that at least 50% more food will need to be produced (Alexandratos and Bruinsma, 2012) to feed the world's population which is projected to grow to 9.5 billion in 2050.

Rice provides 21% of energy and 15% of protein for human better nutrition (Zibaee, 2013). It is ranked first in some Asian countries like India and China (Zhang, 2007). In Malawi, rice is the second important staple food crop after maize (Mzengeza, 2010). In Tanzania, rice is the second major and popular food crop after maize in terms of production volume, farmers involved and cultivated area (FAOSTAT, 2015).

Ballan (2013), reported that overall, there is an estimated global need for an additional 116 million tons of rice by 2035 as compared to439 million tons production in 2010. Malawi has an estimated annual rice production of 99,272tons from a total of 50,146 hectares of rice paddy area (Kanyika *et al.*, 2007) grown as rainfed lowland, upland and irrigated rice.

Lowland rice production can either be rainfed or irrigated. Generally, rainfed lowland rice ecosystems lack water supply and / or water control hence subjected to flooding or drought (Anonymous, 2010) and (Balasubramanian *et al.*, 2007). According to Ballan (2013), upland rice, is a unique rice ecotype that can be grown on upland fields where soil remains aerobic. There are several rice genotypes which can either be

landraces (Modi, 2004) with traits vital for crop advancement (Jameel *et al.*, 2015), improved varieties and Near Isogenic Lines (NILs) (Shashidhar *et al.*,,2012and Prabuddha et al., 2008). The rice landrace are local cultivars that have been grown by farmers for a long time in a particular area.

2.2Grain yield and quality characterization

The main purpose of any breeding programme is to attain high grain yield. A breeder can be working on development of disease resistant or drought tolerant rice varieties (Tomar *et al*, 2016) but by the end of the day need to translate into high yields for the common farmer (Banumathy *et al.,* 2010). Grain yield is usually obtained either from the yield components such as number of productive tillers (panicles) per square metre, spikelets / panicle, fertility percentage (Ripening Ratio), the 1000 grain weight, or net plot. One of the most fundamental considerations by rice breeders in varieties development is good grain quality (Bautista *et al.*, 2009; Bhonsle and Selaphan, 2010). This is the case because even varieties with high yield can be rejected by consumers and traders (Aniekwe, 2010) because of their poor appearance or opaqueness (chalky), cooking and eating qualities (Traore, 2005).The characterization and improvement of rice genotypes should therefore put in consideration of the rice grain yield and quality parameters.

2.3 Importance of rice roots system

A plant root system consists of different kinds of roots that vary in morphology and function. Rice has a fibrous root system which is divided into three categories, namely; seminal roots, mesocotyl roots and nodal roots. The three root classes vary in origin, anatomy and function .The rice seminal root, also known as the embryonic or

radical root is the first root which breaks through the covering very soon after coleorhiza emerges during seed germination. This root grows 3 – 5 cm long within 2 – 3 days after seed germination (Gowdal *et al.*, 2011). There is only one radical root in rice and is usually the longest root before the third – leaf period which lasts up to the seventh - leaf stage or early vegetative stage. Mesocotyl roots are those that grow from the axis between the node of the coleoptiles and the base of the radical and they develop only when the seed is treated with some chemicals or under deep seeding. They usually lack coarseness and branch or lateral roots. Nodal roots are post embryonic roots which emerge from the nodes at the base of the rice plant stem and tillers. They elongate deeply into the soil which later initiate the emergence and growth of branches or laterals from the pericycle and epidermis. The branch or lateral root have been distinguished into three, namely; the L – type, M – type and S – type. The L – type are usually long and course with length range of 0.2 – 0.3mm, M – type are long and course lateral roots without branches and S – type are short, fine, numerous and non – branching lateral roots generally ranging from 0.035 – 0.1 mm. The spatial configuration and distribution of these roots determine root system architecture (Gowdal, *et al.,* 2011; Kanbar *et al.,* 2009; Henry, *et al.,* 2011).

The root system plays fundamental functions in rice growth and development, namely: acquisition of nutrient elements and water (Toorchi *et al.,* 2007), enhancing tolerance of the plant to abiotic stress and anchorage of the plant including biosynthesis of hormones and amino acids. The roots are responsible for absorption of most nutrients and water. Inorganic carbon is absorbed in the form of carbon dioxide mainly by leaves while all the other essential mineral elements are absorbed through root surface from the soil for rice growth. There is high grain yield mainly due to a greater sink

size (total number of spikelets) caused by a larger panicle influenced by increased root activity. One of the most severe abiotic stresses limiting rice productivity in the world is drought (Haider *et. al.,* 2012; Kadioghu, 2012) and has a serious impact on the sustainability of rice yields in rainfed farming system. Drought is a climatic abnormality, characterized by deficient supply of moisture resulting either from sub-normal rainfall, erratic rainfall distribution, higher water need, salt concentrations or a combination of all the factors. The mode of drought resistance with which roots are most likely associated is drought avoidance. Genotypes that have deep, coarse roots with a high ability of branching and penetration, elasticity in leaf rolling, high cuticular resistance, higher root to shoot ratio, and early stomatal closure are reported as component traits of drought avoidance (Wang and Yamauchi, 2006).The mechanism for drought tolerance in rice is accomplished by the ability of the plant to absorb more water from soil (Abbas *et al.*, 2014). Therefore, the key to developing elite rice varieties suitable for water use efficiency is to improve the root system with deep root and high water uptake ability.

Soil salinity is another severe abiotic stress affecting rice production. High salt stress, which occurs at both cellular and the entire plant levels, disrupts homeostasis in water potential and ion distribution. Great changes in ion and water homeostasis lead to molecular damage, growth arrest and even death of the plant. Roots therefore play a fundamental role in the exclusion of sodium and chloride (Na^+ and Cl^-) ions for plants growing in saline soils.

Although the understanding about rice root has been expanded in the last decades, there remains much to be done about root morphology and physiology, especially in

the genetics of roots. There is a close relation between above ground traits and underground roots, providing an alternative approach for rice genetic improvement. However, root research is still a consuming and difficult work, because it is largely influenced by the complex underground environment, hence a need to find methods of studying them and inclusion of molecular markers.

2.4 Methods of root phenotyping

The growth of roots, morphology and distribution are closely related to many factors such as genetics, growth stage, tillage, soil water and nutrients, soil temperature and other soil properties. The studying of the root architecture is not a simple process due to the complex nature of the roots as they are hidden in the soil. There are several methods of studying the roots of rice plants in a somehow simpler way (Han et al., 2016) among which some of them include; root sampling by using a root box pin - board method. This method enables us to collect the entire root system with minimum disturbance to its structure. This can also be used to evaluate the response of root system development and plant water use precisely.

Glass rhizotrons is also another method of studying roots. In this method, plants are gown in thin rhizotrons with glass sides that are filled with soil and inclined at 15º. Photographs are taken and non - destructive assessment made of root traits such as rooting angle and depth whenever needed.

The basket method of root phenotyping is also used to study roots. In this method, the average growth angle of rice nodal roots is evaluated more easily. The advantage of this method is that it enables researchers to quantitatively determine which accession

is a shallow- or deep-rooting type. This method can also be used in several experimental conditions ranging from field to hydroponic culture.

Furthermore, the use of PVC tubes is also another method of studying roots. In this method plants are gown in PVC tubes that are filled with soil. For rice, 20-cm-wide and 100-cm-long tubes are recommended but the sizes vary depending on the number of days the plants are expected to be grown in the soil and plant space. The study can be done in a greenhouse or in an open field conditions. It is the latter method that the screen house experiment presented in this paper adopted.

2.5 Markers for rice breeding

2.5.1 Morphological markers

The marker- assisted breeding is traced back a long time to the use of classical or morphological markers as an assisting tool for selection of plants with desired characteristics in breeding programs (Jameel *et al.*, 2015). The markers used in early history of plant breeding mainly included visible morphological traits, such as leaf shape, flower color, pubescence color, seed shape, awn type and length, leaf rolling, ligule shape and colour, pod color, and seed colour, among others. These morphological markers generally represent genetic polymorphisms which are easily identified and manipulated. Some of these markers are linked with other agronomic traits and thus can be used as indirect selection criteria in practical breeding. However, morphological markers available are limited, and many of these markers are not associated with important economic traits (for example; grain yield and quality) and even have undesirable effects on the development and growth of plants; hence calls for molecular markers.

2.5.2 Molecular markers

Molecular marker technique is a tool for selecting such complex traits as root and yield, and permit molecular plant breeders to detect genetic loci controlling traits for drought tolerance / resistance, grain yield, aroma, and grain recovery among others without having to measure the phenotype (Yoshida *et al.,* 2010). This helps in reducing breeding time and labour need to conduct field work (Gowda *et al.,* 2011). Different molecular markers namely; Simple Sequence Repeat (SSR), Sequence Cleaved Amplified Region (SCAR), Amplified Fragment Length Polymorphism (AFLP), Random Amplified Polymorphic DNA (RAPD), Restriction Fragment Length Polymorphism (RFLP), and Single Nucleotide Polymorphism (SNP) (Brara, 2015; Hossain *et al.*, 2007; Srividhya *et al.*, 2011) are being used not as a replacement for but a valued supplement to conventional breeding. Molecular markers, for example; Simple Sequence Repeats (SSRs), have proven vital in determination of genetic diversity within and among species (Shashidhar *et al.,* 2014; Etemad *et al.*, 2012; Ahmad, 2015). Basically, Simple Sequence Repeats (SSRs) are also referred to as microsatellite and are the most commonly used molecular markers. They are generally PCR dependent markers which are cost effective, highly reproducible, discriminatory efficiency (Ballan, 2013) and detecting any polymorphism of a particular trait (Jameel *et al*., 2015; Hong *et al.,* 2010) for further varieties development.

Microsatellite Markers have been used for characterization of genetic diversity (Hosan *et al.,* 2010) in different plant species such as wheat (Tomar *et al.,* 2016).The genetic diversity of both cultivated and wild species have also been examined in rice (Afiukwa *et al.,*2016).

It is from this background that the present study was undertaken to assess the genetic diversity of 15 selected Faya rice genotypes to screen out the grain yield and root architecture in order to select diversified parents having desirable traits.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Plant materials

The fifteen (15) selected Faya rice genotypes sourced from Lifuwu Agricultural Research Station in Malawi were the plant materials used in this study. All the genotypes are *Oryza sativa* land races suitable for lowland ecosystem.

Table 1: List of selected Faya rice genotypes and their origin

SR NO.	ENTRY IDENTITY	NAME OF GENOTYPE	ORIGIN
1	T1	Mw 1685	Malawi
2	T2	Faya 14 M 69	Malawi
3	T3	Acc 9290	Malawi
4	T4	Faya Mafuta 1	Malawi
5	T5	Acc 18028	Malawi
6	T6	Faya Kalonga	Malawi
7	T7	Acc 5934	Malawi
8	T8	Acc 18037	Malawi
9	T9	Faya Makanjira	Malawi
10	T10	Acc 17323	Malawi
11	T11	Acc 5933	Malawi
12	T12	Faya Zambia	Zambia
13	T13	Acc 17344	Malawi
14	T14	Faya Mafuta 2	Malawi
15	T15	Acc 9293	Malawi

Note: Acc = Accession

3.2 Methods

3.2.1 Screen House (PVC) Experiment

3.2.1.1 Characterization of the root traits and other growth parameters in PVC pipes using morphological markers.

The selected Faya rice genotypes were grown in the screen house conditions using the polyvinyl chloride (PVC) tubes of 100 cm height and > 15 cm diameter laid out in a

Randomized Complete Block Design (RCBD) in order to evaluate the morphological traits. The PVC pipes were used in the screen house in order to easily study the root architecture and other growth parameters so as to complement field studies. The experiment was conducted at Lifuwu Agricultural Research Station in Malawi, during the 2017/2018 rainy season commencing in November, 2017 and ending in May, 2018.

There were three (3) replicates and the fifteen (15) selected genotypes constituted the experimental treatments. The PVC pipes, which represented each hill, were spaced at 25 x 25 cm so as to follow the recommended field spacing normally used for the rice crop. The pipes were buried in the ground to a depth of 10 cm each filled with clay loam soil. Four (4) PVC pipes were used as hills in which each genotype was planted per replicate. Three pre-germinated seedlings were directly planted into each PVC pipe and thinned to one (1) at 10 days after seedling emergence (DASE). The recommended cultural practices such as fertilizer applications were done at 10 days after seedling emergency (DASE) and 40 days after seedling emergency (DASE) for NPK and Urea respectively. The fertilizer rate was 2.05 g per hill (one PVC pipe) representing 120 kg per hectare for each of NPK basal dressing and Urea top dressing fertilizers. Water was applied at 2 days interval except the week of fertilizer application in which the frequency was increased to everyday. Weeding was practiced using hands and was done upon appearance of the weeds.

The observations on the following morphological features were recorded at the respective plant stages; number of tillers (NT) per hill, number of days to flowering, flag leaf length (FLL) and width, basal leaf length and width, panicle length, plant

height, number of panicles per plant, number of days to maturity, number of grains (spikelets) per panicle, 1000 grain weight, and grain yield, were assessed, and analyzed.

Number of days to 50% flowering: This is recorded as number of days when approximately half (50%) of the plants have headed.

Number of tillers per hill: This parameter was accomplished by counting the total number of tillers per hill / station during maturity stage of the crop.

Spikelet fertility percentage (Filling grain ratio): Total number of filled and unfilled grains (spikelets) per panicle was counted to calculate the spikelet fertility in a panicle. The following formula was applied to get the actual percentage;

Spikelet fertility percentage = Filled grains/ Unfilled Grains x 100

Flag leaf length: A flag leaf is the last leaf in a rice plant and its length was measured in centimeters using a ruler from the ligule to the tip of the blade on five plants that were sampled.

Flag leaf width: This was measured in centimeters using a ruler at the widest segment of the flag leaf on five sampled plants.

Leaf blade length: This was measured in centimeters from the ligule to the tip of the blade on five representative plants and the mean value was eventually calculated. The leaf of interest is that lying below the flag leaf in a rice plant.

Leaf blade width: This parameter was measured on the same highest leaf below the flag leaf on which length was collected for the five representative plants

Panicle length: This was measured in centimeters from the panicle node to the tip of the panicle using a ruler.

Number of panicles per plant: The number of panicles was recorded per hill for all the plants and averages taken for all the three replicates of the treatment.

Number of days to maturity: This was recorded as the date on which approximately 80% of the grains on the panicle were fully ripened and ready for harvesting.

Plant height: This was measured in centimeters (cm) using a plant height ruler at maturity stage from the soil surface to the top of the spike excluding the awns (for the genotypes which posses awns).

Number of grains (spikelets) per panicle: This was counted using a grain counter as the number of grains obtained from each panicle.

Grain yield / plant: The grains weight of individual plants was recorded in grams using a digital balance. The averages for all the three replicates were taken and equated to yield per hectare after adjusting the moisture content of the grain to 14 %.

In order to separate the root architecture from the upper part of the plants during harvest, the shoots were cut at the base and the pipes filled with water for overnight to loosen the soil. The following day, the pipes were relieved of the soil and the roots thoroughly washed using a water horse pipe.

Rice root architectural phenotyping

The root traits morphological data such as maximum root length (MRL), root number (RN), fresh and dry Root weight, fresh shoot weight, dry shoot weight, root / shoot ratio, and root volume (root thickness), were recorded after root washing as discussed below.

Fresh root mass (g): This parameter was recorded in grams using a digital balance. As a process, the roots were cleared and blotted with filter paper in order to remove any excess water and the fresh weights were eventually measured.

Dry root mass (g): The roots were oven - dried at 70 ^{o}C for 72 hours and the dry weight captured in grams using a digital balance.

Fresh shoot weight (g): The shoots weight of each genotype was recorded using a digital weighing balance after cutting them into small pieces of < 10 cm.

Dry shoot weight (g): The shoots were then placed in envelopes and oven dried at 70 ^{o} C for 72 hours (three days) followed by recording of the weight using a digital balance.

Maximum root length: This was recorded in centimeters from the crown to the root tip as the length of the longest root of a particular plant. It was achieved using a measuring ruler. The Maximum Root Length gives the plant potential to absorb moisture and nutrients in deeper soil layer for its use.

Root number: The total number of roots per plant at crown region was determined for each plant. The method was simply counting the number of roots available in each plant. This trait is important for the physical strength and potential for root system architecture of the plant.

Root volume or root thickness: The Root volume was measured in milliliter (ml) which is equivalent to cubic centimeters (cc) using water displacement procedure. In this method, a beaker of known volume was filled with water and the respective plant roots were placed in the same beaker. The volume of water which came out after placing the roots was regarded as the actual root volume of the plant roots in question. This trait was studied because it gives the plant the ability to permeate a large volume of soil.

Root to shoot ratio (R / SR): This relationship trait was determined by dividing the measurements of the roots by those of the shoots.

Grain length: This was recorded on 10 randomly selected grains from the base of the lowermost glumes to the tip of the fertile lemma or palea using a caliper in millimeter (mm).

Grain width: This parameter was measured on 10 representative plants using a caliper as a distance across the fertile lemma and palea at the widest point in millimeter (mm).

Brown rice shape: This was measured by dividing the grain length value with that of the grain width of the respective genotype.

1000 grain weight: The one thousand (1000) grains were counted using an electronic grain counter prior to determining the weight using a digital weighing balance.

3.2.2 Field experiment

3.2.2.1 Evaluation of grain yield, quality and other growth parameters of the genotypes using morphological markers in field conditions

3.2.2.1.1 Plant materials

The same genotypes used in the screen house as elaborated in Table1, above were also used in the field condition to accomplish this specific objective.

3.2.2.1.2 Methods

The fifteen (15) selected Faya rice genotypes were also grown in the field conditions. The field experiment was also laid out in a Randomized Complete Block Design (RCBD) in order to evaluate the morphological traits. The experiment was conducted at Lifuwu Agricultural Research Station experimental farm in Malawi; during the 2017 / 2018 rainy season starting in December, 2017 to May, 2018.The experimental area received a rainfall amount of 1420 mm during the season in question. The experiment was replicated three (3) times. Each treatment was planted in a plot measuring 5 m x 0.5 m (gross area of 2.5 m^2).The spacing between rows was 25 cm x

25 cm. The plants were also spaced at 25 cm x 25 cm and the net area for grain yield harvesting was 1 m^2 (4 m x 0.25 m). There was a 50 cm space separating each replicate whereas a 30 cm space was adopted to separate the plots. The genotypes were randomly allocated to the plots as illustrated in the figure below.

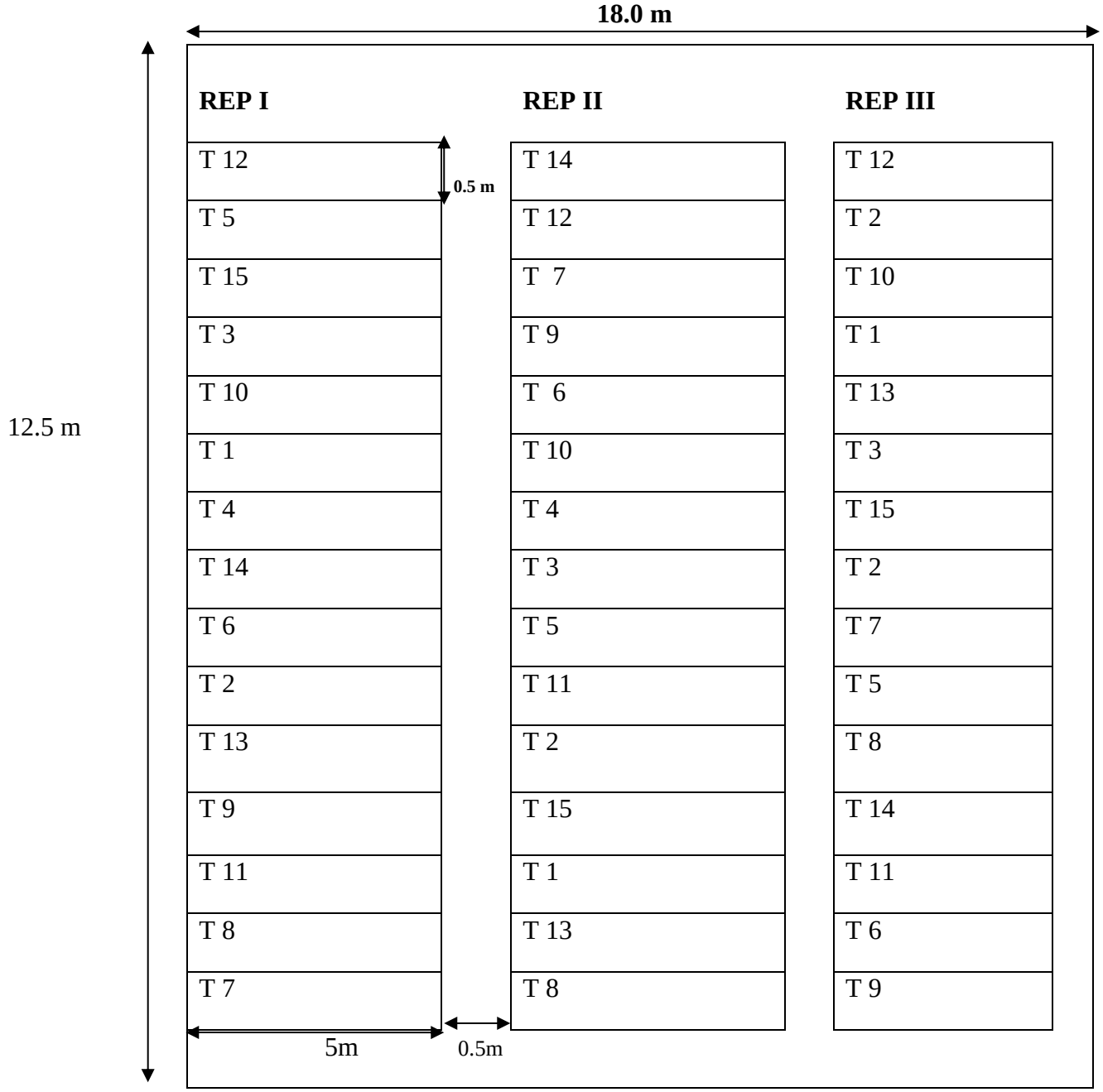

Figure 1: Field lay out for the fifteen (15) studied Faya rice genotypes

3.2.2.1.3 Data collection and analysis

The growth morphological data such as plant height, panicle length, basal leaf length and width, leaf blade colour, basal leaf sheath colour, flag leaf length and width, ligule shape and colour, leaf blade pubescence, auricle presence / absence and colour, lemma and palea colour, stigma colour, panicle types, panicle exsertion, panicle altitude of branches, apiculus colour, awning, sterile lemma colour were recorded. Moreover, number of spikelets (grains) / panicle, 1000 grain weight, number of days to 50% flowering, no of days to maturity, spikelet fertility percentage, panicle threshability, number of tillers per plant/hill, number of panicles per plant were also recorded. Grain quality traits such as chalkiness, translucency, amylose content, gelatinization temperature, gel consistency, brown rice size (length, width) and brown rice shape were collected (based on descriptor from Bioversity International (IRRI) and (WARDA) (2007). Grain yield for the genotypes was eventually recorded. In the case of the field condition, sixteen plants from the middle row of each plot (i.e. 1 m^2 net plot) were harvested, threshed and air-dried. The total grain weight for each plot was measured in grams and converted to tons / ha at 14% moisture content

Data analysis was done for analysis of variance (ANOVA) using Genstat 16^{th} edition software. Correlations were established as used by Pearson (n) excel procedure (Abdallah *et al.,* 2016) to illustrate the relationships between root architecture and other growth traits with grain yield. The agglomerative hierarchical clustering for dendrogram was done using XLSTAT 2018 Version on the Euclidean distance matrix following the Ward's linkage procedure on the 25 morphological markers. Principal Component Analysis (PCA) was also performed by using the XLSTAT 2018 Version.

The twenty five (25) morphological markers in field condition also comprised parameter measurements of traits in the screen house and were recorded as follows;

Number of tillers per hill: This parameter was accomplished by counting the total number of tillers per hill (plant) during maturity stage of the crop.

Number of days to 50% flowering: This was achieved by recording the number of days taken by each genotype from transplanting to opening of the first flower in about 50% of the plants grown either in the field or screen house conditions.

Number of days to maturity: This was recorded as the date on which about 80% of the grains on the panicle were fully ripened and ready for harvesting.

Spikelet fertility percentage: It was achieved by counting the number of filled grains and total spikelets per panicle and converted into percentage as described by International Rice Research Institute (IRRI) (2013). The total number of filled and unfilled grains per panicle was therefore counted to calculate the spikelet fertility in a panicle. The following formula was applied to get the actual percentage;

Spikelet fertility percentage = Filled grains / Unfilled grains x 100

Flag leaf length: Flag leaf is the last leaf in a rice plant. It was measured in centimeters using a ruler from the ligule to the tip of the blade on five plants that were randomly sampled.

Flag leaf width: It was measured in centimeters using a ruler at the widest segment of the flag leaf on five randomly sampled plants.

Flag leaf altitude: This was measured from five samples near the collar at the angle of attachment between the flag leaf and the main panicle axis during anthesis.

Leaf blade length: This was measured in centimeters from the ligule to the tip of the blade on five representative plants. The leaf of interest is that lying below the flag leaf in a rice plant.

Leaf blade width: This parameter was measured on the same highest leaf below the flag leaf on which length was collected for the five representative plants

Leaf blade pubescence: This involved visual assessment and by touching, rubbing fingers over the leaf surface from the tip downwards during late vegetative stage.

Leaf blade altitude: This parameter was recorded during late vegetative stage prior to heading. It was recorded by observing the position of the leaf blade tip in relation to its base scored on the leaf below the flag leaf.

Basal leaf sheath colour: It was achieved through visual appearance of the outer surface of the sheath during late vegetative stage.

Panicle length: This was measured in centimeters from the panicle node to the tip of the panicle using a ruler.

Number of panicles per plant: The number of panicles was recorded per hill for all the plants and averages taken for all the three replicates of the treatment.

Plant height: This was measured in centimeters using a plant height ruler at maturity stage from the soil surface to the top of the spike excluding the awns (for the genotypes which posses awns).

Number of grains (spikelets) per panicle: This includes the number of grains per panicle regarding both field and unfilled grains. It was obtained by counting the grains from each panicle using a digital grain counter.

Panicle exsertion: This was recorded as the crop approached maturity by observing the way the plant is exserted above the sheath of the flag leaf.

Panicle threshability: This was done in order to assess the percentage of the grains that can be removed by grasping the panicle with the hand and applying a slight rolling pressure with the palm and fingers.

Panicle altitude of branches: This refers to the compactness of the panicle, classified according to its mode of branching, angle of primary branches and spikelet density captured as the crop approached maturity.

Lemma and palea colour: Lemma is the larger and lower part of two bracts that contain the flower while the palea is the smaller upper part of two bracts that contain the flower and later the seed. Both of these structures offer protection by covering the flower and eventually the seed, and collectively are referred to as the hull of the seed. These were recorded by observing the plants after anthesis to hard dough stage.

Lemma shape of apiculus: This was captured after harvest of the genotypes for shape of the grain tip.

Sterile lemma presence and colour: This was observed on five representative plants**.**

Apiculus colour: This is a small pointed tip of the spikelet as a late observation parameter at maturity stage of the crop.

Auricle presence / absence and colour: The sheath is the leaf part which wraps the leaf .At the junction point between the leaf and the collar is where the auricle can be found depending on the variety. The auricle colour is also obtained at late vegetative stage for the genotypes possessing auricles.

Awning: This was recorded for the presence and distribution of awns along the panicle from flowering to maturity.

Ligule presence and colour: This was collected during late vegetative stage for those possessing ligule.

Ligule shape: This was recorded from five representative plants during the late vegetative stage through observation.

Rice grain quality traits

Milling recovery and degree of milling: Milling recovery is the total milled rice obtained out of paddy, expressed as weight percent of milled rice (including broken) obtained from a sample of paddy. Milling of rice increases its shelf life and whiteness, a physical property that the consumers do desire.

Hundred grams of rough rice/paddy (rice that the husk/hull has not been removed) were weighed. The moisture content was determined using a digital grain moisture meter. The measured paddy was dehulled with testing husker machine and the resulting brown rice and husks were weighed separately. The brown rice was milled in a testing miller for 30 seconds. The bran was weighed and the weight of the total milled rice was determined. Degree of Milling (DOM) is the amount of bran left on milled rice kernels and this also affects the milled rice paste viscosities.

The following equations were used to determine the milling traits of rice samples.

% Milling Recovery = MRW / WoP x 100; where MRW = Milled Rice Weight and WoP = Weight of paddy.

Chalkiness: The acceptance of rice by consumers is also dependent on chalkiness, which is a kernel-appearance trait. The opaque area in the rice kernel s referred to as chalk or white belly and is highly not acceptable by most consumers. The main cause of chalkiness is a malformation of starch granules which comprise air spaces between them leading to staining of the same.

Translucency: The translucency involved visual examination of the grains at daylight followed by judging the grains into groups of either cloudy, opaque or translucent.

Amylose content: Amylose content is a vital index for establishing the quality and flavor or taste of rice. In this study, it was not assessed due to lack of laboratory equipment such as spectrometer at the time of data handling.

Gelatinization temperature by alkali-digestion value: This is a simpler approach of detecting the energy needed to melt starch in the rice grain. In the present study, it was achieved by soaking seven (7) rice grains of each genotype for 16 hours in 1.7 % KOH as a similar procedure described by Bioversity International 2007in rice standard evaluation for gelatinization temperature.

Gel consistency: The rice sample of 0.1 g for each genotype was ground and placed in a test tube with thymol blue of 0.025% in ethanol (0.2 ml) and potassium hydroxide (KOH) of (0.2N, 2 ml). The test tubes were then shaken to ensure contents are mixed. This was followed by boiling of the contents in the test tube for 15minutes; resting for 7 minutes and then placed in an ice-bath for < 20 minutes (time was partly modified for a higher duration as compared to that illustrated Bioversity International 2007 descriptor, for ease of handling of the samples). After cooling, the test tubes were laid flat on graph paper for at least 1 hour. The distance that the gel travelled was then recorded as the gel consistency.

Grain length: This was recorded on 10 representative grains from the base of the lowermost glumes to the tip of the fertile lemma or palea using a caliper in millimeter (mm).

Grain width: This parameter was measured on 10 representative plants using a caliper as a distance across the fertile lemma and palea at the widest point in millimeter (mm).

Brown rice shape: This was captured by dividing the grain length value with that of the grain width of the respective genotype.

1000 grain weight: The one thousand (1000) grains were counted using an electronic grain counter prior to capturing the weight using a digital weighing balance. In order

to get the appropriate weight, the moisture content of each genotype was recorded and the respective 1000 grain weight adjusted to 14 % moisture content.

Grain yield / ha: In the case of the screen house (PVC) condition, this trait was obtained from the net plot area of four (4) hills per replicate representing 0.75 $m^2$of the total harvest area and converted to grain yield per hectare (t / ha) at 14 % moisture content for each genotype. The moisture content was measured using an Autocomp Grainmini moisture meter. In the case of field experiment, the net area for grain yield harvesting was 1 m^2 (4 m x 0.25 m).

3.2.3Laboratory Experiment

3.2.3.1 Molecular examination of some root traits and grain yield of the genotypes.

3.2.3.1.1 Plant Materials.

The specific objective "to determine diversity of grain yield and some root traits of the genotypes using Simple Sequence Repeats (SSR) molecular markers" was accomplished using the same plant materials of selected fifteen (15) Faya rice genotypes. The plant materials were of diverse Faya rice landraces obtained from Lifuwu Agricultural Research Station. The evaluation of genetic diversity of these rice landraces involved ten (10) Simple Sequence Repeat (SSR) marker out of the initially planned fourteen (14) SSR markers. Four (4) SSR primers were not used because they comprised wrong reverse primers and/or a missing reverse primer from the reagent supplier. Table 2 illustrates the list of SSR primers used in the present study.

3.2.3.1.2 Methods.

The 15 genotypes were grown in pots in the screen house followed by DNA extraction at 21 days after seedling emergence.

3.2.3.1.2.1 DNA Extraction.

Genomic DNA was isolated from young green leaves using DNA extraction kit (product) imported from Zymo Research – USA. DNA extraction was done using the following protocol (a completely different protocol from the earlier proposed CTAB method); as were guidelines from the DNA extraction kit:

1. The 150 mg of finely cut rice leaves were added to a ZR Bashing Bead™ Lysis Tube (2.0 mm). 750 µl Lysis Solution (15 ml equivalent in this case) was then added to the tube.

   The Genomic Lysis Buffer (15 ml) was prepared and added to beta – mercaptoethanol 75 ml (i.e. 500µl per 100 ml equivalent).
2. The samples were ground by acid washed sand (instead of bead beater), followed by further grinding using a Disruptor Genie ™ at 13000 rpm.
3. Furthermore, centrifugation of the ZR Bashing Bead™ Lysis Tube containing samples (2 mm) in a micro centrifuge at a 13000 rpm was done. Centrifugation was conducted in order to separate the liquid from semi –solid particles as DNA may be in the liquid component at this stage.
4. The 400 µl supernatant was transferred to a Zymo - Spin™ IV spin filter (Orange Top) in a collection tube and centrifuged at 8000 rpm
5. 1200 µl of Genomic Lysis Buffer was added to the collection tube from step 4 above and mixed.
6. 600 µl of the mixture from step 5 was transferred to a Zymo – Spin ™ IIC Column in a collection tube and centrifuged at a revolution of 13,000 rpm.
7. The flow through was discarded from the collection and stage 6 processes were repeated.

8. 200 µl DNA Pre – Wash Buffer was added to the Zymo - Spin™ IIC columnin a new collection tube and centrifuged at 13,000 rpm
9. 500 µl DNA g – Wash Buffer was added to the Zymo - Spin™ IIC columnin a new collection tube and centrifuged at 13,000 rpm
10. The Zymo - Spin™ IIC column was transferred to a clean 1.5 ml micro centrifuge tube and 75 µl DNA Elution Buffer was added directly to the column matrix, followed by centrifugationat 8000 rpm
11. The Zymo - Spin™ IV – HRC Spin Filter (Green Top) was snapped at the base and placed into a clean collection tube. This was followed by centrifugation at 13,000 rpm.
12. The eluted DNA was then transferred to a prepared Zymo - Spin™ IV – HRC Spin Filter (Green top) in a clean 1.5 ml micro centrifuge tube and centrifuged at 8000 rpm.

3.2.3.1.2.2 Checking the quality of DNA

DNA quality was checked by;

- Preparing agarose gel which was a mixture of buffer TDE (150 ml) and agarose (0.8 %).
- The mixture was placed in a microwave for (3 – 4 minutes) and thereafter allowed to cool
- Ethidium Bromide was added to the mixture in the casting tray for easy visualization and was waited to settle for 30 minutes.
- Lamda was for genomic DNA and Ladder (100 Bp) were placed at the first two wells for comparisons.

- Loading die (1 µl) was used for allowing the samples not to mix with buffer, but to stay on the wells. Current was allowed to flow for 1 hour before checking.

The DNA was found to be of high quality for running PCR and / or other downstream applications.

3.2.3.1.2.3 PCR amplification.

PCR, a polymerase chain reaction technique was done followed by electrophoresis using agarose gel electrophoresis (AGE).The polymerase chain reaction was done in the Veriti 96 well Thermal cycler for 2 hours. The total reaction mixture was 26 µl which comprised 2 Master Mix (12.5 µl), Forward and Reverse Primers (1.0 µl), Nuclease Free Water (10.5 µl) and DNA (2 µl).The programmable PCR thermal controller set for 32 cycles which comprised each cycle included94ºC for 5 minutes, 94 ºC for 1 minute, annealing temperature depending on the primer (table 1) for 1 minute, 72 ºC for 1 minute, 72 ºC for 5 minutes, and – 4 ºC for storage (hold).The gel solution was composed of 3g agarose in 150 ml TAE buffer where 2% Ethidium was added after it had cooled from the microwave heat. The loading dye was gently mixed with the DNA of each genotype and deposited into the corresponding well beginning with the Ladder (50 Bp). The PCR products were electrophoresed on the gel solution, and analyzed under the Ultra violet (UV) trans-illuminator for DNA detection followed capturing of band pictures.

Scoring of Band: The gels were scored for computer analysis on the basis of the presence and / or absence of the amplified products on each well. If a product was present, it was indicated as one (1) and if absent; it was indicated as zero (0) across all fifteen (15) Faya rice genotypes.

3.2.3.1.2.4 Data analysis

The genetic similarity was analyzed using Jaccard similarity coefficient based on the UPGMA in XLSTAT 2018 Version described by Ballan (2013) for the 2013.3 Version. Polymorphic Information Content (PIC) was calculated applying the following procedure:

PIC = 1 - $\sum P^2$ where P is the frequency of i^{th} allele. This formula was also reported by Joachim (2015) and Ballan (2013).

Principal Component Analysis (PCA) was also performed using the XLSTAT 2018 Version.

The list of SSR markers used and their corresponding sequence have been illustrated in the Table 2 below.

Table 2: List of 10 SSR markers and their sequence used in the study

SR. NO	MARKER	CHR NO	AMPLICON SIZE (BP)	ANN TEMP (^{0}C)	FORWARD (F) AND REVERSE (R) SEQUENCES	TRAIT (S)	SOURCE
1	RM 212	1	112-136	52.5	F: CCACTTTCAGCTACTACCAG R: CACCCATTTGTCTCTCATTATG	MRL, NT	Oraibi et al., (2014)
2	RM 213	2	139	57	F: ATCTGTTTGCAGGGGACAAG R: AGGTCTAGACGATGTCGTGA	RN	Gramene
3	RM 215	9	148	59	F: CAAAATGGAGCAGCAAGAGC R: TGAGCACCTCCTTCTCTGTAG	MRL	Joachim (2015)
4	RM 231	3	168-182	58.5	F: CCAGATTATTTCCTGAGGTC R: CACTTGCATAGTTCTGCATTG	GY	Ballan (2013)
5	RM 242	9	225	58	F: GGCCAACGTGTGTATGTCTC R: TATATGCCAAGACGGATGGG	MRL, DRW	Ballan (2013)
6	RM 248	7	102	59.2	F: TCCTTGTGAAATCTGGTCCC R: GTAGCCTAGCATGGTGCATG	GY	Gramene
7	RM 262	2	154	58.3	F: CATTCCGTCTCGGCTCAACT R: CAGAGCAAGGTGGCTTGC	RT	Ballan (2013)
8	RM 315	1	133	53.5	F: GAGGTACTTCCTCCGTTTCAC R: AGTCAGCTCACTGTGCAGTG	RN, PH, PL	Mahalingam et al., (2013)
9	RM 3810	1	105	55.4	F: ACGAAGGAACTACCCGTGTG R: CGCACATGTTACTCTAGCGG	RT	Gramene
10	RM 331	8	176	55	F:GAACCAGAGGACAAAAATGC R:CATCATACATTTGCAGCCAG	RL, NT	Afiukwa et al., (2016)

CHAPTER FOUR

4.0 RESULTS

In order to achieve the set objectives for this study, experiments were conducted in the screen house, laboratory and field conditions at Lifuwu Agricultural Research Station and Sokoine University of Agriculture in 2017 /2018. For an easy presentation, the results and discussion of these experiments are described under Screen house (PVC) experiment, Field experiment and Laboratory experiment.

4.1Performance of 15 Faya rice genotypes in screen house (PVC) experiment

4.1.1 Grain yield and growth parameter traits

The average performance of the selected fifteen (15) Faya rice genotypes for different studied traits is illustrated in Table 3. The observations followed the characterization and evaluation procedure of studying traits using morphological markers.

Table 3: Mean performance of selected 15 Faya Rice Genotypes for the 10 quantitative traits in PVC pipes (Screen House)

TRT NO	GENOTYPE NAME	GRY (ton / ha)	PLH (cm)	NPP	TPP	PAL (cm)	LBL (cm)	LBW (cm)	FLL (cm)	FLW (cm)	SPP
1	Mw 1685	3.2	138.2	14.3	18.0	21.9	50.0	1.2	23.1	1.4	101.2
2	Faya 14 M 69	3.5	100.6	16.0	21.3	25.5	30.6	1.3	33.3	1.2	104.3
3	Acc 9290	2.1	147.6	22.6	27.6	26.3	47.3	0.9	28.9	1.2	121.3
4	Faya Mafuta 1,	2.6	156.8	17.3	20.6	27.3	44.7	1.1	21.8	1.3	174.7
5	Acc 18028	2.7	156.8	17.6	20.6	25.5	53.0	1.2	29.6	1.4	160.0
6	Faya Kalonga	2.9	107.2	15.6	16.0	27.4	44.5	1.2	30.3	1.4	228.9
7	Acc 5934	2.2	152.9	18.0	24.0	25.1	51.7	1.0	31.0	1.3	111.1
8	Mw 18037	2.6	166.3	13.6	14.0	24.9	48.6	1.3	26.6	1.5	178.1
9	Faya Makanjira	2.2	138.6	21.6	24.0	22.9	43.4	1.1	28.7	1.3	86.7
10	Acc 17323	2.9	151.3	18.0	19.3	25.4	50.2	1.2	29.8	1.4	206.6
11	Acc 5933	2.5	145.4	20.0	18.3	25.1	51.4	1.1	29.5	1.3	147.7
12	Faya Zambia	2.7	158.7	14.0	16.6	25.0	42.2	1.2	21.4	1.5	209.5
13	Acc 17344	2.7	169.7	17.0	13.6	25.5	56.4	1.4	32.6	1.6	191.9
14	Faya Mafuta 2	2.7	164.9	19.0	21.3	28.6	46.2	1.1	25.1	1.3	215.2
15	Acc 9293	3.0	146.2	15.6	20.3	23.7	54.9	1.0	31.8	1.2	149.7
Grand mean		2.75	146.74	17.39	19.73	25.38	47.72	1.19	28.28	1.41	159.12
F pr		0.050	<.001	0.084	0.007	<.001	<.001	<.001	0.002	<.001	<.001
LSD (5 %)		0.780	16.18	5.70	6.46	1.91	8.26	0.15	5.83	0.16	65.97
SE		0.382	5.602	1.974	2.238	0.664	2.863	0.055	2.019	0.058	22.84
Range		2.1 – 3.5	100 – 169.7	18.6– 22.6	13.6 - 27.6	21.9 - 28.6	30.6 – 56.4	0.9 – 1.4	21.4 – 33.3	1.2 – 1.6	86.7 – 228.9
CV %		17.0	6.6	19.7	19.6	4.5	10.4	8.0	12.4	7.1	24.9

Note: GRY = Grain yield; PLH = Plant height; NPP = Number of Panicles per Plant; TPP = Tillers per plant; PAL = Panicle Length; LBL = Leaf Blade Length; LBW = Leaf Blade Width; FLL = Flag Leaf Length; FLW = Flag Leaf Width; SPP = Spikelets per panicle, SF = Spikelet fertility.

4.1.1.1 Grain yield (ton / ha).

Significant differences ($P < 0.050$) were observed among the selected rice genotypes for this trait. Specifically, Faya 14 M 69 depicted the average maximum yield of 3.5 tons per hectare while the minimum yield was exhibited by Accession 9290 with grain yield of 2.1 tons per hectare. The grand mean value for this trait was 2.75 tons per hectare.

4.1.1.2 Plant height (cm).

There were very highly significant differences ($P < 0.001$) for this trait amongst the rice genotypes. The data illustrate that genotype Mw 17344 had the maximum height of 169.7 cm while Faya 14 M 69 attained the minimum height of 100.6 cm. All the genotypes except two were tall with plant height of more than 110 cm.

4.1.1.3 Panicle number.

The number of panicles per plant depicted significant differences ($P = 0.044$) among genotypes and Accession 9290 attained the maximum mean number of panicles per plant of 22.67. On the other hand, the minimum mean number of panicles per plant of 13.6 was attained by Accession 18037 which was at par with Faya Zambia with 14 panicles / plant.

4.1.1.4 Tiller number.

This trait showed highly significant differences among the studied rice genotypes as evidenced by the probability value ($P = 0.007$). The mean maximum and minimum values of 27.67 and 13.67 were attained for Accession 9290 and Accession 17344 respectively.

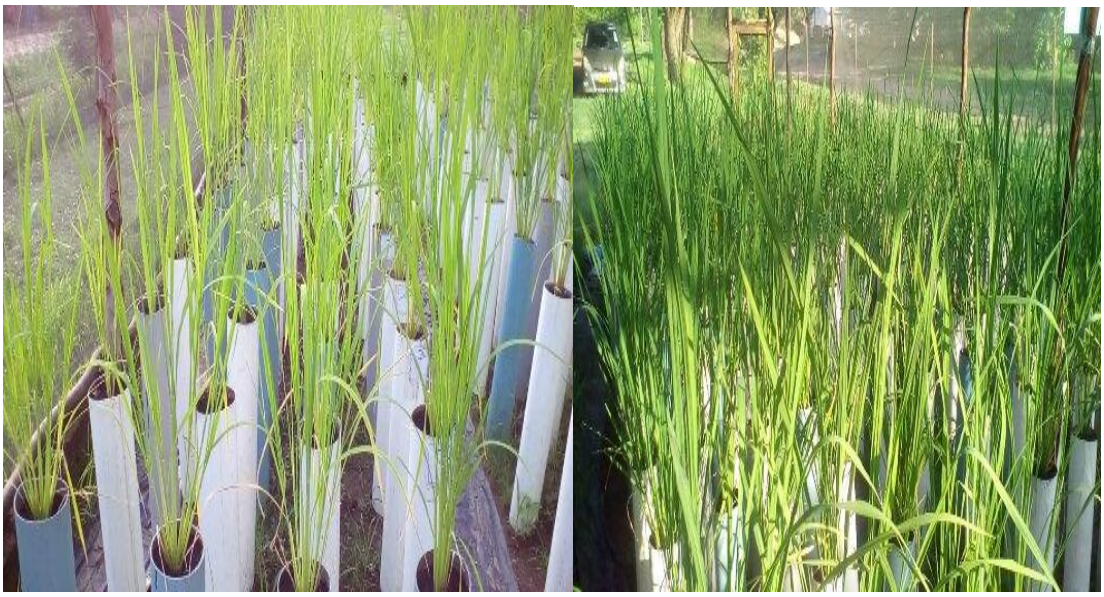

Figure 2: Early and late vegetative stages with high tillers formation of 15 Faya rice genotypes grown in PVC pipes

4.1.1.5 Panicle length (cm).

There were very highly significant differences ($P < 0.001$) among the selected rice genotypes for this trait. Furthermore, Faya Mafuta 2 had the mean maximum panicle length among all the selected rice genotypes with 28.67 cm and the minimum panicle length was attained by genotype Mw 1685 with 21.96 cm.

4.1.1.6 Leaf blade length.

There were very highly significant differences ($P < 0.001$) observed among the studied rice genotypes for this trait. From the results, it was noted that Mw 18037, had the mean longest leaf of 67 cm whereas the shortest was 30.67 cm for Faya 14 M 69.

4.1.1.7 Leaf blade width (cm).

Very highly significant differences were observed for this trait among the studied genotypes with the probability value ($P < 0.001$). In addition, Accession 17344 depicted the mean maximum width of 1.45 cm and the minimum leaf blade width value was for Accession 9290 (0.942 cm).

4.1.1.8 Flag leaf length (cm).

This trait exhibited highly significant differences among the studied genotypes and had a probability value (P = 0.002). Faya 14 M 69 attained the average maximum value of 33.38 cm while Faya Zambia gave the mean minimum value of 21.42 cm which was closely at par with Faya Mafuta 1 with flag leaf length of 21.88 cm

4.1.1.9 Flag leaf width (cm)

Very highly significant differences (P < 0.001) were observed among the rice genotypes for this trait. From the results, it was noted that Acc 17344 had the mean widest leaf of 1.692 cm whereas the narrowest was observed in Accession 17344 (1.225 cm) which was closely at par with Faya 14 M 69 (1.292 cm).

4.1.1.10 Number of spikelets per panicle

This trait exhibited very high significant differences among the studied rice genotypes as evidenced by p < 0.001 on the analyzed data. Furthermore, Faya Kalonga attained the average maximum value of 228.9 grains per panicle while the minimum value of 86.7 was achieved in Faya makanjira.

4.1.2 Root Architectural and other phenotypic Traits

The studied genotypes performed differently in terms of root architectural traits and the results are presented in Table 4.

Table 4: Mean performance of selected 15 Faya rice genotypes for the root and other traits grown in PVC pipes (Screen house)

TRT NO	GENOTYPE NAME	FRM (g)	RON	MRL (cm)	FSM (g)	ROV (cc)	DRM (g)	DSM (g)	R /S R	NDM
1	Mw 1685	148.1	262.0	51.3	74.3	191.7	95.7	69.3	1.4	122.0
2	Faya 14 M 69	115.9	367.0	62.3	39.4	291.7	58.6	43.5	1.5	161.0
3	Acc 9290	398.6	329.3	70.0	88.1	350.0	138.7	76.1	1.7	164.0
4	Faya Mafuta 1,	208.3	387.3	49.6	68.1	175.0	76.8	60.9	1.2	156.0
5	Acc 18028	326.2	317.3	76.3	113.3	350.0	132.0	88.3	1.5	156.0
6	Faya Kalonga	101.2	163.7	32.0	29.1	141.7	36.9	33.7	1.1	131.0
7	Acc 5934	342.0	280.0	69.6	72.5	208.3	86.5	71.4	1.1	158.0
8	Mw 18037	326.1	383.0	68.0	75.0	250.0	97.8	72.0	1.4	150.0
9	Faya Makanjira	210.9	230.3	45.6	67.9	150.0	126.9	68.7	1.8	146.0
10	Acc 17323	334.4	305.3	61.5	74.3	291.7	119.9	73.1	1.6	157.0
11	Acc 5933	295.3	277.7	58.3	94.4	225.0	83.8	73.5	1.1	160.0
12	Faya Zambia	329.5	350.7	59.6	68.2	275.0	110.8	67.6	1.70	152.0
13	Acc 17344	324.1	316.0	56.1	114.6	300.0	80.6	87.9	1.0	156.0
14	Faya Mafuta 2	295.1	266.0	56.6	101.8	250.0	97.9	77.2	1.2	156.0
15	Acc 9293	383.4	271.3	82.3	78.4	300.0	87.8	65.0	1.4	148.0
Grand mean		275.9	300.4	59.9	77.0	250.0	95.4	68.5	1.4	151.5
Range		101.2 – 398.6	163.7 – 387.3	32.0 – 82.3	29.1 – 114.6	141.7 – 350.0	36.9 – 138.7	33.7 – 88.3	1.0 – 1.8	122.0 - 164
F pr		<.001	<.001	<.001	<.001	0.108	0.041	0.039	0.837	0.00
LSD (5%)		129.2	81.9	18.5	31.3	147.4	54.7	28.2	0.9	0.00
SE		44.766	28.369	6.430	10.844	51.05	18.95	9.784	0.325	0.00
CV %		28.1	16.4	18.6	24.3	35.4	34.4	24.7	39.1	0.00

Note: FRM = Fresh Root Mass, MRL = Maximum Root Length, ROV= Root Volume, GRL = Grain Length, GRW = Grain Width, TGW = Thousand Grain Weight, RON = Root Number, FSM = Fresh Shoot Mass, DRM = Dry Root Mass, DSM = Dry Shoot Mass, R / S R = Root / Shoot Ratio, NDM = Number Of Days to Maturity

4.1.2.1 Fresh root mass (g)

For this character, very highly significant differences ($P < 0.001$) were observed among the genotypes with Accession 9290 depicting the mean maximum value of 399 grams, while the minimum value of 101 grams was recorded in Faya Kalonga.

4.1.2.2 Root number

This trait exhibited very high significant differences ($P < 0.001$) among the genotypes. More specifically, Faya Mafuta 1 had a maximum root number (387.3) and the minimum mean value (163.7) was found in Faya Kalonga.

4.1.2.3 Maximum root length (cm):

Very highly significant differences ($P < 0.001$) were observed among the studied genotypes for maximum root length. Accession 9293 exhibited maximum value (82.3 cm), whereas the minimum value was obtained in Faya Kalonga with a value of 32 cm.

Figure 3: A comparison of Accession 9293 longest root with the shortest root of Faya Kalonga grown in PVC pipes

Figure 4: Comparison of root length of some selected Faya rice genotypes grown in PVC pipes.

4.1.2.4 Fresh shoot mass (g)

Very highly significant differences were exhibited among the studied genotypes for this character. The mean maximum fresh shoot weight was recorded in Accession 17344 (114.6 g) whilst the minimum value was exhibited in Faya Kalonga (29.1 g)

4.1.2.5 Root volume (cc)

Non - significant differences were observed among the genotypes for this trait. However, Accession 9290 exhibited the mean maximum value of 350 cc and was non - significantly at par with that of Accession 18028 (350 cc). The mean minimum value was obtained in Faya Kalonga (142 cc).

4.1.2.6 Dry root mass (g)

Significant differences (P = 0.041) were exhibited for this trait among the studied genotypes. The average maximum magnitude of 138.7 g was attained by Accession 9290 while the minimum (36.9 g) was achieved for Faya Kalonga and grand value was 95.4 g.

4.1.2.7 Dry shoot weight (g)

This trait showed significant differences (P = 0.039) among the studied genotypes. Furthermore, Accession 18028 exhibited mean maximum mass of 88.3 g and was closely at par with Accession 17344 which had a weight of 87.9 g.

4.1.2.8 Root/shoot ratio

The analyzed data exhibited non significant differences for this trait among the studied genotypes. Besides, Faya Makanjira exhibited the maximum value of 1.84 where as the minimum value was attained by Accession 17344 (1.02).

4.1.1.9 Number of days to maturity

There were not significant differences in terms of number of days to maturity among the studied genotypes. However, it was noted that Accession 9290 had the longest number of days to mature while Mw 1685 had the shortest average number of days to reach maturity, which were 164 days and 122 days respectively.

4.1.3 Grain quality traits

Table 5: Mean performance of selected 15 Faya rice genotypes grown in screen house (PVC) pipes

TRT NO	GENOTYPE NAME	GR L (mm)	GRW (mm)	GRS	DT F 50%	TGW (g)	SPF (%)
1	Mw 1685	9.6	3.2	2.9	96	35.6	96.9
2	Faya 14 M 69	9.4	2.6	3.5	114	34.9	92.0
3	Acc 9290	8.7	2.5	3.4	134	23.2	90.3
4	Faya Mafuta 1	9.2	2.5	3.6	102	26.2	96.4
5	Acc 18028	9.2	2.8	3.2	108	29.3	96.6
6	Faya Kalonga	8.1	2.4	3.3	100	26.4	92.8
7	Acc 5934	9.1	2.6	3.4	118	27.9	95.0
8	Acc 18037	9.5	2.7	3.4	112	31.3	97.1
9	Faya Makanjira	9.8	2.6	3.8	110	28.0	94.9
10	Acc 17323	9.4	2.7	3.5	118	26.2	95.7
11	Acc 5933	9.3	2.8	3.3	114	26.5	96.7
12	Faya Zambia	9.8	2.8	3.4	106	29.1	97.7
13	Acc 17344	9.1	2.6	3.4	119	30.7	97.0
14	Faya Mafuta 2	9.0	2.5	3.6	117	23.3	97.7
15	Acc 9293	8.9	2.6	3.3	100	27.2	98.7
Grand mean		9.5	2.7	3.4	111.2	28.4	95.7
F pr		NS	NS	NS	NS	<.001	<.001
SE		0.00	0.00	0.00	0.00	0.00	0.00
CV %		0.00	0.00	0.00	0.00	9.1	1.9

GRL = Grain Length, GRW = Grain Width, GRS = Grain Shape, DTF = Days to 50 % Flowering, SPF = Spikelet fertility, TGW = Thousand Grain Weight. NDM = Number, NS = Non – Significant.

4.1.3.1 Grain length

The analyzed data illustrated non – significant differences for this trait among the studied genotypes. However, a comparison among the genotypes illustrated that Faya makanjira (9.89 mm) had the maximum length though was closely at par with Faya Zambia (9.8 mm) and Mw 1685 (9.62). On the other hand, Faya Kalonga depicted the lowest mean length among the group valued at 8.13 mm.

4.1.3.2 Grain width

Non – significant difference was exhibited among the studied genotypes for this trait. However, the analyzed data shows that mean maximum grain width is found in genotypes Mw 1685 valued at 3.22 mm while the minimum value is in Faya kalonga (2.45 mm).

4.1.3.3 Brown grain shape

There was not significant difference for this trait among the studied genotypes. The maximum grain shape was recorded in Faya Makanjira (3.8) whereas the minimum value was in Mw 1685 (2.98).

4.1.3.4 Days to 50 % flowering.

There were non – significant differences observed for days to 50% flowering among the studied genotypes. Days to 50% flowering among the rice genotypes ranged from 96 to 134 and the grand mean value of 112.2 days. The minimum number of days to 50 % flowering was 96 and was observed in Mw 1685 whereas Accession 9290 exhibited maximum days of 134 to 50 % flowering.

4.1.3.5 One thousand (1000) grain weight

The analyzed data exhibited very highly significant differences ($P < 0.001$) among the studied genotypes for this trait. The mean maximum 1000 grain weight was attained in Mw 1685 (35.68 g) and was closely at par with that of Faya 14 M 69 (34.96 g) while the minimum value was in Accession 9290 (23.27 g) and was also closely at par with Faya Mafuta 2 (23.34 g).

4.1.3.6 Spikelet fertility (%)

Very highly significant differences were exhibited on this trait among the studied genotypes as evidenced by the $p < 0.001$ value on the analyzed data. It was also noted that the average maximum value of 98.78 % was achieved in Accession 9293 while the minimum value of 90.31 % was attained by Accession 9290.

4.1.4 Phenotypic traits correlations

Correlation analysis was done on the phenotypic data in order to establish the magnitude of relationships between pairs of traits. Great interests were those correlations between grain yield and root architecture as have been the main targets of this study though some grain quality and growth parameters were also included. Table 6 below illustrates the outcome of the existing associations among thirteen (13) traits for genotypes grown in the screen house using PVC pipes.

Table 6: Phenotypic traits correlations for the genotypes grown in the screen house using (PVC) pipes

TRAIT	FRM	GRL	RON	MRL	FSM	TGW	ROV	NDM	GRY	PLH	SPP	SPF	TPP
FRM	1.00												
GRL	0.048	1.00											
RON	0.294*	0.413*	1.00										
MRL	0.747**	0.141	0.459*	1.00									
FSM	0.665**	0.145	0.189	0.462*	1.00								
TGW	-0.450*	0.468**	0.229	-0.003	-0.207	1.00							
ROV	0.640**	-0.006	0.482*	0.771**	0.521**	-0.029	1.00						
NDM	0.558**	0.068	0.564**	0.507**	0.373*	-0.388*	0.570**	1.00					
GRY	-0.510**	-0.009	0.018	-0.047	-0.377*	0.583**	0.088	-0.350*	1.00				
PLH	0.740**	0.267*	0.371*	0.379*	0.785**	-0.282*	0.291*	0.314*	-0.505**	1.00			
SPP	0.093	-0.343*	0.008	-0.216	-0.169	-0.345*	0.021	-0.064	0.151	0.153	1.00		
SPF	0.147	0.603**	0.178	0.061	0.381*	0.260*	-0.188	-0.215	0.027	0.613**	0.256*	1.00	
TPP	0.268*	-0.078	0.004	0.286*	0.226	-0.369*	0.249	0.465*	-0.481*	-0.035	-0.633**	-0.600**	1.00

***Significant correlation at 0.05 level (2-tailed); **Significant correlation at 0.01 level (2-tailed).**

FRM = Fresh Root Mass, GRL= Grain Length, RON = Root Number, MRL = Maximum Root Length, FSM = Fresh Shoot Mass, TGW = Thousand Grain Weight, ROV = Root Volume, NDM = Number of Days to Maturity, GRY = Grain Yield, PLH = Plant Height, SPP = Number of Spikelets per Panicle, SPF = Spikelet Fertility, TPP = Tillers Per Plant.

4.1.4.1 Fresh root mass

Fresh root mass positively correlated with all traits except grain yield and 1000 grain weight. However, some correlations were not significant.

4.1.4.2 Grain length

Grain length exhibited positive associations with all traits (although some correlations were not significant) except number of tillers per plant, number of spikelets per panicle, root thickness, and grain yield.

4.1.4.3 Root number

Positive correlation was exhibited for root number with all other characters. However, significant and positive correlation was observed with maximum root length, root thickness, number of days to maturity and plant height.

4.1.4.4 Maximum root length (cm)

Maximum Root Length exhibited positive and significant correlation with such traits as fresh root mass, root number, fresh shoot mass, root thickness, number of days to maturity, number of tillers per plant, and plant height while with other traits were not significant. On the other hand, there was negative and non – significant association for the same trait with 1000 grain weight number of spikelets per panicle and grain yield.

4.1.4.5 Fresh shoot mass (g)

This trait exhibited positive and significant relationship with fresh root mass, maximum root length, root volume / root thickness, number of days to maturity, spikelet fertility, and plant height. On the other hand, negative and significant association was exhibited for the same trait with grain yield.

4.1.4.6 Thousand grain weight (g)

There was positive and significant correlation for 1000 grain weight with such characters as grain length, spikelet fertility and grain yield. However, negative and significant association was attained for the same trait with fresh root mass, number of days to maturity, number of spikelets per panicle, number of tillers per plant and plant height.

4.1.4.7 Root volume (cc)

Positive and significant correlation was exhibited for root volume with such traits as fresh root mass, root number and maximum root length including fresh shoot mass, number of days to maturity, and plant height.

4.1.4.8 Number of days to maturity (NDM)

The number of days to maturity exhibited positive and significant correlation with fresh root mass, root number, maximum root length, fresh shoot mass, root thickness, number of tillers per plant and plant height. On the other hand, negative and significant relationship was exhibited for the trait in question with 1000 grain weight and grain yield.

4.1.4.9 Grain yield (tons / ha)

There was positive and significant association for grain yield with 1000 grain weight and plant height. However, such traits as fresh root mass, fresh shoot mass, number of days to maturity, number of tillers per plant and plant height depicted negative and significant association with the trait in question.

4.1.4.10 Plant height (cm)

Plant height was positively and significantly correlated with all the traits except number of spikelets per panicle which was non - significant. Furthermore, the same trait illustrated negative and significant relationship with the remaining traits such as 1000 grain weight and grain yield with an exception of number of tillers per plant

4.1.4.11 Number of spikelets per panicle

This trait exhibited positive and significant correlation with spikelet fertility only. However, the same trait showed negative and significant association with grain length, 1000 grain weight and number of tillers per plant.

4.1.4.12 Spikelet fertility

Spikelet fertility exhibited positive and significant correlation with such traits as grain length, fresh shoot mass, 1000 grain weight, and number of spikelets (table 6)

4.1.4.13 Number of tillers per plant

Number of tiller per plant positively associated with fresh root mass, maximum root length, root thickness and number of days to maturity. However, the same trait correlated negatively and significantly with number of spikelets per panicle, grain yield and spikelet fertility.

4.2 Performance of the selected 15 Faya rice genotypes in field experiment

The screen house experiment was conducted in order to complement the field experiments which gave the outcome presented in Table 7 below.

Table 7: Mean performance of selected 15 Faya rice genotypes in field condition

TRT NO	GENOTYPE NAME	GRY (ton / ha)	PLH (cm)	NPP	TPP	PAL (cm)	LBL (cm)	LBW (cm)	FLL (cm)	FLW (cm)	SPP
1	Mw 1685	3.3	143.7	13.6	12.0	22.1	39.3	1.1	33.0	1.1	124.
2	Faya 14 M 69	4.2	140.4	14.1	16.0	26.6	42.3	1.1	30.1	1.0	185.0
3	Acc 9290	2.5	128.9	11.8	13.5	25.5	46.6	1.1	30.7	1.2	192.0
4	Faya Mafuta 1,	3.1	114.2	9.0	9.8	31.2	54.1	1.3	36.2	1.4	265.7
5	Acc 18028	2.6	130.7	9.3	9.6	27.9	52.7	1.3	35.7	1.3	237.3
6	Faya Kalonga	2.8	93.2	7.7	7.7	29.0	50.8	1.3	33.5	1.6	267.3
7	Acc 5934	3.2	140.1	11.5	12.9	27.2	50.1	1.1	34.5	1.3	194.0
8	Acc 18037	2.4	138.7	7.6	8.2	28.3	45.0	1.2	34.8	1.6	242.3
9	Faya Makanjira	2.6	118.3	15.1	14.1	24.2	46.7	1.2	26.4	1.1	96.7
10	Acc 17323	2.4	131.6	8.5	8.6	26.8	52.5	1.2	35.5	1.3	236.7
11	Acc 5933	2.3	129.4	10.1	10.0	26.2	49.2	1.2	32.1	1.3	200.3
12	Faya Zambia	2.9	139.9	6.9	7.3	28.6	52.8	1.4	33.1	1.6	246.7
13	Acc 17344	2.6	138.0	7.4	8.1	27.3	52.3	1.3	42.8	1.5	280.7
14	Faya Mafuta 2	2.5	156.0	8.2	9.3	31.7	52.9	1.2	37.5	1.4	274.3
15	Acc 9293	3.0	120.7	11.9	11.4	24.7	43.7	1.0	34.4	1.0	164.0
Grand mean		2.8	131.5	10.3	10.4	27.1	48.7	1.2	34.0	1.3	213.8
Range		2.3 – 4.2	93.2 – 156.0	6.9 – 14.1	7.3 – 16.0	22.1 – 31.7	39.3 – 54.1	1.0 – 1.4	26.4 – 42.8	1.0 – 1.6	124. 0 – 280.7
F pr		0.015	0.374	<.001	<.001	<.001	0.001	0.229	<.001	<.001	<.001
LSD (5%)		0.865	42.4	2.5	2.6	1.9	6.8	0.2	4.5	0.1	65.1
SE		0.300	14.679	0.897	0.915	0.688	2.38	0.086	1.563	0.036	22.55
CV %		18.1	19.3	15.0	15.1	4.4	8.5	12.0	7.9	4.6	18.3

Note: GRY = Grain yield; PLH = Plant height; NPP = Number of Panicles per Plant; TPP = Number of tillers per plant; PAL = Panicle Length; LBL = Leaf Blade Length; LBW = Leaf Blade Width; FLL = Flag Leaf Length; FLW = Flag Leaf Width; SPP = Spikelets per Panicle.

4.2.1 Yield and growth parameter traits

4.2.1.1 Grain yield (ton/ha)

Highly significant differences (P = 0.01) were exhibited among the studied genotypes for this trait. Faya 14 M 69 had the mean maximum yield of 4.201 tons per hectare while the minimum yield was exhibited in Accession 5933 valued at 2.330 tons per hectare.

4.2.1.2 Plant height (cm)

There were not significant differences for this trait amongst the studied genotypes. However, the analyzed data showed that Faya mafuta 2 had the average maximum height of 156 cm while Faya Kalonga attained the mean minimum height of 93.2 cm.

4.2.1.3 Number of panicles per plant

The number of panicles per plant showed very highly significant differences ($P < 0.001$). The mean maximum number of panicles per plant was attained by Faya 14 M 69 with the value of 16.03. On the contrary, the minimum mean value of 7.33 panicles per plant was attained by Faya Zambia.

4.2.1.4 Tiller number

There were very highly significant differences for this trait among the studied genotypes ($P < 0.001$). The mean maximum and minimum values of 16.03 and 7.33 were achieved for Faya Makanjira and Faya Zambia respectively.

4.2.1.5 Panicle length (cm)

There was very highly significant variation among the studied genotypes for this trait with a probability value of ($p < 0.001$). The maximum value was achieved in Faya Mafuta 2 (31.78 cm) and was closely at par with Faya Mafuta 1 (31.2 cm) while the minimum mean magnitude was in Mw 1685 (22.15 cm).

4.2.1.6 Leaf blade length (cm)

This character exhibited very highly significant differences among the studied genotypes with a probability value ($p < 0.001$). The longest mean value of 54 cm was attained in Faya mafuta 1, whereas the shortest was in Mw 1685 with the value of 39.31 cm.

4.2.1.7 Leaf blade width (cm)

This trait exhibited significant differences as evidenced by a ($p < 0.001$) value observed among the studied genotypes. From the data, it was noted that Faya Zambia had the mean widest leaf of 1.4 cm whereas the narrowest was attained in Accession 9293 with value of 1.067 cm.

4.2.1.8 Flag leaf length (cm)

These traits showed very highly significant difference of $p < 0.001$ among the studied genotypes. It was also discovered that Accession 17344 attained the average maximum value of42.83 cm and the minimum value was for Faya Makanjira (26.22 cm)**.**

4.2.1.9 Flag leaf width (cm)

There were very highly significant differences ($P < 0.001$) for this trait among the studied. Besides, the mean maximum value was attained in Faya Zambia (1.62 cm) which was closely at par with Mw 18037 (1.60 cm) and Faya Kalonga (1.606 cm). On the other hand, the average minimum value was attained by Accession 9293 (1.06 cm) and was closely at par with Faya 14 M 69 (1.086 cm).

4.2.1.10 Number of spikelets per panicle

The studied genotypes exhibited very highly significant differences ($P < 0.001$) on this trait. The average maximum number of spikelets per panicle was exhibited in Accession 17344 (280.7) while the minimum was attained in Faya Makanjira (96.7).

Table 8: Mean performance of selected 15 Faya rice genotypes in field condition

TRT NO	GENOTYPE NAME	GRL (mm)	GRW (mm)	GRS	GMR (%)	DTF 50%	NDM	TGW (g)	SPF (%)	Scent (Aroma)
1	Mw 1685	9.8	3.2	3.0	75	95	122	25.5	95.6	Scented
2	Faya 14 M 69	10.2	3.0	3.3	75	103	141	21.0	94.9	Scented
3	Acc 9290	10.6	2.7	3.9	74	99	144	18.1	95.5	Scented
4	Faya Mafuta 1,	10.1	2.7	3.6	77	109	136	19.7	95.7	Scented
5	Acc 18028	10.2	3.0	3.3	77	112	136	20.2	97.1	Scented
6	Faya Kalonga	10.0	3.0	3.3	75	106	131	21.7	97.5	Scented
7	Acc 5934	10.4	2.8	3.6	75	112	138	21.6	94.4	Scented
8	Mw 18037	10.1	3.0	3.3	77	112	130	21.4	97.2	Scented
9	Faya Makanjira	10.3	2.8	3.6	78	96	127	23.8	92.4	Scented
10	Acc 17323	10.1	2.9	3.5	76	110	137	20.1	95.6	Scented
11	Acc 5933	10.1	3.0	3.3	75	113	140	19.3	95.1	Scented
12	Faya Zambia	10.2	3.0	3.3	77	112	132	23.8	96.1	Scented
13	Acc 17344	10.4	3.0	3.4	78	109	136	21.8	96.4	Scented
14	Faya Mafuta 2	10.4	2.7	3.7	75	108	136	17.9	96.9	Scented
15	Acc 9293	10.1	2.7	3.6	74	98	128	21.1	95.9	Scented
Grand mean		10.24	3.1	3.4	76	106	134.2	21.10	95.9	**All genotypes are aromatic**
Range		9.8 – 10.6	2.7-3.2	3.0 -3.9	74 - 78	95-113	122-144	17.9-25.5	94.4–97.2	
F pr		NS	NS	NS	NS	NS	NS	<.001	0.008	
LSD (5%)		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
SE		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
CV %		0.00	0.00	0.00	0.00	0.00	0.00	8.3	1.6	

Note: GMR = Grain Milling Recovery, GRL = Grain Length, GRW = Grain Width, GRS = Grain Shape, DTF = Days to 50 % Flowering, SPF = Spikelet fertility, TGW = Thousand Grain Weight. NDM = Number of Days to Maturity.

4.2.2 Grain quality and other traits

4.2.2.1 Grain length

Non – significant differences were exhibited for this trait among the studied genotypes. However, average maximum value of 10.61 mm was obtained in Accession 9290 and the minimum was 9.86 for Mw 1685.

4.2.2.2 Grain width

There was non – significant difference among the studied genotypes for this trait. However, the analyzed data depicts that mean maximum grain width is found in genotype Mw 1685 valued at 3.25 mm while the minimum value is in Accession 9290 (2.71 mm).

4.2.2.3 Brown grain shape

There were non - significant differences for this trait among the studied genotypes. The maximum grain shape was recorded in Accession 9290 (3.91mm) whereas the minimum value was in Mw 1685 (3.03 mm).

4.2.2.4 Grain milling recovery (%)

There was not significant difference among the studied genotypes for this trait. However, it was noted that the maximum milling recovery was 78 % for genotypes Faya Makanjira and Accession 17344. The minimum value was 74 % captured in Accession 9290 and Accession 9293.

4.2.2.5 Number of days to 50% flowering

There was non - significant difference for number of days 50% flowering among the studied genotypes. However, differences in magnitude was noticed as four (4) genotypes took a maximum of 112 days to 50% flowering, namely; Accession 18028, Accession 18037, Accession 5934 and Faya Zambia while the minimum number of days was 95 and was exhibited by Mw 1685.

4.2.2.6 Number of days to maturity

Non – significant difference was observed among the studied genotypes for the number of days to maturity. However, Accession 9290 exhibited the average maximum number of days to maturity (144 days) while Mw 1685 had the earliest number of days to maturity (122 days).

4.2.2.7 1000 grain weight

The analyzed data illustrated very highly significant differences with a probability ($_p<$ 0.001) among the studied genotypes for this trait. The mean maximum 1000 grain weight was 25.52 mm for Mw 1685 while the minimum value was in Accession for Faya Mafuta 2 with a magnitude of 17.94 mm.

4.2.2.8 Spikelet fertility (%)

There were significant differences (P = 0.008) among the studied genotypes for this trait. Besides, Faya Kalonga exhibited the average maximum value of 97.5 % and was closely at par with Accession 18037 (97.2%) and Accession 18028 (97.1). The mean minimum value was attained by Faya Makanjira (92.4 %).

4.2.2.9 Scent (Aroma)

All the genotypes were found to be scented (aromatic) after cooking (Table 8).

4.2.2.10 Chalkiness (white belly)

In this study, all the genotypes had no chalk except three (Faya Makanjira, Accession 9293 and Accession 18037) which had minor chalkiness.

4.2.2.11 Translucency

The studied rice genotypes gave different results on this trait as a majority of them (10 genotypes) depicted opaque grains. The opaque was observed in Mw 1685, Faya 14 M 69, Faya Mafuta 1, Faya Mafuta 2, Faya Zambia, Accession 9293, Accession 18028, Accession 17323, Accession, Faya Kalonga and Accession 17344. The translucency was observed in Accession 5933, Accession 5934, and Accesion 9290 whereas the cloudy was exhibited in Faya Makanjira and Accession 9293. These results represent 66.7 %, 20 % and 13 % for opaque, translucency and cloudy grains respectively.

4.2.2.12 Gelatinization temperature by alkali-digestion value

The results showed that Accession 9293, Accession 18037 and Faya Makanjira were not affected by alkali digestion. These therefore belong to the low alkali digestion with high temperature (> 74 ^{o}C). The rest of the genotypes; Mw 1685, Faya 14 M 69, Acc 9290, Faya Mafuta 1, Acc 18028, Faya kalonga, Acc 5934, Acc 17323, Acc5933, Faya Zambia, Acc 17344, and Faya Mafuta 2 belong to the intermediate gelatinization temperature (70 – 74 ^{o}C).

4.2.2.13 Gel consistency

The results indicated that majority of the genotypes had an intermediate gel consistency types although individual values differed. The genotypes such as Faya 14 M 69 (48 mm), Accession 9290 (45 mm), Faya Mafuta 1 (52 mm), Accession 18028 (46 mm), Accession 9293 (60 mm), Faya Makanjira (46 mm), Accession 17323 (45 mm), Accession 5934 (47 mm), Faya Zambia (52 mm), Accession 17344(58mm), Faya mafuta 2 (51 mm) and Accession 9293 (55 mm) are all intermediate because they fall on the gel length range of (41- 60 mm). However, Mw 1685 (40 mm), Accession 18037(30 mm), Accession 5934 (39 mm) and Faya Kalonga (40 mm)

exhibited a hard types of gel consistency which range from (36 mm – 40 mm). Genotypes which were grouped as intermediate had a soft gel while those categorized as high possessed a hard gel.

4.2.3 Phenotypic traits correlations

Correlation analysis was also done on the phenotypic traits for rice genotypes which were grown in field condition. An exception of the traits is noticed since the root architectural traits only depended on the screen house (PVC) work hence have not reappeared in the field data. Table 9 below illustrates the correlation existing among the ten (10) traits of the studied genotypes.

Table 9: Phenotypic traits correlations for the genotypes grown in field condition

Trait	GRY	PLH	NPP	TPP	PAL	LBL	NDM	SPP	TGW	SPF
GRY	1.00									
PLH	-0.538**	1.00								
NPP	0.587**	-0.647**	1.00							
TPP	0.572**	-0.602**	0.976**	1.00						
PAL	-0.139	0.236	-0.641**	-0.576**	1.00					
LBL	-0.444*	0.308*	-0.692**	-0.651**	0.749**	1.00				
NDM	-0.016	-0.249	-0.051	0.068	0.369*	0.388*	1.00			
SPP	-0.266*	0.372*	-0.848**	-0.788**	0.856**	0.742**	0.404*	1.00		
TGW	0.203	0.138	0.167	0.054	-0.502**	0.054	-0.794**	-0.447*	1.00	
SPF	-0.206	0.506**	-0.749**	-0.723**	0.516**	-0.723**	0.037	0.752**	-0.251*	1.00

***Significant correlation at 0.05 level (2-tailed); **Significant correlation at 0.01 level (2-tailed).**

Note: GRY = Grain Yield, PLH = Plant Height, NPP = Number of Panicles per Plant, TPP = Number of Tillers per Plant, PAL = Panicle Length, LBL = Leaf Blade Length, SPF = Spikelet Fertility, NDM = Number of Days to Maturity, SPP = Number of Spikelets per Panicle, TGW = Thousand Grain Weight.

4.2.3.1 Grain yield (tons / ha)

Positive and significant correlations were exhibited for grain yield with number of panicles per plant and number of tillers. On the other hand, negative and significant association was attained for the trait in question with plant height, leaf length, and number of spikelets per panicle.

4.2.3.2 Plant height (cm)

Plant height was positively and significantly correlated with leaf length, number of spikelets per panicle and spikelet fertility. However, negative and significant relationships were observed for the trait in mention with number of days to maturity, number of tillers, number of panicles per plant and grain yield (Table 9).

4.2.3.3 Number of panicles per plant

There was positive and highly significant correlation for the number of panicles per plant with grain yield and number of tillers per plant. However, negative and significant correlation was attained for this trait with plant height, panicle length, leaf length, number of spikelets per panicle and spikelet fertility.

4.2.3.4 Number of tillers per plant

The number of tillers per plant demonstrated positive and significant correlation with grain yield and number of panicles per plant. On the other hand, negative and significant association was exhibited for the same trait with plant height, panicle length, leaf length, number of spikelets per panicle and spikelet fertility.

4.2.3.5 Panicle length (cm)

Positive and significant correlation was exhibited for panicle length with leaf length, number of days to maturity, number of spikelets per panicle and spikelets fertility. On the contrary, this trait had negative and significant association with number of panicles per plant, number of tillers and 1000 grain weight.

4.2.3.6 Leaf length (cm)

Leaf Length exhibited positive and significant correlation with plant height, panicle length, number of days to maturity and number of spikelets per plant. However, negative and significant association was noticed for the trait in question with spikelet fertility.

4.2.3.7 Number of days to maturity (NDM)

Positive and significant relationships were exhibited for the number of days to maturity with panicle length, leaf length and number of spikelets per panicle. On the same trait, negative and significant correlation was attained with 1000 grain weight.

4.2.3.8 Number of spikelets per panicle

The number of spikelets per panicle showed positive and significant association with plant height, panicle length, leaf length and number of days to maturity. On the other hand, negative and significant correlation was attained for this trait with grain yield, number of panicles per plant, number of tillers and 1000 grain weight.

4.2.3.9 One thousand grain weight (g)

The trait exhibited negative and significant correlation with panicle length, number of days to maturity number of spikelets per panicle and spikelet fertility. However, all the other traits correlated non - significantly with the trait in question.

4.2.3.10 Spikelet fertility (%)

The trait exhibited positive and significant correlation with plant height, panicle length and number of spikelets per panicle. However, the same trait had negative and significant association with number of panicles per plant, number of tillers per plant, leaf length and one thousand grain weight.

4.2.4 Rice qualitative traits

4.2.4.1 Apiculus colour

Apiculus is the small pointed portion of palea or lemma tips depending on whichever is longer. In this study, five (5) genotypes were scored to have straw clour and the remaining ten (10) genotypes showed brown tawny colour representing 33.3% and 66.7% respectively.

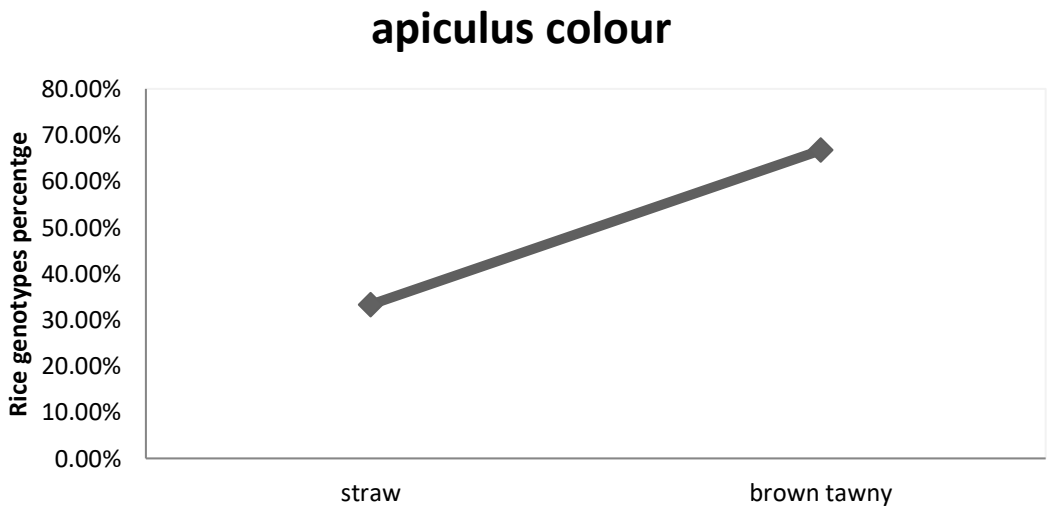

Figure 5: Percentage of apiculus colour

4.2.4.2 Basal leaf sheath colour

Green colour was observed in ten (10) genotypes namely; Mw 1685, Faya 14 M 69, Accession 9290, Faya Mafuta 1, Accession 18028, Accession 5934, Accession 18037, Faya Makanjira, Accession 5933 and Accession 17344 representing 66.7 %. Furthermore, such genotypes as Faya Kalonga, Accession 17323, Faya Zambia and Faya Mafuta 2 exhibited a green with purple lines colour. This stands for 26.7 % of the entire studied genotypes. Only one genotype, Accession 9293, exhibited purple colour on this trait and this caters for 6.6 % of the studied genotypes

4.2.4.3 Ligule shape and colour

This was another trait vital for characterization of rice. In this work, all the studied genotypes had similar ligule shape of 2 – creft. Besides that, all the ligules of the studied genotypes were whitish in colour illustrating lack of variation in both traits.

4.2.4.4 Leaf blade colour

Leaf blade color was another qualitative trait that was used to characterize the rice genotypes. In this study all the rice genotypes exhibited a green colour except Accession 9293 which had a light green colour.

4.2.4.5 Leaf blade pubescence

In this study, it was noted that all the genotypes were pubescent.

4.2.4.6 Panicle exsertion

This trait is very fundamental for the identification of rice cultivars because it is very clear as the crop stand in the field at early maturity stage. The studied genotypes showed variation for this trait because nine (9) genotypes were observed to be well exserted, four (4) were moderately well exserted whereas two (2) were exserted partly.

4.2.4.7 Auricle presence / absence and color

The studied genotypes were categorized as all enriched with auricles basing on the observation. Besides that, it was also noted that all the genotypes had light green auricles.

4.2.4.8 Flag leaf altitude

In this study, nine (9) genotypes exhibited an erect behavior on this trait. In addition, semi – erect (intermediate) behavior on this trait was noticed in three (3) genotypes and the remaining three (3) genotypes depicted horizontal behavior. Therefore the erect, semi – erect (intermediate) and horizontal treatments shared the levels of 60 %, 20 % and 20 % respectively. The figure 5 below illustrates the variation levels in percentage on the flag leaf of the genotypes.

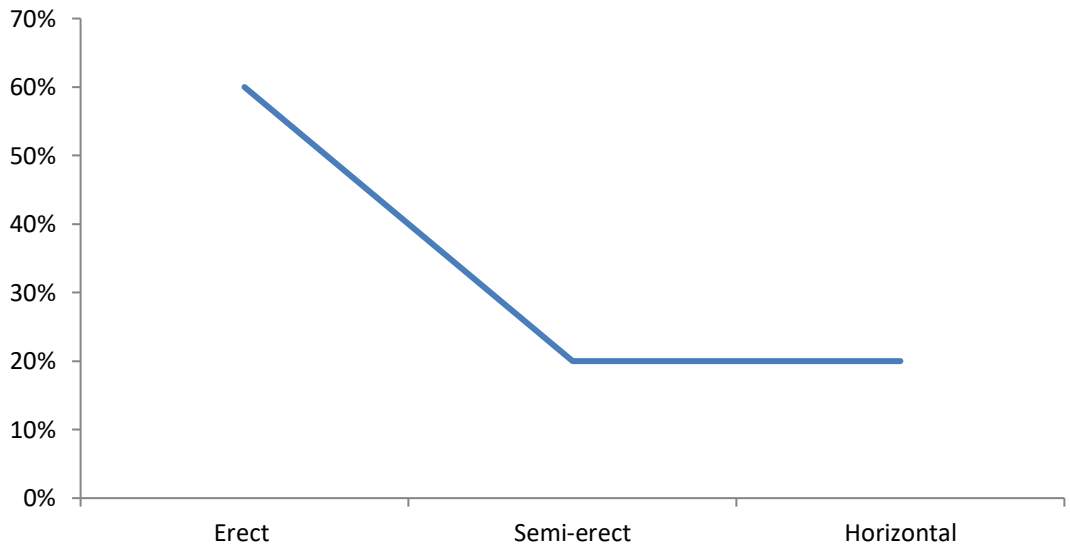

Figure 6: Percentage of flag leaf altitude

4.2.4.9 Panicle altitude of branches

The studied genotypes behaved differently to this trait. Basically, an erect mode of branching was exhibited in four (4) genotypes, namely; Accession 9290, Faya 14 M 69, Accession 5933 and Faya Zambia whereas open (spreading) types of branching was observed in Faya Kalonga, Accession 5934and Accession 17323 , and the remaining genotypes had semi – erect (semi – compact panicle) mode of branching.

4.2.4.10 Lemma and palea colour

Lemma and palea of most of the genotypes evaluated had straw color 155 (81.15%). Nineteen (9.95%) of the genotypes had brown furrows and thirteen (6.81%) had brown color on lemma and palea. In addition, two (1.05%) of the genotypes had black color, one (0.52%) had purple and one (0.52%) had purple spots.

4.2.4.11 Sterile lemma colour

Sterile lemma is the flowerless bract at the base of spikelet. All the genotypes had straw color except Faya Makanjira which depicted gold colour representing 93.3 % and 6.7 % respectively.

4.2.4.12 Awning

This trait was considered in order to detect the presence or absence of awns in the studied genotypes. It was noted that all the genotypes were awnless except Accession 17323, Faya Makanjira and Accession 9293 which were partly awned. This represents 80 % and 20 % for the awnless and partly awned genotypes respectively.

4.2.5 Agglomerative Hierarchical Clustering

The agglomerative hierarchical clustering was done using XLSTAT on the Euclidean distance matrix following the Ward's linkage procedure. The dendrogram was constructed using twenty five (25) quantitative morphological, grain quality, and root architectural traits for the fifteen (15) Faya rice genotypes. The rice genotypes were grouped into four (4) clusters after the analysis and depicted the following categories; cluster 1 comprised Mw 1685 only, cluster 2 consisted of Faya 14 M 69 and Faya Kalonga. In addition, cluster 3 composed of seven (7) genotypes such as Accession

9290, Faya Mafuta 1, Accession 5934, Faya Makanjira, Accession 5933, Faya Mafuta 2 and Accession 9293, and cluster 4 consisted of five genotypes, namely; Accession 18028, Accession 18037, Accession 17323, Faya Zambia and Accession 17344 as shown in figure 6.

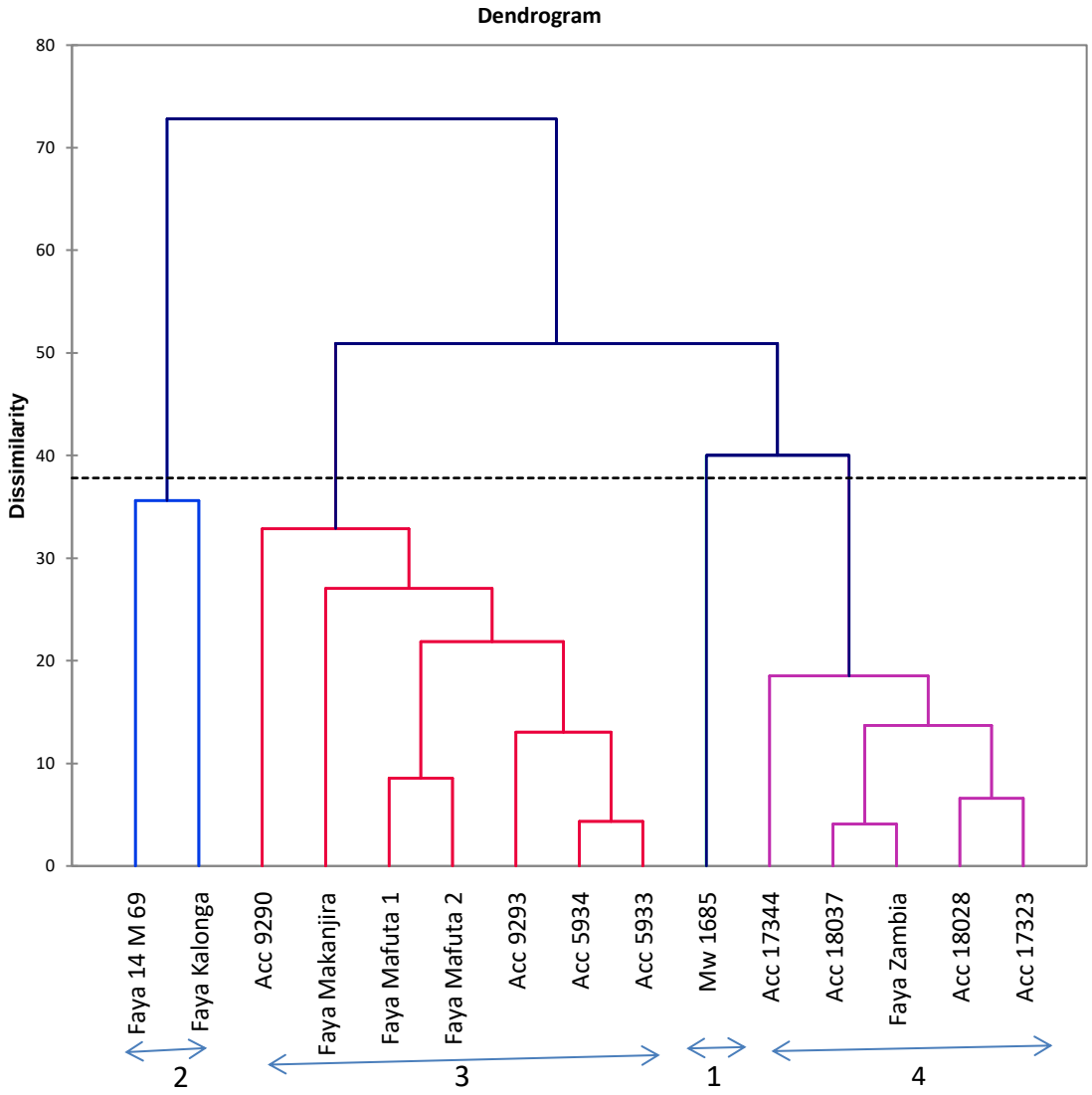

Figure 7: Dendrogram using agglomerative clustering method illustrating the profile of 15 Faya rice genotypes based on morphological, grain quality and root architectural characters.

Furthermore, the clustering analysis gave results on mean value of each trait. It was therefore noted that the maximum cluster mean values for grain length (9.62), grain width (3.22), 1000 grain weight (35.68) and spikelet fertility (96.98) were exhibited in cluster 1.In cluster 2, the maximum centroid values were obtained in such traits as grain yield, panicle length and flag leaf length with magnitudes of 3. 2, 26.4 and 31.8 respectively. In addition, cluster 3 maximum mean values were obtained in number of panicles per plant, (19.2), number of tillers per plant (22.33), days to maturity (155.4), grain shape (3.5) and days to 50% flowering (113.5). Cluster 4 comprised a majority of the traits with the maximum values and these include; plant height (160.56), leaf length (50.11), leaf width (1.3), flag leaf width (1.5), number of spikelets per panicle (189.2), fresh root mass (328.06), root number (334.46), maximum root length (64.33), fresh shoot mass (89.13), root volume (293.34), dry root mass (108.26), dry shoot mass (77.8) and root / shoot ratio (1.44). Generally, cluster 2 comprised the lowest mean performing traits whereas cluster 4 yielded the highest mean traits of the studied genotypes.

Table 6 shows the centroids / means of the 25 morphological, grain quality and root architectural traits of the 15 Faya rice genotypes in four (4) clusters.

Table 10: Cluster centroids of 25 morphological, grain quality and root architectural traits of the 15 Faya Rice Genotypes

TRAIT	C L U S T E R			
	1	**2**	**3**	**4**
Grain yield	3.212	3.287	2.521	2.764
Plant height	138.200	103.900	150.343	160.560
Panicles /plant	14.360	15.835	19.201	16.068
Tillers/plant	18.000	18.665	22.333	16.868
Panicle length	21.960	26.495	25.619	25.292
Leaf length	50.000	37.625	48.560	50.118
Leaf width	1.200	1.271	1.081	1.305
Flag leaf length	23.170	31.880	28.156	28.044
Flag leaf width	1.483	1.350	1.333	1.537
Spikelets / panicle	101.200	166.600	143.771	189.220
Fresh root mass	148.100	109.050	304.800	328.060
Root number	262.000	265.350	291.700	334.460
Maximum root length	51.330	47.165	61.763	64.334
Fresh shoot mass	74.300	34.310	81.637	89.138
Root volume	191.700	216.700	236.900	293.340
Dry root mass	95.790	47.800	99.826	108.262
Dry shoot mass	69.390	38.655	70.436	77.804
Root / shoot ratio	1.412	1.384	1.424	1.488
Days to maturity	122.000	146.000	155.429	154.200
Grain length	9.620	8.780	9.191	9.442
Grain width	3.220	2.550	2.619	2.758
Grain shape	2.980	3.430	3.507	3.416
Days to 50 % flowering	96.000	107.000	113.571	112.600
Thousand grain weight	35.680	30.705	26.086	29.382
Spikelet fertility	96.980	92.460	95.711	95.711

4.2.6 The Principal Component Analysis (PCA).

The principal component analysis (PCA) for the 15 Faya rice genotypes produced results for factor scores, Eigen value, variability percentage and cumulative percentages. The analyses lead to the emergence of five (5) Principal Components. The first principal component had a variance cumulative magnitude of 93.504 % whereas the entire five components comprised a variance cumulative value of 99.59 %. The traits associated with the maximum first principal component variance cumulative percentage were root number, fresh root mass, root volume, number of spikelets per panicle, days to maturity, days to 50 % flowering and spikelet fertility with values of 9.492, 8.246, 7.183, 3.504, 3.185, 1.437 and 0.792 respectively. Furthermore, characters associated with the second principal component variance cumulative percentage were number of spikelets per panicle (1.675), root number

(1.026), days to maturity (0.604) and spikelet fertility (0.5). In addition, the third principal component was related to number of spikelet per panicle (1.879) and fresh root mass (0.867).

The fourth principal component had only plant height trait (0.592) as its associating trait with a high positive contribution towards the available variance cumulative value (99.13 %). The fifth principal component was correlated with such a trait as dry root mass with the value of 0.596. The levels of discrimination for the principal axes exhibited by Eigen values were 14.026, 0.438, 0.274, 0.134 and 0.068 for principal components 1, 2, 3, 4 and 5 respectively. In this regard, the Eigen discrimination values were highest in the first principal component and lowest in the fifth component, and that was true also for the variance percentage with highest value of 93.504 % and lowest magnitude of 0.456 %. Table 11 illustrates Principal Component Analysis (PCA) for the factor scores, Eigen values, variability percentage and variance cumulative percentage of the 25 morphological, grain quality and root architectural traits for the 15 Faya rice genotypes. The graph of the first and second principal component using 25 morphological markers / traits also agree with the clustering pattern already presented despite minor differences. In that graph, it has been illustrated that most of the genotypes are clustered together at the left side, depicting that they share common attributes. For example, T3, T4, T7, T9, T11, T14, T5 which belong to cluster 3 have also been grouped together. However, other genotypes which are in cluster four have been grouped together with those of cluster three in the third component of the plot. Treatments 1, 2 and 4 have been scattered in the second component whereas treatment 6 is in the first component of the plot and this means they are more variable from the rest. In a related situation, the graph of the first and

second principal components also grouped the 25 traits of the genotypes under the study.

Results showed that number of spikelets per panicle, root number and fresh root mass were clustered in the first, second, and third component respectively. The rest of the remaining traits were clustered together at the centre of the plotted graph. Figure 7is a graph for the first and second principal components of the 15 Faya rice genotypes basing on the 25 morphological, grain quality and root architectural traits while figure 8is the same graph but having an illustration of the 25 traits and their corresponding components.

Table 11: Factor scores, Eigen values, variability and variance cumulative percentage of 25 morphological, grain quality and root architectural traits for the five principal components

Character	Principal 1	Principal 2	Principal 3	Principal 4	Principal 5
Grain yield	-3.299	-0.093	-0.063	-0.107	-0.167
Plant height	2.973	0.222	0.153	0.592	0.234
Number of panicles / plant	-2.655	-0.055	-0.043	-0.015	-0.047
Number of tillers /plant	-2.554	-0.057	-0.095	-0.014	-0.032
Panicle length	-2.308	0.078	0.011	-0.043	-0.082
Leaf length	-1.327	0.049	0.098	0.077	0.065
Leaf width	-3.368	-0.111	-0.062	-0.103	-0.177
Flag leaf length	-2.180	0.054	-0.004	-0.083	0.000
Flag leaf width	-3.358	-0.111	-0.061	-0.101	-0.175
Number of spikelets /panicle	3.504	1.675	1.879	-0.157	-0.248
Fresh root mass	8.246	-2.373	0.867	0.293	-0.352
Root number	9.492	1.026	-1.488	0.322	-0.616
Maximum root length	-0.848	-0.195	-0.173	-0.140	-0.066
Fresh shoot mass	-0.084	-0.420	-0.032	0.097	0.183
Root volume	7.183	-0.215	-0.310	-1.515	0.353
Dry root mass	0.721	-0.475	-0.324	0.413	0.596
Dry shoot mass	-0.443	-0.230	-0.101	0.176	0.167
Root /shoot ratio	-3.358	-0.115	-0.066	-0.101	-0.171
Number of days to maturity	3.185	0.604	0.032	0.278	0.349
Grain length	-3.014	-0.067	-0.068	-0.067	-0.132
Grain width	-3.302	-0.104	-0.065	-0.097	-0.166
Grain shape	-3.270	-0.099	-0.060	-0.092	-0.165
Days to 50 % flowering	1.437	0.401	0.052	0.184	0.357
Thousand grain weight	-2.164	0.114	-0.138	-0.033	-0.008
Spikelet fertility	0.792	0.500	0.062	0.238	0.301

Eigen value	**14.026**	**0.438**	**0.274**	**0.134**	**0.068**
Variability %	**93.504**	**2.921**	**1.824**	**0.890**	**0.456**
Variance Cumulative %	**93.504**	**96.425**	**98.249**	**99.13**	**99.59**

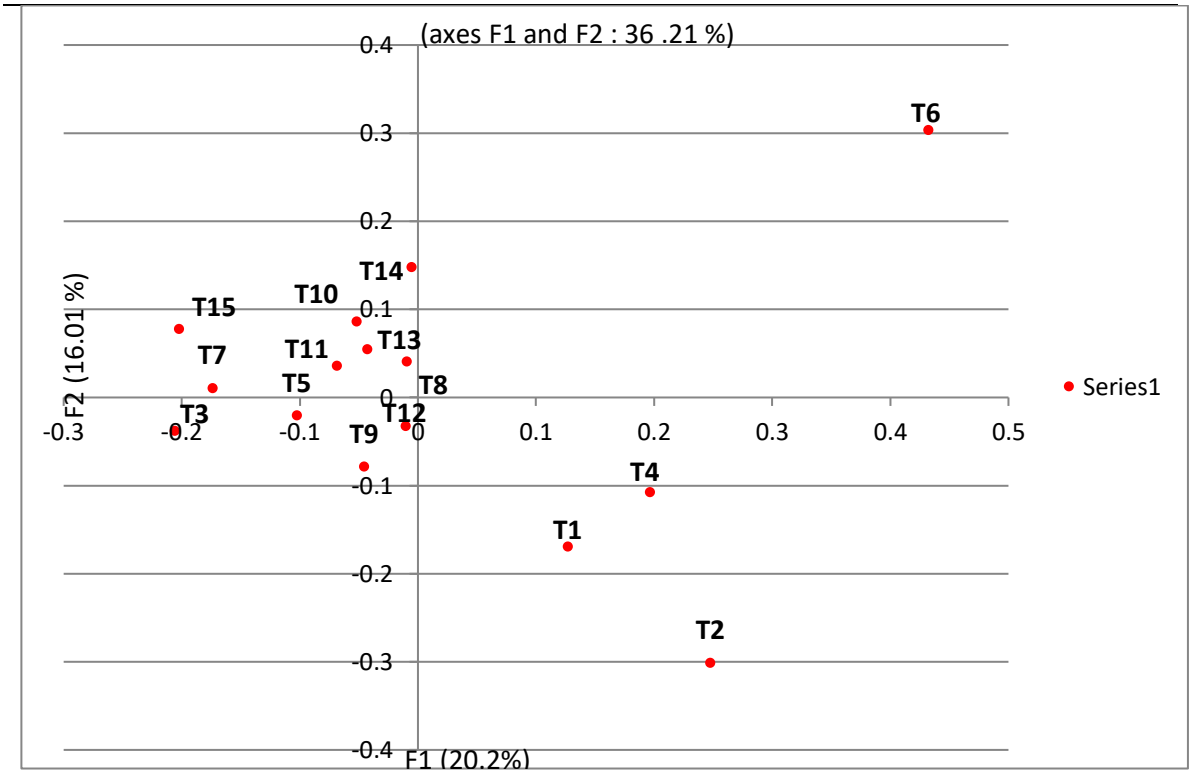

Figure 8: First and second principal components illustrating relationships of 15 Faya rice genotypes based on 25 morphological, grain quality and root architectural traits.

Note:

T1 = Mw 1685

T2 = Faya 14 M 69

T3 = Acc 9290

T4 = Faya Mafuta 1

T5 = Acc 18028

T6 = Faya Kalonga

T7= Acc 5934

T8 = Acc 18037

T9 = Faya Makanjira

T10 = Acc 17323

T11 = Acc 5933

T12 = Faya Zambia

T13 = Acc 17344

T14 = Faya Mafuta 2

T15 = Acc 9293

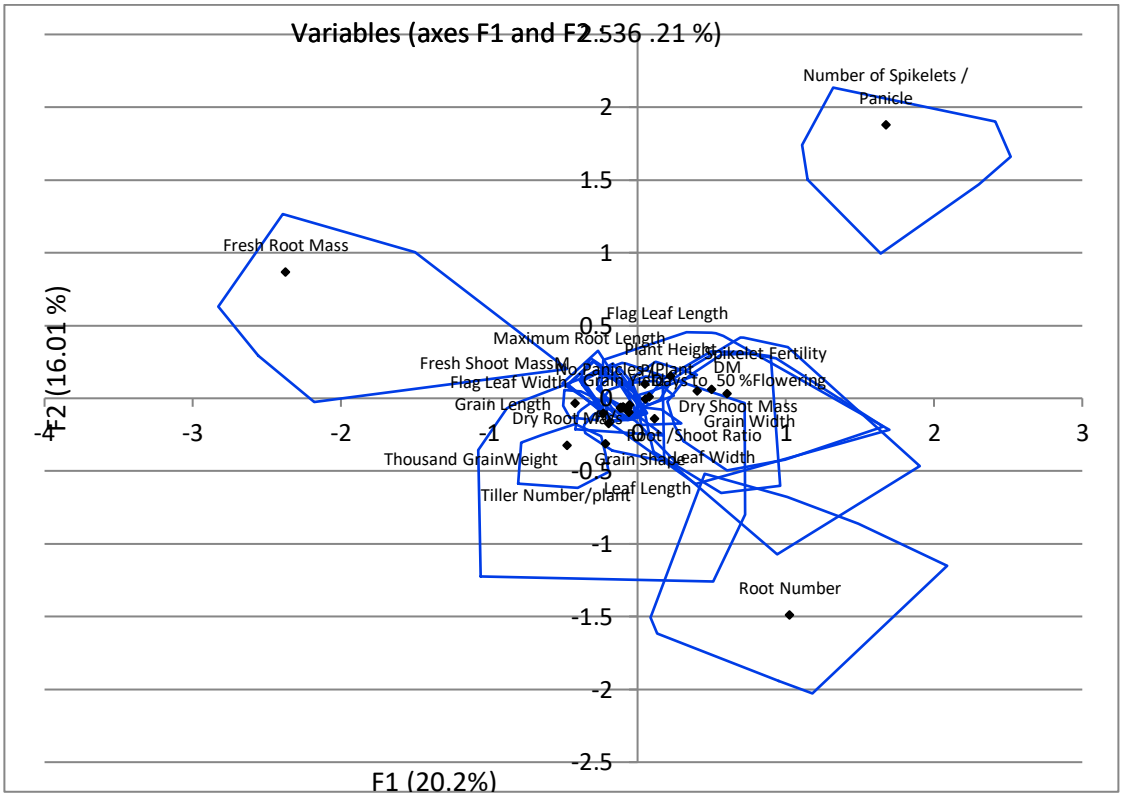

Figure 9: First and second principal components illustrating relationships of 25 morphological, grain quality and root architectural traits.

4.3 Performance of the genotypes based on molecular (SSR) marker studies.

In this study a total of ten (10) SSR primers were used for the fifteen (15) Faya rice genotypes and all those markers turned out to be polymorphic for the target traits. The markers yielded a total of 142 bands and each primer had an average of 14.2 bands amplified after running the PCR. The primer base pair bands ranged from the minimum 102 bp (RM 248) to the maximum 225 bp (RM 242) and were realized on the banding patterns of each marker. In total, 63 alleles were scored and the average number of alleles per primer was 6.3 which ranged from 2 to 8 alleles. There were three markers recorded for a maximum of eight (8) alleles namely; RM 213, RM231 and RM248 whereas three other markers had six alleles each, such as RM 212, RM

315 and RM331. The minimum number of two (2) alleles was obtained in RM215 where as RM 242 and RM262 scored 7 alleles each. The Polymorphism Information Content (PIC) was tabulated for each marker and this is fundamental for the measurement of in formativeness of the studied genotypes scores. The PIC ranged from 0.46 for RM 231 to 0.98 for RM 215 and the mean values was 0.75. The results for each marker have been presented in the plates below. The letter T (which has ranged from T1 to T15) at the top of each plate represents the genotypes studied such that T1 = Mw 1685, T2 = Faya 14 M 69, T3 = Acc 9290, T4 = Faya Mafuta 1, T5 = Acc 18028, T6 = Faya Kalonga, T7= Acc 5934, T8 = Acc 18037, T9 = Faya Makanjira, T10 = Acc 17323,T11 = Acc 5933, T12= Faya Zambia, T13 = Acc 17344, T14 = Faya Mafuta 2, T15 = Acc 9293and**L** stands for the Ladder used with a size of 50 Bp. The number of alleles per primer, PIC values and number of amplified bands have been illustrated in Table 5 below.

4.3.1 RM212

This marker is associated with tiller number and maximum root length and is located on chromosome 1 (Price *et al,* 2002; Shashidhar *et al.,* 2010). Thirteen of the studied genotypes showed presence of bands for this marker and two (2) depicted absences. The marker amplified six (6) alleles with size ranging from 89 to 113bp. This marker showed PIC value of 0.78and the expected product size for this marker was 112bp.

Figure 10: Primer RM 212

4.3.2 RM213

The marker is located on chromosome 2, linked to the qTRN2.2 and is associated with root number (Hemamalini *et al.,* 2000; Hue *et al.,* 2018).It amplified a total of eight alleles with 120 to 161 Bp. Fourteen (14) of the studied genotypes showed presence of bands for this marker and one (1) depicted absence. The marker showed PIC value of 0.67 and expected product size for allele in this marker was 139 Bp.

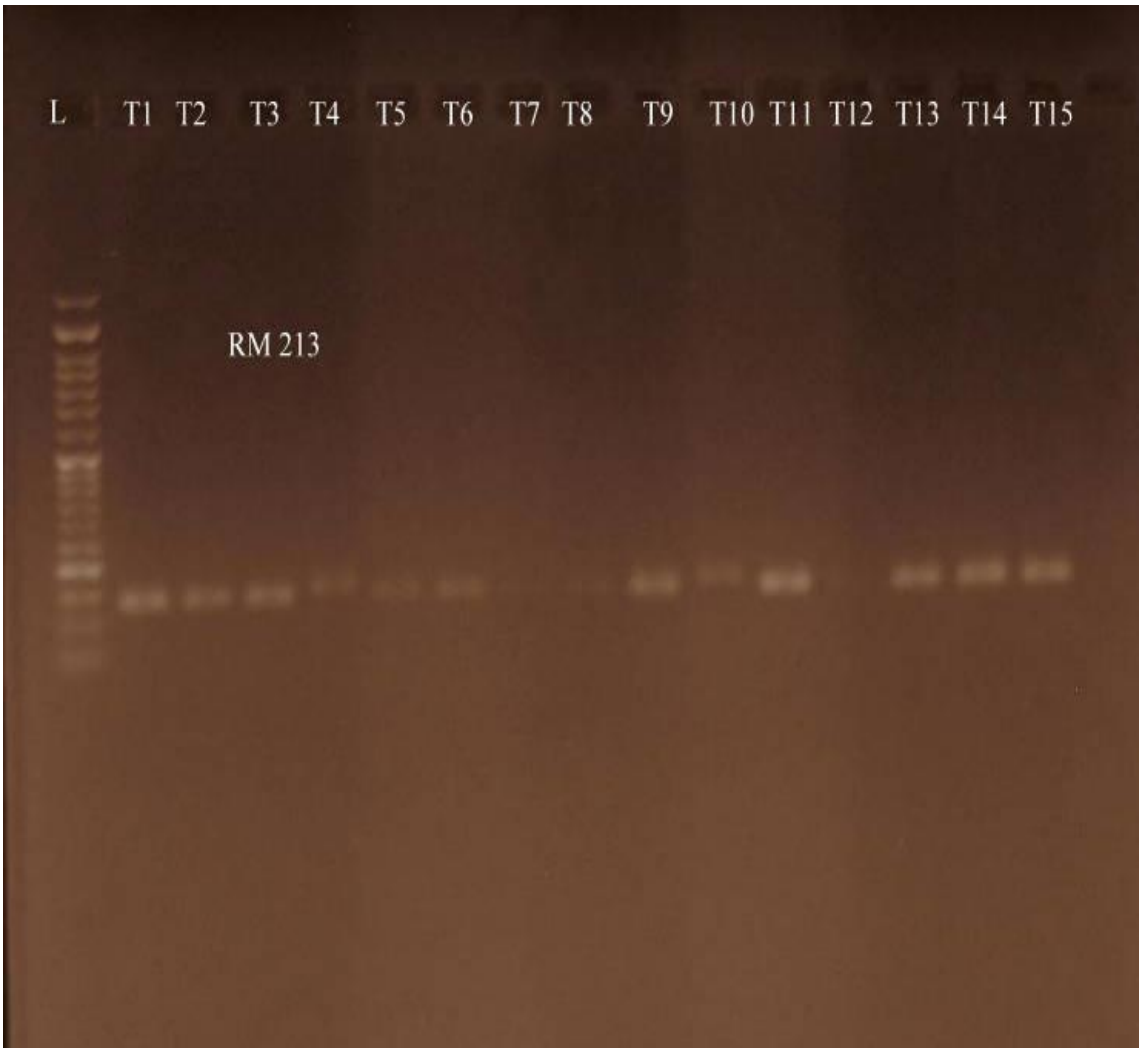

Figure 11: Primer RM 213

4.3.3 RM215

The marker is located on chromosome 9, linked with QTL, qPh1.1 and associated to plant height as well as maximum root length (McCouch *et al.*, 2003). All the studied genotypes showed presence of bands for this marker. It amplified two (2) alleles with the size ranging from 139 to159 Bp. It showed PIC value of 0.98 and the expected product size for allele in this marker was 148 Bp.

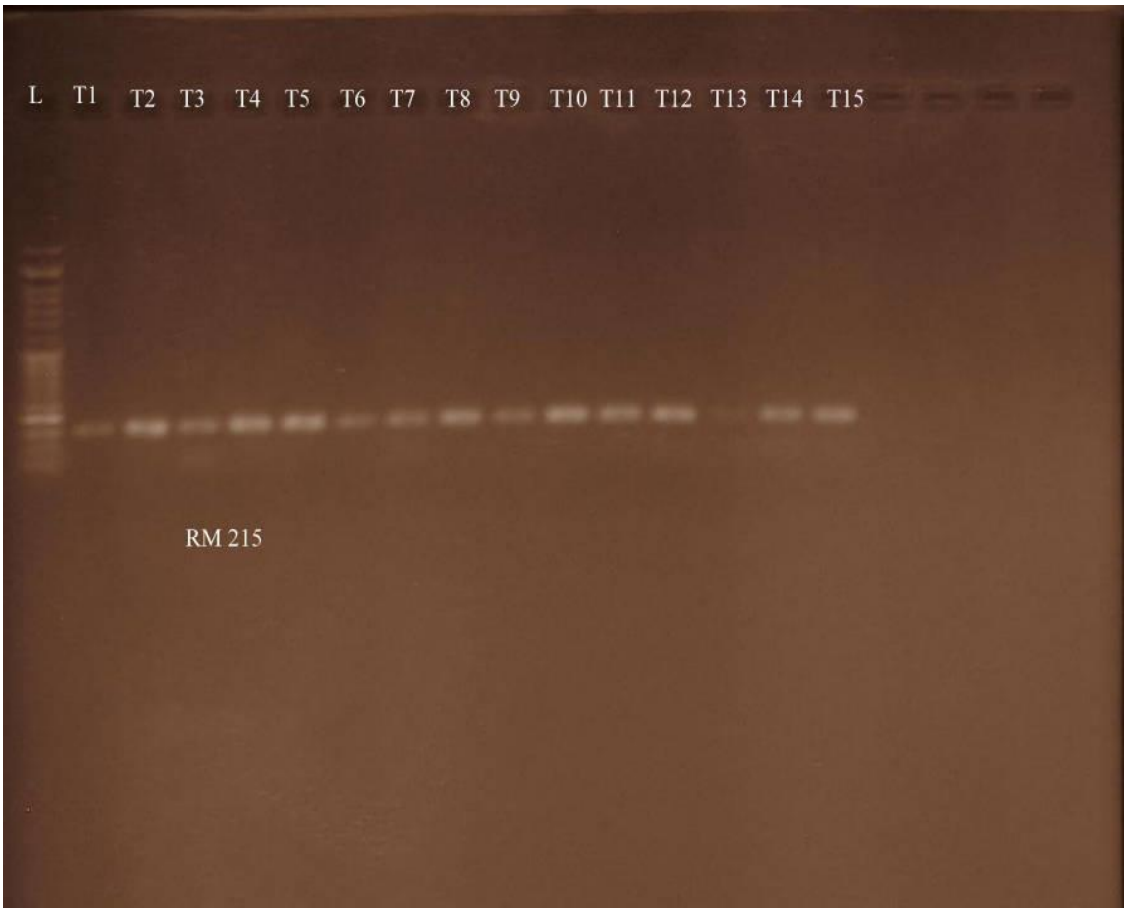

Figure 12: Primer RM 215

4.3.4 RM231

The marker is linked to the Quantitative Trait Loci (QTL, qGY3.1) for grain yield, (Ballan 2013), and is found on chromosome 3. It amplified eight (8) alleles with a size ranging from 168 to 182 Bp. All the studied genotypes showed presence of bands for these markers. It illustrated the PIC value of 0.46 and the expected product size for allele in this marker was 168 Bp.

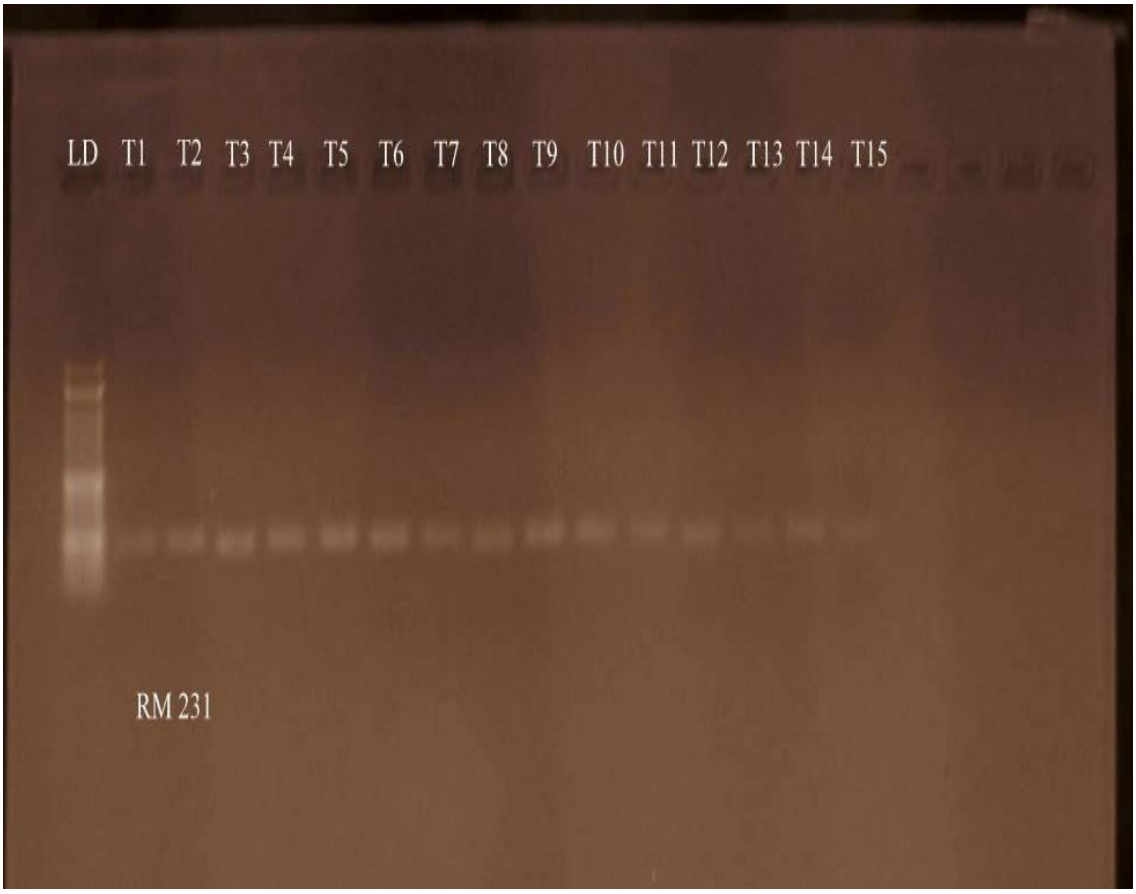

Figure 13: Primer RM 231

4.3.5 RM242

RM 231 is located on chromosome 9, linked to the QTL, qph9.1s and the traits plant height, maximum root length and deep root weight (Shashidhar *et al.,* 2010). Among the studied genotypes, thirteen (13) showed presence of bands for this marker and two (2) depicted absence. It amplified seven (7) alleles with size ranging from 163 to 216bp. This marker showed PIC value of 0.82 and the expected product size for allele in this marker was 225bp.

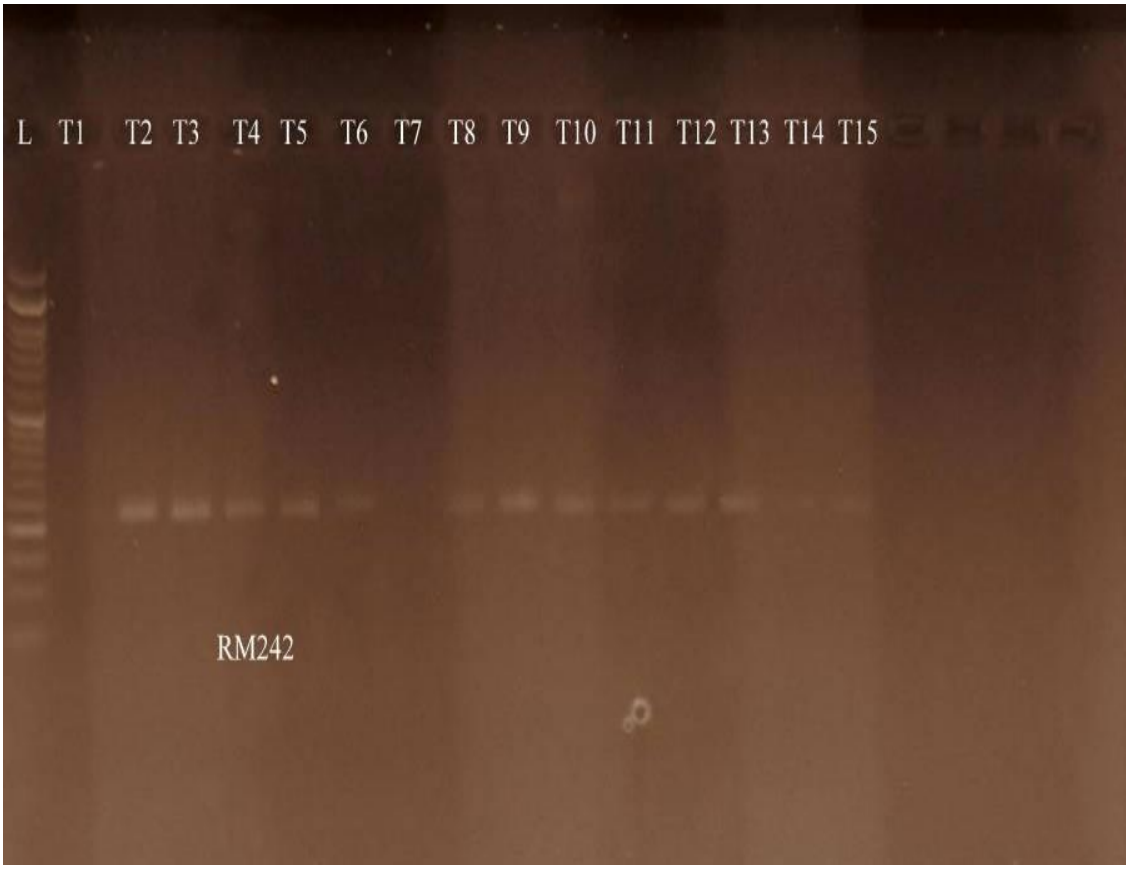

Figure 14: Primer RM 242

4.3.6 RM248

RM 248 is located on chromosome 7, and is linked to the QTL, qGY9 for grain yield (www.gramene.org). Among the studied genotypes, fourteen (14) showed presence of bands for this marker and one (1) depicted absence. It amplified eight (8) alleles with a size ranging from 67 to 96bp. It showed PIC value of 0.67 and the expected product size for allele in this marker was 102bp.

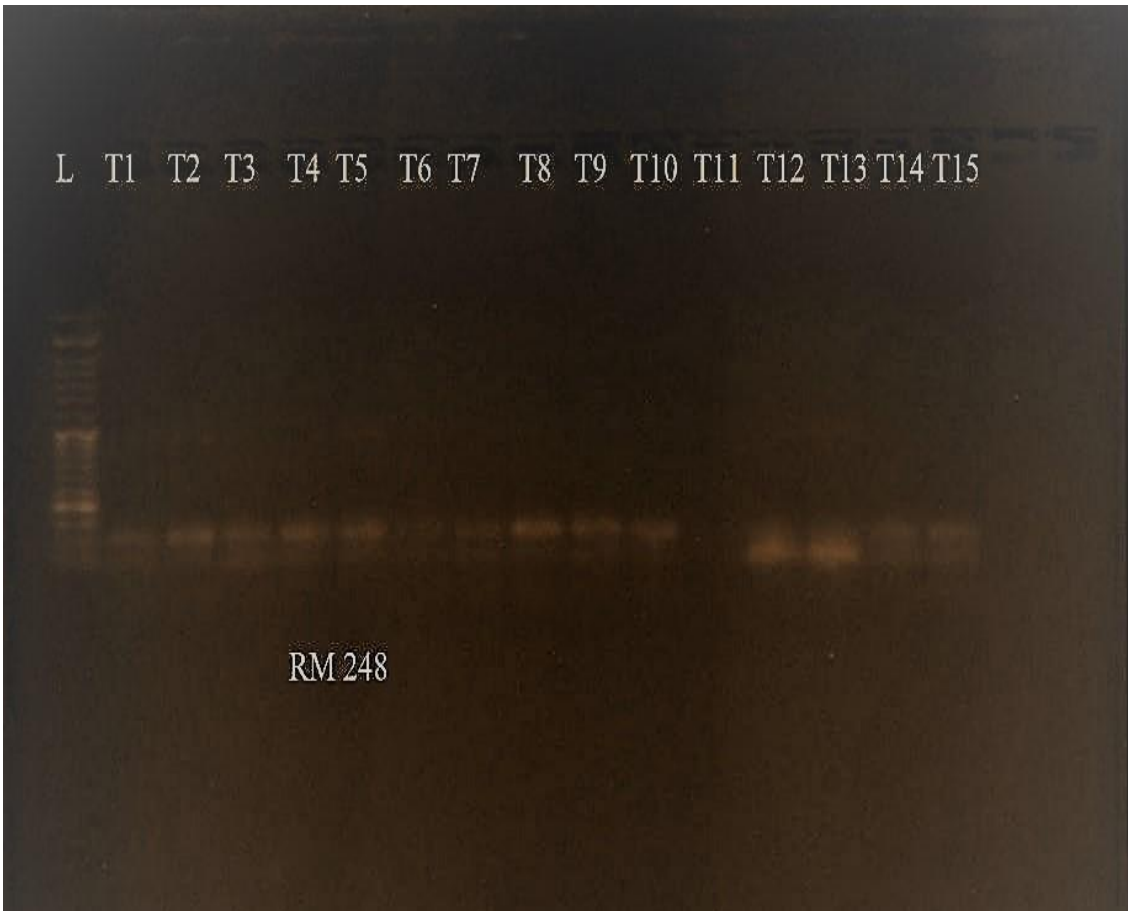

Figure 15: Primer RM 248

4.3.7 RM262

The marker is located on chromosome 2, linked to the QTL, qRTH-2 for root thickness (Yano *et al*., 2008). All the studied genotypes showed presence of bands for this marker. It amplified a total of seven (7) alleles with a size ranging from 129 to 173 Bp. It showed the PIC value of 0.78.

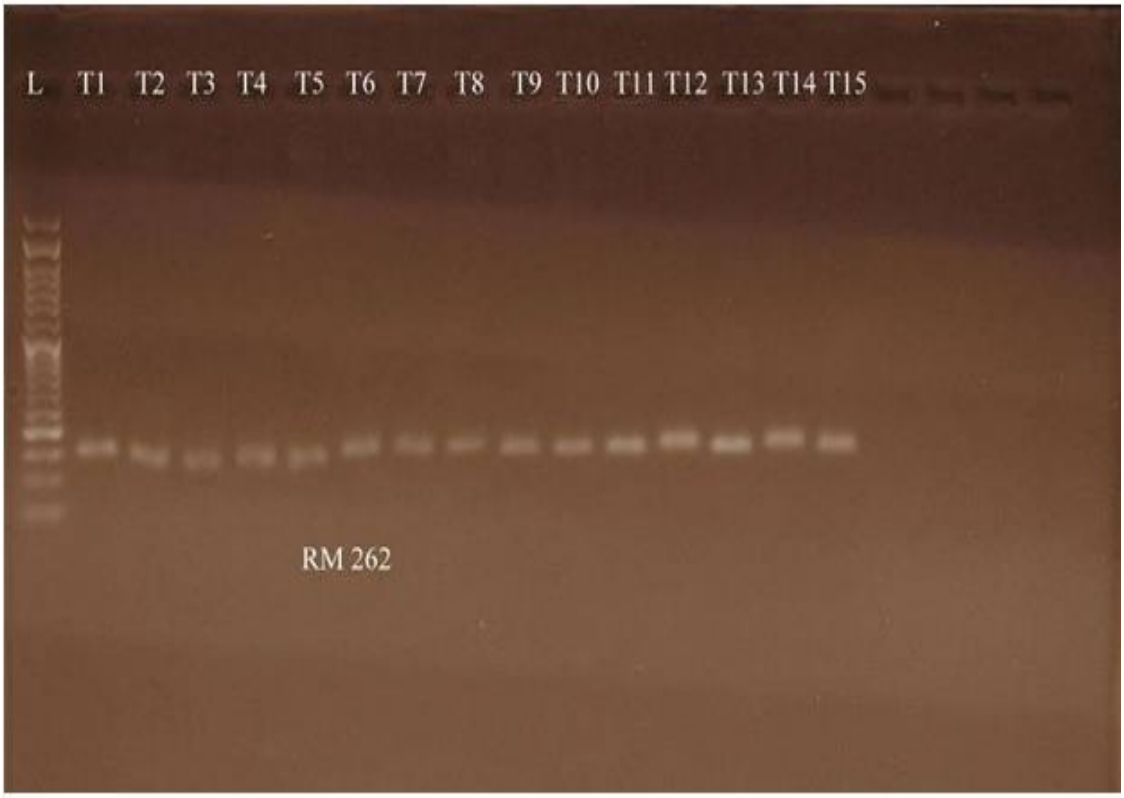

Figure 16: Primer RM 262

4.3.8 RM315

RM 315 is located on chromosome 2, linked to the QTLs, qDTY1.1 and ph1.1 for the trait root number (Vikram *et al.,* 2011). Among the studied genotypes, fourteen (14) showed presence of bands for this marker and one (1) depicted absence. It amplified total seven (6) alleles with size ranging from 134 to 157 Bp. The PIC value for this marker was 0.78 and the expected product size for allele was 133bp.

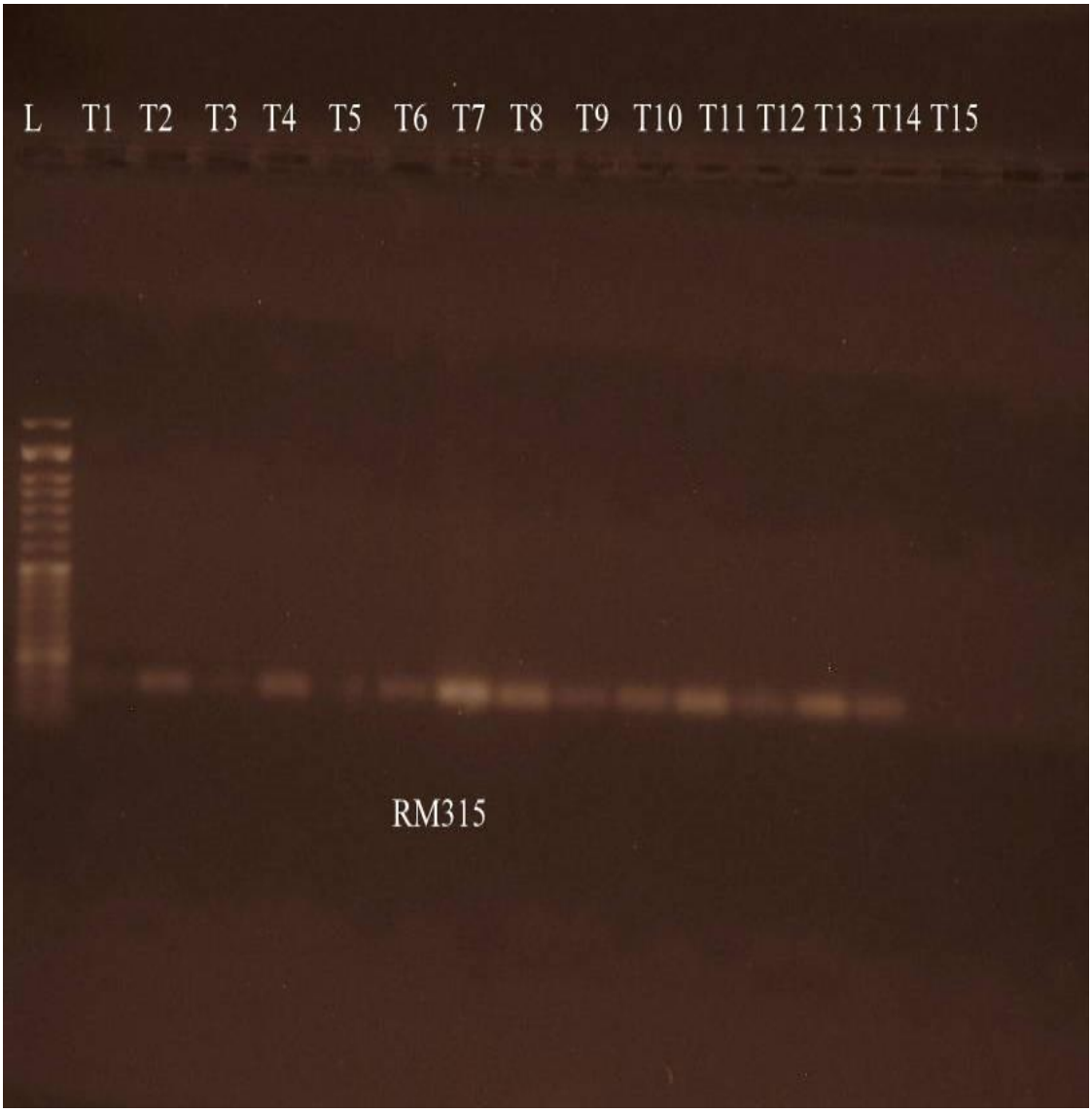

Figure 17: Primer RM 315

4.3.9 RM 331

The marker is for root length and number of tillers traits (www.gramene.org). All the studied genotypes showed presence of bands for this marker. It amplified six (6) alleles with size ranging from 176 to 200 Bp and the PIC value was 0.84.

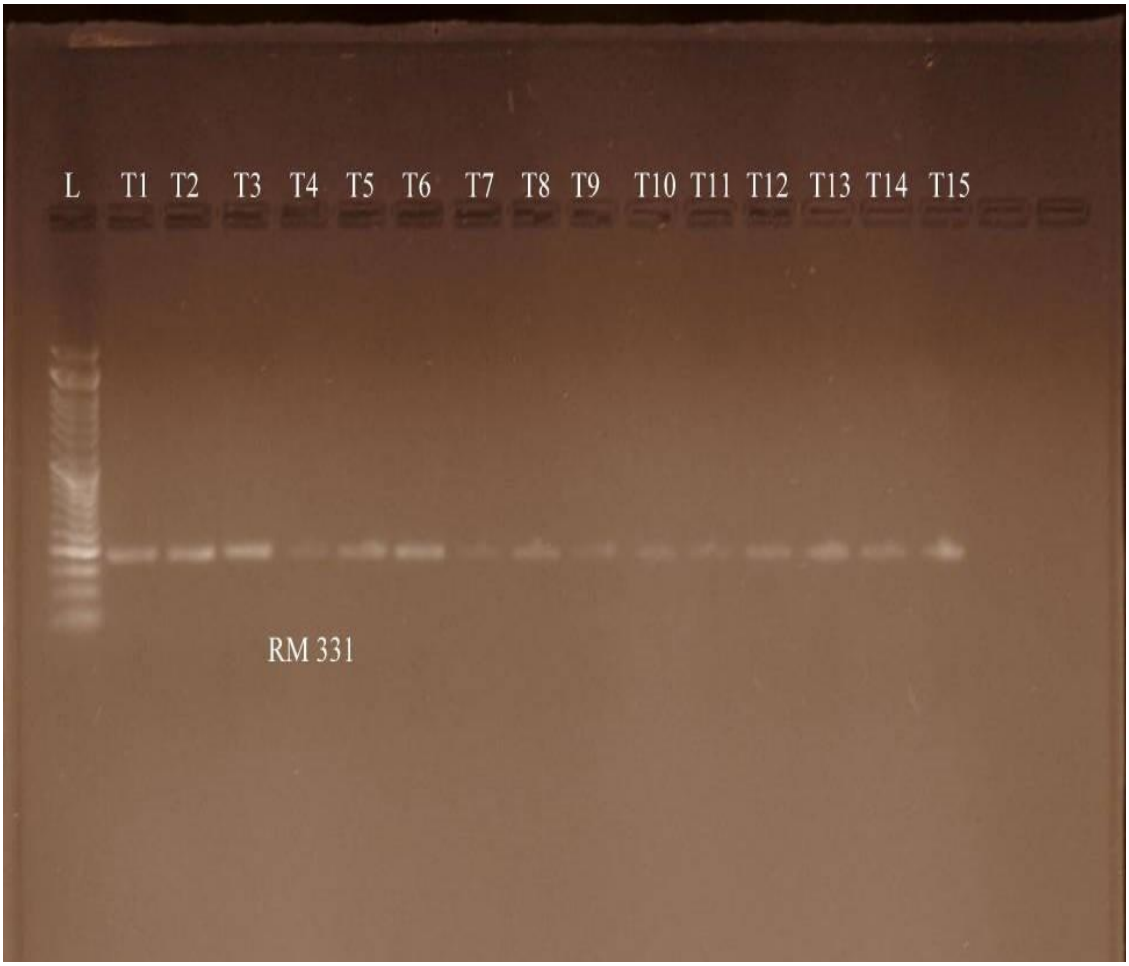

Figure 18: Primer RM 331

4.3.10 RM 3810

The marker is located on chromosome 1 and is linked to QTL, qRTH-1 for the trait root thickness (Yano *et al.*, 2008). Thirteen of the studied genotypes showed presence of bands for this marker and two (2) depicted absences. It amplified five (5) alleles with size ranging from 78 to 104 Bp. It showed PIC value of 0.72 and the expected product size for allele in this marker was 105bp.

Figure 19: Primer RM 3810

Table 12: Illustration of number of amplified bands, number of alleles per primer, and PIC.

SR NO	LOCUS NAME	BANDS AMPLIFIED	NUMBER OF ALLELES	PIC
1	RM212	13	6	0.78
2	RM213	14	8	0.67
3	RM215	15	2	0.98
4	RM231	15	8	0.46
5	RM242	13	7	0.71
6	RM248	14	8	0.67
7	RM262	15	7	0.78
8	RM315	14	6	0.81
9	RM331	15	6	0.84
10	RM3810	13	5	0.85
Total		141	63	
Mean		14.1	6.3	0.75

4.4 Genotypic similarity.

The 15 studied Faya rice genotypes illustrated some similarity and/ or dissimilarity among themselves (figure 19). The least similarity index magnitude was detected for Acc 5934 and Faya Mafuta 2 (0.118) then seconded by Mw 1685, Faya 14 M 65, Accession 9290, Faya Mafuta 1, Accesion 18028, Faya Kalonga, Mw 18037, Faya Makanjira, Accession 17323, Accession 5933, Faya Zambia, and Accession 17344 (all with a magnitude of 0.126 each). The third index value was attained in Acc 9293 (0.135) and was the highest of the group. These values imply that Acc 5934 and Faya Mafuta 2 are genetically similar; and Mw 1685, Faya 14 M 65, Accession 9290, Faya Mafuta 1, Accesion 18028, Faya Kalonga, Mw 18037, Faya Makanjira, Accession 17323, Accession 5933, Faya Zambia, and Accession 17344 are also genetically similar. Accession 9293 has illustrated to be uniquely dissimilar to the rest of the genotypes as evidenced by its lone index, however, the index differences with the other genotypes is small.

The dendrogram obtained using the molecular data of 10 SSR loci depicted three clusters, namely; I, II and III (Figure 19). Again, the genotypes have been grouped in their clusters as illustrated in Table 13. The uniqueness of Acc 9293 in terms of maximum root length on the phenotypic level has also been felt on the molecular level as it stands on its own cluster from the rest and this may bring calls for a possible introgression of QTLs for this trait.

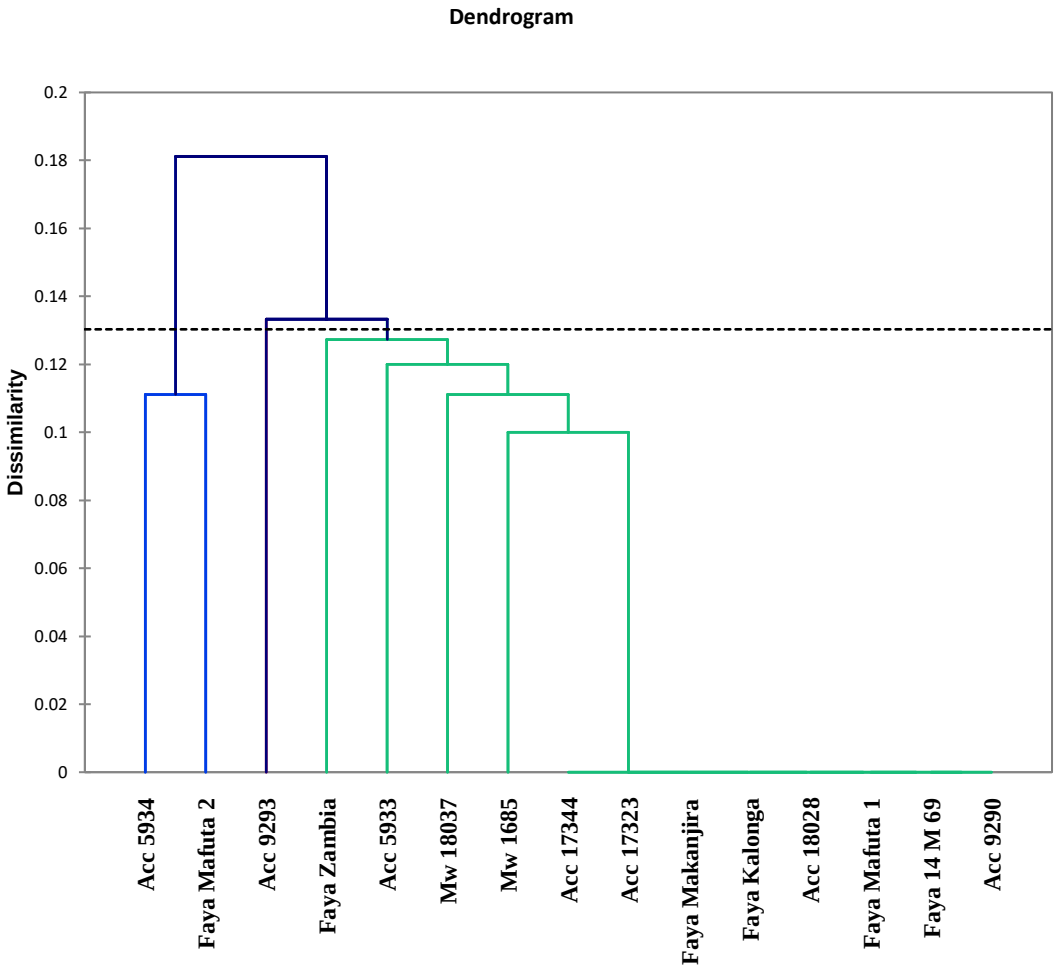

Figure 20: Clustering of 15 Faya rice genotypes constructed using UPGMA based on Jaccard's coefficient attained from 10 SSR marker analyses.

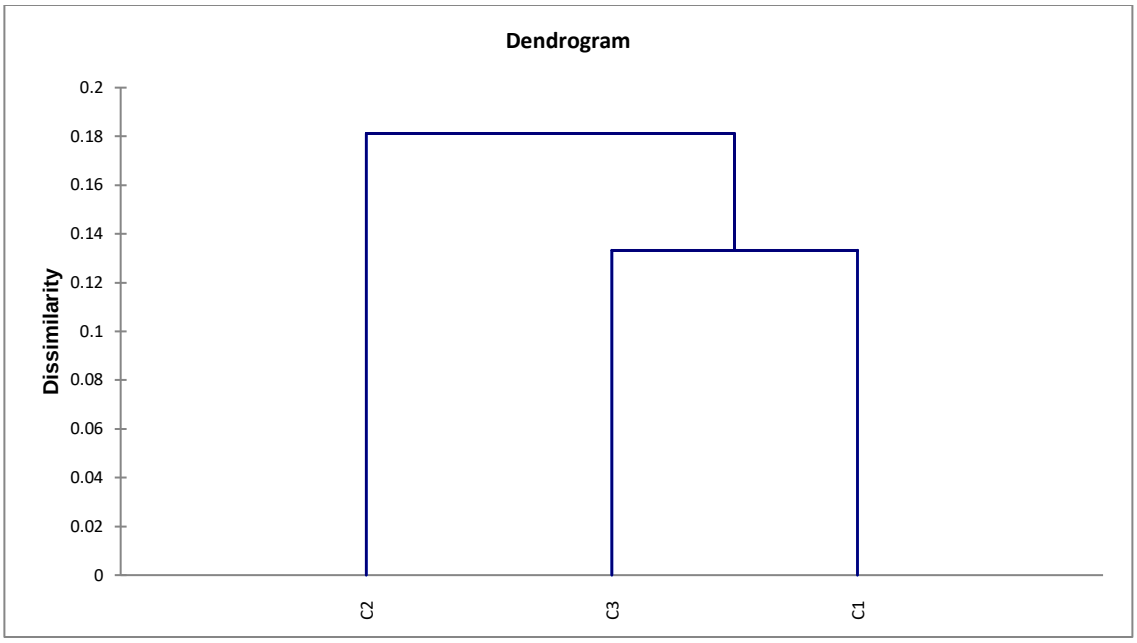

Figure 21: Clusters of 15 Faya rice genotypes formed using UPGMA based on Jaccard's coefficient for the 10 SSR markers.

Table 13 illustrates the grouping of 15 Faya rice genotypes by clustering using UPGMA based on Jaccard's coefficient.

Table 13: Grouping of 15 Faya rice genotypes by clustering using the SSR marker data.

CLUSTER	NUMBER OF GENOTYPES	IDENTITY OF GENOTYPES	NAME OF GENOTYPES
1	12	T1, T2, T3,T4, T5, T6, T8, T9, T10 T11, T12, T13	Mw 1685, Faya 14 M 65, Accession 9290, Faya Mafuta 1, Accesion 18028, Faya kalonga, Mw 18037, Faya makanjira, Accession 17323, Accession 5933, Faya Zambia, Accession 17344.
2	2	T7, T14	Accession 5934, Faya Mafuta 2
3	1	T15	Accession 9293

4.5 Principal component analysis.

The genotypic variation was studied by Principal Component Analysis for determination of genetic diversity of the Faya rice under study. The analysis was done using XLSTAT 2018 version by involving 10 SSR markers on 15 rice genotypes. The results greatly agreed with those of the clustering pattern and the dendrogram although minor deviations were noticed.

The plot showed that most of the genotypes that were in cluster I were grouped closer together in the PCA and those in Cluster II were at the far right though away from each other. However, it was noted also that Acc 9293 which belonged to Cluster III had grouped close to some of the genotypes for Cluster I, whereas Mw 1685 was far below from the rest implying that it is not very related to them.

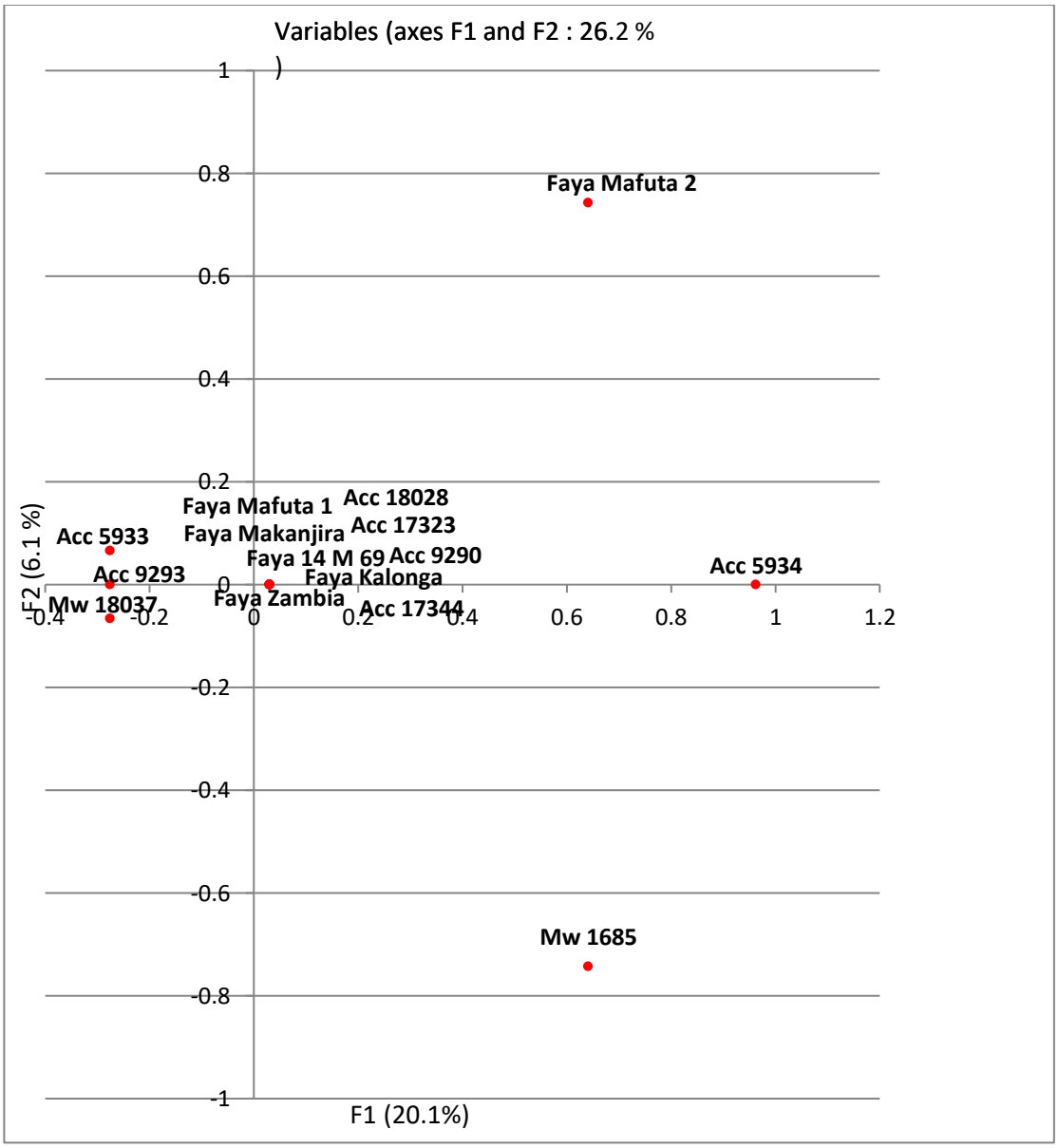

Figure 22: First and second principal components depicting relationships of 15 Faya rice genotypes based on 10 SSR markers.

CHAPTER FIVE

5.0 DISCUSSION

5.1 Morphological Traits Characterization

Morphological traits characterization is very fundamental for scientists in general and rice breeders in particular when studying crop diversities in order to identify superior traits that can be used for further crop improvement. In this study, fifteen (15) selected Faya rice genotypes were characterized based on twelve (12) quantitative growth parameter traits, five (5) root traits, seven (7) grain quality traits, and twelve (12) qualitative traits captured during different respective growth stages of particular parameters. Each character has been discussed below in three categories of screen house (PVC), field and laboratory (SSR) work.

5.1.1 Screen house (PVC) conditions

5.1.1.1Yield and growth parameter traits

Grain yield is the main target of any breeding programme and in the present study it differed significantly among the genotypes. Abade *et al.*, (2016) also reported similar findings for their study of characterization and this depicts a true character of land races.

Generally, regarding the obtained data for plant height, the genotypes have been grouped into semi dwarf (< 110 cm) and tall (> 130 cm) as guided by International Rice Research Institute (IRRI) (1996) descriptor for standard evaluation. In this case, two genotypes namely; Faya 14 M 69 and Faya kalonga were grouped as semi dwarf while the rest of the genotypes were categorized as tall. This implies that breeders can

use one of these traits in order to either achieve lodging resistance from semi dwarf or desirable yielding ability characteristics of tall varieties as also reported by (Joachim, 2015).

Basically, panicle number per plant is an important parameter in contributing towards yield and in this study eleven (11) genotypes were described as having a medium number of panicles (14 - < 20) and the other four (4) as possessing a high number of panicles per plant (> 20).

Generally, the data illustrated that there were defective tillers in Accession 9290 because it exhibited less number of panicles / plant than the reproductive tillers and this is speculated to be a genetic factor. The results also indicate that most of the genotypes studied have a high tillering ability. Furthermore, the number of tillers per plant also differed greatly among the studied genotypes. Three categories existed for this trait as one (1) genotype attained a very high number of tillers / plant (more than 25 tillers per plant). Good number of tillers (20 - < 25 tillers / plant) was noticed in seven (7) genotypes whereas medium number of tillers was attained in the remaining genotypes. Allah *et al.,* (2010), reported that an increased number of tillers per plant would increase mutual shading within the plant which retards root growth more than shoots. For these reasons a highly tillered plant tends to have a short root system. In this study, similar findings were exhibited as high tillering genotypes possessed relatively short roots. Sajid *et al.,* (2015), reported that tiller number is another yield attributing trait. The trait of vigorous tillering can be desirable in certain environments, such as in direct seeding where weeds seriously reduce yield of rice and greater vigour can help in suppression of weeds (Len *et al.,* 2000).

Panicle length is one of the most fundamental characters assessed by rice breeders in yield related experiments, due to the fact that longer panicles with more filled grains will likely lead to higher yield. The four (4) genotypes belong to a category of medium panicle length (21 – 25 cm) whereas the rest of the studied genotypes had a long type of panicle (26 – 30 cm). The results of this kind on panicle length are a true indicator of the ability of the genotypes to give high yield. The present study is in agreement with the findings reported by Pachauri *et al.,* (2017), in which most of the accessions belonged to a panicle range of 26 – 30 cm in length. However, in the same report of Pachauri *et al.,* (2017), it was emphasized that panicle length is not the only factor contributing towards high grain yield. Similar results were also realized by Joachim (2015) during the characterization study except that short panicle lengths were reported in that study.

From the observations, it was noted that Acc 18037, had the mean longest leaf whereas the shortest was for Faya 14 M 69.Very highly significant differences were observed for leaf blade width among the studied genotypes. Accession 17344 depicted the mean maximum width and the minimum value was in Accession 9290.Similar results were reported by Nachimuthu (2012) and Seetharam *et al.,* (2009) during the characterization work of a mixture of land races.

Flag leaf area, which is a product of flag leaf length and flag leaf width is a very important trait in rice because it is responsible for transfer of assimilates to the developing grains. In the present study, flag leaf length exhibited great variation among the studied genotypes. Faya 14 M 69 attained the average maximum value while Faya Zambia gave the mean minimum value which was closely at par with Faya

Mafuta 1. In addition**;** flag leaf width exhibited very highly significant differences among the studied genotypes.

5.1.1.2 Root phenotypic trait studies

Fresh Root Mass (g) differed significantly among the studied genotypes. In a related study, Liu *et al.,* (2004), carried out an experiment under screen house conditions in order to compare *wild species of Oryza* for root and other drought – adaptive traits. The findings were that *wild species* of rice possess superior root growth under drought stress conditions; evident by an increase in total root mass or a proportion of root mass in deeper soil layers. In the present study, fresh root mass had shown to increase significantly for some genotypes within the group where others had minimal values. Genotypes with increased root number had also relatively high yields compared to those with less. Similar findings were reported by Sandhu *et al.,* (2016), and it was also noted that the rice plants have better nutrient uptake if they possess high number of roots compared to those with less. In the present study, genotypes with high number of roots have the potential to produce higher yield than their counterparts. Gowdal *et al.,* (2011), also reported that high number of roots have a positive effect on the rice plants especially during flowering for enhanced grain filling.

The maximum root depth that roots reach is genetically determined and varies substantially between cultivars grown in a similar condition although environmental effects cannot be fully excluded (Gowdal *et. al.,* 2011). In this study, genotypes performed differently and Accession 9293 exhibited the maximum root length. The majority of the genotypes can be described as deep rooting. Some of the genotypes showed shallow rooting behavior with Faya Kalonga leading the group. These results suggest that the deep rooting genotypes might be at an advantage in terms of reaching

the water table and nutrient uptake especially during dry spell (drought) as are constitutive traits (Kamoshita *et al.,* 2008), and leached nutrient conditions respectively. Similar results on deep rooting were reported by Gowdal *et al.,* (2011) using different rice genotypes. Len *et al*., (2000) and Allah (2004) also reported that genotypes with a greater root length increment had superior drought recovery and maintained transpiration during the following severe drought period.

Among the studied genotypes, fresh shoot mass (g) was variable with the average being 77.1g. The range between the lightest shoot to the heaviest was 29.1 g to 114.6 g respectively. Len *et al.,* (2000), reported that genotypes with superior traits have the ability to maintain turgor or leaf water potential especially during stress. Basing on this trait, Accession 18028 (113.4 g) and Accession 17344 (114.6 g) would form the stronger parents for hybridization to improve root mass trait.

In terms of root volume, the available variation among the studied genotypes implies that a bigger area is occupied by the genotypes with large root volume. These findings mean that genotypes such as Accession 9290, Accession 18028, Accession 17344 and Accession 9293 have the potential to absorb larger quantities of nutrients owing to their big volumes than those with small root volumes like Faya Kalonga. This is achieved by the fact that roots form mutualistic associations with key soil micro – organisms such as bacteria and micorrhizal fungi to aid them in their quest for nutrients. This means increased root volume would increase the diameter for oxygen absorption which is also used by such organisms. Henry *et al.*,(2012), reported in a similar way, that unlike in other cereal crops, rice roots in well watered conditions feature a sclerenchyma layer that is much more suberized than the exodermis and it

consists of tightly packed cells of smaller diameter than other cells in the outer part of the roots. Collectively, the cell layers of the outer part of roots in rice form a barrier which inhibit radial oxygen loss (eventually used by micro – organisms) while at the same time allowing water uptake and are capable of retaining root water under drought. Roots with a large thickness, in this case greater volume have been reported to have the ability of penetrating a soil hardpan (Comas *et al.,* 2013). According to Jeong *et al.,* (2013), increased root diameter developed by over – expression of OsNAC5, leads to increased yield by a 9 % - 26 % magnitude.

Dry root mass (g) differences were non - significant, with Accession 9290 exhibiting maximum size and Faya Kalonga exhibiting the minimum value. Ballan (2013), reported the opposite results on this trait when studying 40 rice genotypes in the net house condition. Dry shoot mass just like fresh shoot mass, was variable among the genotypes as weight declined in proportional to the fresh shoot mass values after oven drying.

Root / shoot ratio is a measure of the allocation of resources between different plant components and did not differ significantly among the genotypes of the present study. Gowdal *et al.,* (2011) emphasized the need of a deep root / shoot ratio in rice as a vital trait for absorption of soil moisture and nutrient in deeper soil layers. Kondo et al., (2003) reported genetic variation in root / shoot ratio among the *Oryza species* and within *subspecies* of Japonica and Indica rice tested under field conditions. This is however not in agreement with the findings of the present study within the group of Faya rice land races. It is speculated in this work that the growth environments might have different effects on the rice genotypes for this trait.

5.1.1.3 Grain Quality Traits

The genotypes performed non – significantly different on grain length despite that, individual values varied among the genotypes. Generally, all the genotypes were described as long – grained (> 7.5 mm) according to International Rice Research Institute (IRRI) (2013). However, one genotype (Mw 1685) had been grouped as medium (2.1 – 3.0) and the rest of the genotypes were categorized as slender (over 3.0) in terms of grain shape. Abade *et al.,* (2016) in the characterization work of 20 different rice strains as cultivars found different results which ranged from short, long to extra long grains. Joachim (2015), in the characterization work of rice genotypes from East and Southern Africa (ESA) region also reported different results in which grain length ranged from short, medium, long to extra long and the grain shape from bold, medium to slender. The results in the present study therefore imply that, for this trait, the rice genotypes may be closely related within the group of Faya strains. The implication of this is that any of these Faya strains may be used to improve the grain length in a breeding program.

5.1.1.4 Correlations of traits

There was positive association between fresh root mass with other characters. Ballan (2013) reported a similar positive trend of results on all the traits except for spikelet fertility and plant height which were negatively correlated. However, fresh root mass had negative association with other traits. In addition, grain length exhibited positive association with a majority of traits. Positive correlation was exhibited for root number with all other characters. Toorchi *et al.,* (2006) reported a similar trend for maximum root length and grain yield with the trait in question. Furthermore, the maximum root

length exhibited positive and significant correlation with such traits as fresh shoot mass, root thickness and number of days to maturity. These findings are in agreement with the results reported by Ballan (2013), where all but spikelet fertility correlated positively with the trait in question. On the other hand, the present study showed negative association for the same trait with 1000 grain weight, number of spikelets per panicle and grain yield.

5.1.2 Field Condition

5.1.2.1 Grain yield and growth parameters

Grain yield is the main focus of many breeding programmes and the characterization work of this study in particular. The rest of the genotypes have shown to be lower yielding basing on the analyzed data despite that they also possess other vital traits for crop improvement. This data, therefore, depict a great variation existing among the studied genotypes despite being from the same Faya rice strain. Based on the 1000 - grain weight attained for each of the studied genotype, it was found that they belong to two categories of low (15-20g) and medium (21-25g). In that regard seven genotypes were classified as having the low 1000 grain weight whereas the remaining eight genotypes belong to the category of medium 1000 grain weight. International Rice Research Institute (IRRI) (2009) reported that longer grains are lighter in weight than medium or bold grains but the contrary was observed in this study for field conditions. In the present study again, the same genotypes performed differently on this trait as they agreed with the above report of IRRI (2009) when grown in screen house condition and this implies that there was genotype x environmental interaction.

Tiller number per plant ranged from few (7.33 tillers) to moderate (16.03 tillers) and very few genotypes showed defective tillers at panicle formation.

Generally the very highly significant differences mean that the genotypes have different filling ratio / fertility percentage per panicle such that those with larger values have the potential of giving less unfilled grains.

The number of spikelets per panicle showed positive and significant association with plant height, panicle length, leaf length and number of days to maturity. On the other hand, negative and significant correlation was attained for this trait with grain yield, number of panicles per plant, number of tillers and 1000 grain weight. This implies that in the current study, number of spikelets per panicle had a negative contribution towards yield as its component

Generally all the studied genotypes can be described as tall in terms of plant height except Faya Kalonga (93.2 cm) and this is in agreement with International Rice Research Institute (IRRI) 1996 which describes that any genotypes >110 cm is regarded as tall.

5.1.2.2 Grain Quality Traits

Pachauri *et al.,* (2017), reported that grain length is a fundamental quality trait. In those findings, 80 % of the accessions were categorized as short to medium group while few of the accessions were observed as long grained. In the present study, grain length exhibited non – significant differences among the studied genotypes. However, Accession 9290 possessed the maximum length and the minimum was for Mw 1685.The results means that all the genotypes in the present study have extra - long grains (> 7.5) (IRRI, 2013). Similar findings were reported by Abade *et al.,* (2016). Mzengeza *et al.,* (2010), reported the genetic analysis of three characteristics of grain size, namely; grain length, grain shape and 1000 grain weight. In those findings, Faya

Mpata had the longest and most slender grains (8.0 mm long and 3.0 respectively), and was classified as extra – long. In the present study, similar findings have been reported and this illustrates the superiority of Faya rice genotypes for grain length trait.

Brown rice shape showed non - significant differences among the studied genotypes. However, it means all the genotypes in the present study have a slender type of grain shape (> 3 mm). According to Joachim (2015), a mixture of grain shapes were observed during the characterization work of various land races from East and Southern Africa (ESA) region. The present findings for this trait therefore indicate that genotypes within the group are more closely related such that their computed grain shape belongs to the same category than a mixture of strains/ land races.

Grain milling recovery (%) exhibited non - significant difference among the studied genotypes. However, it was noted that Faya Makanjira and Accession 17344 exhibited the maximum milling recovery percentage. The minimum milling recovery was captured in Accession 9290 and Accession 9293. Similar findings were reported by Joachim (2015), however, a lower milling recovery percentage ranging from 61.28 to 71.73 % was reported in that study and that represent the closeness of relationship of the genotypes for this trait in the present study. In terms of scent or aroma, all the genotypes in this study were found to be scented (aromatic) after cooking. This is a true characteristic of Faya rice genotypes as previous workers on Faya 14 M 69 reported its aromatic status as one distinguishing character, (Abade *et al*., 2016).

5.1.2.3 Correlations

Grain yield is the end product of the interaction of different interrelated traits. A thorough understanding of the interaction of characters among themselves had been of great use in plant breeding. In the present study, grain yield showed positive association with three traits and negatively with the rest of the traits. These results mean that grain yield in this study depended more on those traits with positive contributions than those with negative. Ballan (2013), reported similar results except that only plant height correlated negatively. These results imply that selection of the genotypes for improvement of grain yield should be based on those traits that positively and significantly contribute towards the trait in question

Toorchi *et al.,* (2006), reported positive and significant association of plant height with spikelet fertility and grain yield. In the present study, similar findings have been exhibited as plant height positively correlated with panicle length, leaf length, number of spikelets per panicle, 1000 grain weight and spikelet fertility. However, negative relationships were observed for the trait in mention with number of days to maturity, number of tillers, number of panicles per plant and grain yield. Positive correlations were exhibited for the number of panicles per plant with grain yield, number of tillers per plant, and 1000 grain weight. This was in great agreement with the findings reported by Toorchi *et al.,* (2006) and Ballan (2013).Positive results of similar nature were also reported by Abade *et al.,* (2016). Babu *et al.,* (2012), also reported that yield attributing traits revealed significantly positive association of grain yield per plant with number of productive tillers per plant. The report also emphasized the need to consider selection for these traits in order to improve yield.

Positive correlation was exhibited for panicle length with some traits. The present results are in agreement with the results reported by Kalyan *et al.,* (2017) for plant height and number of spikelets per panicle. On the contrary, this trait was negatively associated with grain yield, number of panicles per plant, number of tillers and 1000 grain weight. Leaf length exhibited positive correlation with such traits as plant height, panicle length, number of days to maturity, number of spikelets per plant and 1000 grain weight. However, negative association was noticed for the trait in question with grain yield, number of panicles per plant, number of tillers and spikelet fertility. Number of days to maturity (DM) correlated positively with number of tillers per plant. This implies that the longer the crop stays in the field, the more the chances of producing more tillers and hence high yield. Again, panicle length, leaf length, number of spikelets per panicle and spikelet fertility correlated positively with number of days to maturity, implying that the genetic expression of these traits is also dependent on the length of time the crop stays in the field. Abade *et al.,* (2016) reported similar findings. On the same trait, negative correlation was attained with grain yield, plant height, number of panicles per plant and 1000 grain weight. These results imply that traits such as plant height did not influence grain yield in a positive trend as such yield was influenced by other traits.

The number of spikelets per panicle showed positive association with plant height, panicle length, leaf length, number of days to maturity and spikelet fertility. On the other hand, negative correlation was attained for this trait with grain yield, number of panicles per plant, number of tillers and 1000 grain weight. Similar results were reported by Igbal *et al.,* (2018), for number of effective tillers plant-1. Positive correlation was exhibited for 1000 grain weight with grain yield, plant height, number

of panicles per plant, number of tillers per plant and leaf length. Similar results were reported by Kalyan *et al.,* (2017) for grain yield. On the contrary, panicle length, number of days to maturity, number of spikelets per panicle and spikelet fertility correlated negatively with the trait in question. This implies that increased number of panicles, tillers and leaf length may cause intra – completion for assimilates which can retard the filling ability of the crop. Similar results were reported by Igbal *et al.,* (2018), for number of days to maturity.

5.1.2.4 Agglomerative Hierarchical Clustering (AHC)

The agglomerative hierarchical clustering was done using XLSTAT on the Euclidean distance matrix following the Ward's linkage procedure. The dendrogram was constructed using twenty five (25) quantitative morphological, grain quality, and root architectural traits for the fifteen (15) Faya rice genotypes. There were four (4) clusters obtained from the analysis, which revealed that one genotype belonged to cluster 1, two genotypes belonged to cluster 2, seven genotypes were in cluster 3 and cluster 4 consisted of five genotypes. Further observations revealed that genotypes within the Faya group that bear the same name, for example, Faya Mafuta 1 and Faya Mafuta 2 were clustered together (cluster 3). Besides, Faya Zambia which is said to have originated from Zambia was also in the same cluster with some Accessions (cluster 4). Cluster 1 was composed of one accession only, and was separated from the rest of the genotype during the clustering pattern. These results indicated that the rice genotypes are diverse regardless sharing the same name or not as evidenced by a mixture of clustering within the Faya strains. These results are in agreement with reports by previous workers. According to Joachim (2015), selection, genetic drift and continuous exchange of genetic materials may cause diversity other than geographical reasons alone and as such genetic diversity should be the basis for selecting parents.

In addition, the clustering analysis gave results on centroid value of each character. It was therefore noted that the maximum cluster mean values for grain length, grain width, 1000 grain weight and spikelet fertility were obtained in cluster 1. In cluster 2, the maximum mean values were shown in such traits as grain yield, panicle length and flag leaf length. Besides that, cluster 3 had maximum mean values in number of panicles per plant, number of tillers per plant, days to maturity, grain shape and days to 50% flowering. Cluster 4 consisted of a majority of the traits namely; plant height, leaf length, leaf width, flag leaf width, number of spikelets per panicle, fresh root mass, root number, maximum root length, fresh shoot mass, root volume, dry root mass, dry shoot mass and root / shoot ratio.

These results imply that a genotype belonging to cluster 1 can be used as a parent for improving grain quality traits, particularly grain size while those belonging to cluster 2 can be used for improving grain yield. Improvement of root architecture such as maximum root length for deeper – soil – layer moisture absorption will require selecting parents from cluster 4. Parents for improving growth duration and the tillering ability could be selected from cluster three (3) as evidenced by the high mean values for related traits. Breeders aiming at improving yield and its components can select parents from cluster 4 as evidenced by the high mean values of related traits for the cluster in question. Since breeding depends on diversity, all the genotypes evaluated in the present study have proven to possess one or more traits that can be used in any breeding program as depicted at both morphological and molecular levels.

5.1.2.5 The Principal Component Analysis (PCA).

The results of Principal Component Analysis (PCA) are very fundamental for elaborating diversity of the rice genotypes. Ashfaq *et al.,* (2012) reported that the four (4) principal components in their study were considered to be more important because they had more than one Eigen value that showed total variation of more than 67% for the rice genotypes under study and that that was enough for determination of genetic diversity. According to Pachauri *et al.,* (2017), the PCA with Eigen values >1 and which explained at least 5% of the variability in the data were taken into account.

In the same report, it was also indicated that the PCA data with about 72.48% cumulative variability among the traits studied should be selected for further explanation. It is in the latter arguments (cumulative variability percentage) that made the present study to consider 5 PCA levels for further elaborations. The Principal Component Analysis (PCA) for the present study gave results for factor scores, Eigen value, variability percentage and cumulative percentages. The first principal component had a variance cumulative magnitude of 93.50 % whereas the five components comprised a variance total value of 99.59 %. The present study therefore agrees with the previous findings to a great extent as the variations are above those reported. Hossain *et al.,* (2007) also carried a report in which it was emphasized that the higher the coefficient, the more effective they will be in discriminating between the genotypes regardless of positive or negative signs but hinted that positive scores contribute greatly to the genetic diversity. Root number, fresh root mass, root volume, number of spikelets per panicle, days to maturity, days to 50 % flowering and spikelet fertility traits that were associated with the maximum first principal component variance cumulative percentage would contribute greatly if selected for hybridization .

Furthermore, characters associated with the second principal component variance cumulative percentage were number of spikelets per panicle, root number, days to maturity and spikelet fertility. In addition, the third principal component which was related to number of spikelet per panicle and fresh root mass would also contribute to any breeding work. The fourth principal component had only plant height trait that would highly contribute positively towards the available variance cumulative value and is the lowest principal component contributor of the group. The fifth principal component was correlated with such a trait as dry root mass that would also be used. The levels of discrimination for the principal axes exhibited by Eigen values ranged from 14.0 to 0.068 from the first to the last principal components respectively. In this regard, the Eigen discrimination values were highest in the first principal component and lowest in the fifth component, and that was true also for the variance percentage depicting that the first component is the best in this study for breeding contributing traits. The majority of genotypes belonging to the first component would therefore be selected during breeding for the target traits mentioned. The least genetic similarity index magnitude detected for and among the genotypes implies that some of the genotypes studied have closely similar genetic constitution while others are distantly similar.

5.1.3 Microsatellite (SSR) markers studies.

The Simple Sequence Repeats (SSRs), also known as Short Tandem Repeats (STRs), microsatellites, or Sequence- Tagged Microsatellite Sites (STMS), Jameel *et al* (2013), are PCR-based markers. They are randomly tandem repeats of short nucleotide motifs (2–6 Bp / nucleotides long). Di-, tri- and tetra- nucleotide repeats, for instance (GT) n, (AAT) n and (GATA) n, are plentiful and widely distributed throughout the animals'

and plants' genomes. The SSR markers have been extensively used in constructing genetic linkage maps, marker-assisted selection, germplasm analysis (Lapitan, 2007) and QTL mapping in plants. Molecular markers have been proven to be powerful tools in the assessment of genetic variation within and among the species. In the present study, a total of 63 alleles were obtained on polymorphic SSR with an average of 6.3 alleles per primer that ranged from 2 to 8. The results obtained were comparable to the range of 2 to 22 alleles per locus reported by Joachim (2015). The Polymorphism Information Content (PIC) value is an evidence of allele diversity and frequency among the varieties (Afiukwa, 2016). PIC value of each marker can be evaluated on the basis of its alleles, Shashriar *et al.,* (2014). In the present study, PIC ranged from 0.46 to 0.98 with an average value of 0.75. The highest PIC value (0.98) was obtained in RM 215 and was considered as the best marker of the entire group. Furthermore, nine (9) primers depicted PIC values of greater than 0.5. This indicates that they are all greatly informative as previous workers recommended that a marker with PIC value of 0.5 and above is fundamental in distinguishing the polymorphism (Pervaiz *et al*., 2009).

In addition, the studied genotypes illustrated three clusters on the dendrogram clustering pattern. The dendrogram obtained using the molecular data of 10 SSR loci depicted three clusters, such as; cluster I, cluster II and cluster III. Most of the genotypes belonged to cluster I and comprised the 12 genotypes. Cluster III and II had one (1) and two (2) genotype (s) respectively. The uniqueness of Accession 9293 in terms of maximum root length on the phenotypic level has also been felt on the molecular level as it stands on its own cluster from the rest and this may bring calls for a possible introgression of QTLs for this trait. In a report by Joachim (2015), it was

noted that varieties that bared the same name were different genetic materials. The same report also noted that varieties from the same country were observed to be phenotypically similar, whereas the genetic results confirmed that they were not similar. The present study also agrees to the same trend for Faya Mafuta 1 and Faya Mafuta 2 which bear the same name and are phenotypically similar, were found to be different as evidenced by the genetic clustering profile. This might also confirm the phenomena of materials due to genetic drift reported by other workers like Jameel *et al.*, (2013). This necessitates the need for complementing morphological markers with molecular markers, as the former is usually affected by the environment.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

The main objective of this work was to characterize grain yield, grain quality and root architectural traits of selected Faya rice genotypes using molecular and morphological markers in order to identify superior genotypes that can be used in subsequent breeding activities for hybridization. The findings of the present study are illustrated in summary form as follows;

1. There is rich genetic divergence for different quantitative and qualitative traits among selected fifteen (15) Faya rice genotypes as evidenced by great variation among traits.
2. The studied root architectural traits exhibited tremendous variation among the studied genotypes, despite that other traits such as root volume and root / shoot ratio showed no variation.
3. All the grain quality traits of the genotype under study showed no variation except 1000 grain weight, spikelet fertility, translucency, chalkiness, gelatinization temperature and gel consistency which had great variation.
4. Since grain yield is the main target of any breeding programme, the present study revealed that this trait correlated positively with some traits and negatively with others. The results imply that the variation exhibited on the traits under evaluation was because of genetic makeup of the studied rice genotypes and not due to the environmental effect.
5. The agglomerative hierarchical clustering using morphological markers grouped the fifteen (15) Faya rice genotypes into four (4) clusters and five

Principal Components while the same genotypes were categorized into three clusters when ten (10) Simple Sequence Repeat (SSR) markers were used for clustering.

6. The Principal Component Analysis (PCA) results revealed that root number, fresh root mass, root volume, number of spikelets per panicle, days to maturity, days to 50 % flowering and spikelet fertility traits that were associated with the maximum first principal component variance cumulative percentage would contribute greatly if selected for hybridization owing to their variation levels.
7. All the ten (10) SSR (Microsatellite) markers that were used in studying the fifteen (15) Faya rice genotypes turned out to be polymorphic for the target traits.
8. The highest Polymerase Information Content (PIC) value was recorded for primer RM215 and all the markers used in this study were neutral, convenient and co-dominant in nature.
9. The screening work using both morphological and molecular (SSR) markers has revealed that the 15 Faya rice genotypes are diverse and would produce significant transgressive segregants if used in subsequent hybridization breeding programmes.

6.2 Recommendations

1. The genotypes such as Faya 14 M 69, Mw 1685, Faya Kalonga, Accession 9293 and Accession 5934 would be utilized for the improvement and development of new rice varieties in a hybridization program for improving grain size and aroma.
2. Breeding programs aimed at improving the maximum root length in order to allow absorption of water from deeper soil layers by the plant(s)and grain quality trait (especially grain shape) could use Acc 9293 and Mw 1685, respectively, as the best parental donors.
3. The genotypes Accession 9293 and Mw 1685 should be considered for further testing for release in Malawi so that they can be grown by farmers due to their desirable traits.
4. All the SSR markers used in this study have proven to be a success in studying the diversity of rice land races as evidenced in the current work where all markers turned out to be polymorphic hence could be used in any rice screening work.
5. Future studies should consider screening the rice genotypes using both molecular and morphological markers for high yielding and drought tolerance for both lowland and upland cultivated rice species as drought is a growing challenge due to climate change phenomena.

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