AGRO-MORPHOLOGICAL CHARACTERIZATION AND GENETIC DIVERSITY OF RICE LANDRACES IN SAVANNA ZONES OF NIGERIA

BY

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DECLARATION

I declare that the work in this dissertation entitled **"Agro-Morphological Characterization and Genetic Diversity of Rice Landraces in Savanna Zones of Nigeria"** has been carried out by me in the Department of Biology, Ahmadu Bello University, Zaria. The information derived from the literature has been duly acknowledged in the text and a list of references provided. No part of this project thesis was previously presented for another degree or diploma at this or any other institution.

Hadiza Usman MUHAMMAD	Signature	Date

CERTIFICATION

This dissertation entitled AGRO-MORPHOLOGICAL CHARACTERIZATION AND GENETIC DIVERSITY OF RICE LANDRACES IN SAVANNA ZONES OF NIGERIA by Hadiza Usman MUHAMMAD meets the regulations governing the award of the degree of Master of Science (M.Sc.) in Biology of the Ahmadu Bello University, and is approved for its contribution to knowledge and literary presentation.

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DEDICATION

This work is dedicated to my late father Muhammad Bello, my mother Maimuna Ibrahim and my children; Hauwa'u, Rahmah and Muhammad.

ABSTRACT

This research was conducted to evaluate the agro-morphological characteristics of rice landraces and their genetic diversity in savanna zones Nigeria. A total of seventy rice landraces from eighteen northern states were utilized for the study. The landraces were sown in polythene bags packed with loamy soil (8kg). A complete randomised design layout with three replicates was adopted. Twenty seven agro-morphological traits (15 qualitative and 12 quantitative agronomic traits) were evaluated based on the internationally accepted standard evaluation system for rice. The genetic diversity of the landraces was also determined based on 21 SSR primers using standard protocol. Results obtained revealed a highly significant variability ($p < 0.01$) among the landraces for all the qualitative and quantitative traits. The cluster analysis for the qualitative traits grouped the landraces into five cluster groups at 60% similarity coefficient. Variability studies indicated that the estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the agronomic traits evaluated. The PCV and GCV are respectively highlighted in grain yield per plant (80.37 and 77.83g), number of filled grains per panicle (78.78 and 76.62), number of panicles per plant (27.18 and 26.51), number of total grains per panicle (24.98 and 24.05) and number of leaves per plant (22.74 and 20.46). The agronomic traits measured showed high broad sense heritability (74.5% - 99.3%) with the exception of days to germination (58.9%). The high yielding landraces were WACOT (9600kg/ha), Yar china-KB (858.18kg/ha), Jamila PLT (589.09kg/ha) and Yar Zaiti (560kg/ha). Significant ($p < 0.01$) positive correlation for number of filled grain per panicle ($r = 0.94$) and number of total grain per panicle ($r = 0.53$) with grain yield was obtained. At 91 % similarity

coefficient, the seventy rice landraces were grouped into three cluster groups based on the agronomic traits evaluated. Landraces from cluster group one had highest mean values for number of leaves per panicle (20.33), number of panicles per plant (20.29), number of filled grains per panicle (63.56), number of total grains per panicle (86.45) and grain yield per plant (8.26g). Landraces in cluster group two had highest mean value for hundred seed weight (2.61g) while landraces in cluster group three showed highest mean values for plant height (71.96cm) and panicle length (22.82cm). Genetic diversity of the rice landraces based on 21 SSR primers detected alleles that ranged from 3 to 6 with an average of 4 alleles per primer. Polymorphic information content ranged from 0.34 to 0.79 with an average of 0.45. The neighbor joining tree based on SSR markers grouped the landraces into 4 cluster groups at 95 % similarity coefficient. In conclusion, although there exist morphological diversity in the rice landraces present in Nigeria savanna zones, however, these landraces are genetically closely associated. This could have resulted from the admixture of landraces over time. Agro morphological diversity obtained could have resulted due to environmental factors. The information from this study could be very useful in identification and selection of suitable parents for use in breeding programmes.

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ABBREVIATIONS

AC	Auricle Colour
AFLP	Amplified Fragment Length Polymorphism
ANOVA	Analysis of Variance
APC	Apiculus Colour
AW	Awning
BC	Before Christ
BLS	Basal Leaf Sheath Colour
CRD	Complete Randomized Design
CBN	Central Bank of Nigeria
CE	Chalkiness of Endosperm
cm	Centimeter
DFF	Days to 50% Flowering
DFID	Department for International Development
DG	Days to Germination
DNA	De-oxyribo Nucleotide Acid
F1s	First Filial Generation
FAO	Food and Agricultural Organization
FAOSTAT	Food and Agricultural Organization Statistics
GCV	Genotypic Coefficient of Variation
GYP	Grain Yield per Plant
ha	Hectares
H_B	Broad Sense Heritability
HSW	Hundred Seed Weight
IBPGR	International Board for Plant Genetic Resources
IC	Internode Colour

IITA	International Institute of Tropical Agriculture
IRRI	International Rice Research Institute
JC	Junctura Colour
Kb	Kilo Bytes
LBC	Leaf Blade Colour
LC	Ligule Colour
LMC	Leaf Margin Colour
LSD	Least Significant Difference
LTC	Leaf Tip Colour
MAF	Major Allele Frequency
Mb	Mega Byte
Mins	Minutes
NA	Number of Alleles
NC	Node Colour
NCRI	National Cereals Research
NERICA	New Rice for Africa
NFG	Number of Filled Grains per Panicle
N-J	Neighbor Joining
NLP	Number of Leaves per Plant
NPP	Number of Panicles per Plant
NTG	Number of Total Grains
NTP	Number of Tillers per Plant
NUG	Number of Unfilled Grains per Panicle
PCR	Polymerase Chain Reaction
PCV	Phenotypic Coefficient of Variation
PHT	Plant Height

PIC	Polymorphic Information Content
PNL	Panicle Length
QTLS	Quantitative Trait Loci
RAPD	Random Amplification of Polymorphic DNA
RFPLS	Restriction Fragment Length Polymorphism
rpm	Revolution per Minute
SC	Seed Colour
SGC	Sterile Glume Colour
SGC	Stigma Colour
SNP	Single Nucleotide Polymorphim
SSR	Simple Sequence Repeats
STMS	Sequence Tagged Microsatellite Sites
Taq	Thermophilus aquaticus
TBE	Tris-borate EDTA Buffer
TE	Tris EDTA Buffer
µl	Micro Litre
UPGMA	Unweighted Pair Group Method of Average Linkage
V	Version
VNTRS	Variable Number of Tandem Repeats

CHAPTER ONE

1.0 INTRODUCTION

Rice is the staple food for more than 3.5 billion people worldwide, which represents around half of the world's population (Xu *et al.,* 2016). Out of the total global arable land, rice is cultivated on approximately 11% annually (Bashir *et al.,* 2010; Manik, 2013). On a global basis, it is planted on an area of 159 million hectares with a production of 685 million tonnes. China is leading in the production of rice with annual production of 193 million tonnes, followed by India (148 million tonnes), Indonesia (60 million tonnes), Bangladesh (47 million tonnes), Vietnam (48 million tonnes) and Thailand (30 million tonnes) (Muhammad *et al.,* 2015). Nigeria is ranked as the 17th major producer in the world and it accounts for about 20% of sub-Saharan Africa's rice imports (Omotola and Ikechukwu, 2006).

Rice is recognized as one of the most important food crops, accounting for more than half of human caloric intake globally. It is generally valued for its high nutritional benefits apart from being rich in calories, it is high in fibre, vitamins, and minerals and low in cholesterol and sodium, suggesting it is a healthy source of energy (Afiukwa *et al.,* 2016). By-products of rice have many uses: Tatamin mat, for example, is made from rice straw, beer or sake brewed from rice, rice bran is used to feed farm animals and rice hull for energy generation; making synthetic fibres and fertilizers (FAO, 2000). In Nigeria, most people depend on rice as their staple food, and rice dominates agricultural production. Nigeria was ranked 12th in the world's list of rice-consuming countries, third in Africa and first in West Africa (FAO, 2011) and rice is a major contributor to internal and sub-regional trade in Nigeria (Oko *et al.,* 2012).

The rice genus, *Oryza* consists of two cultivated species; and more than 20 wild and weedy species. The cultivated species are *Oryza sativa,* which is grown worldwide and indigenous to Asia; and *Oryza glaberrima*, planted on a limited scale in West Africa (Muhammad *et al.,* 2015). The two species can be distinguished in the field especially by differences in ligule shape and panicle branching. *Oryza sativa* have long (40-45mm), pointed and thin ligules and many panicle branches, while *Oryza glaberrima* has short (6mm), oblong and thick ligules and lack secondary branching on the primary branches of the panicle (Sarla and Swamy, 2005). *Oryza sativa* has acquired a broad range of adaptability and tolerance with agronomic traits but susceptible to most African stresses (Semon *et al*., 2005).

Nigerian farmers grow improved cultivars for their high yields, some farmers still grow local landraces because of their adaptation to the local environment and preferred traits. Despite their lower yields, these landraces can serve as useful resources for breeding programs (Vilayheuang *et al.,* 2016). Characterization is a critical step to be carried out to identify accessions and ascertain genetic relationships among genotypes. Characterization and quantification of genetic diversity have been a major goal in evolutionary biology (Kumar, 2016). Genetic diversity reflects the amount of genetic variability amongst individuals or populations within a variety or species. Genetic variability measures the tendency of individuals to vary from one another based on morphometrics or molecular markers (Razak *et al.,* 2016). Knowledge of the genetic diversity and population structure of germplasm collections is an important foundation for crop improvement. Genetic variability in any breeding material is important and a pre-requisite as it provides

not only a basis for selection but also some valuable information regarding the selection of diverse parents for use in a hybridization program (Tandekar and Koshta, 2014).

The pace and magnitude of genetic improvement are generally dependent on the amount of genetic diversity present in a population. Diversity in germplasm is estimated using different methods such as phenotypic, biochemical and DNA polymorphisms (Yadav *et al.,* 2013). Assessment based on plant phenotypes may not be a reliable measure of genetic difference because of the influence of environmental factors. However, they are still important for genetic diversity studies. The combination of morphological and molecular markers provide comprehensive tools for genetic dissection and yield evaluation which is required for selection of genotypes for breeding programs and for genotype documentation (Ahmad *et al*., 2015).

Genetic characterization of crop plants has gained momentum with the advent of polymerase chain reaction (PCR) based molecular markers. Several Molecular markers have been used to characterize crop resources in rice (Kumar *et al.,* 2016). Most researchers have used simple sequence repeat (SSR) markers to examine the genetic diversity, population structure and genetic variation within rice landraces (Das *et al*., 2013). SSR markers have many advantages over other marker systems; it has higher reproducibility which is most important in genetic analysis, co-dominant in nature, bands produced from the same set of primers are intuitively orthologous, abundant in the genome of all species, and well distributed in their genome (Wang *et al*., 1994). SSR markers have been widely applied in rice genetic studies as they are able to detect high levels of allelic diversity which makes them ideal for genetic diversity and intensive genetic mapping studies diversity (McCouch *et al.*,1997).

1.1 Statement of the Research Problem

Nigeria with an estimated population of more than 199,562,930 million persons and population growth rate of 2.60% (Worldometers, 2019), happens to be not only the leading producer of rice in West Africa but also among the leading importers of the commodity. Although endowed with a strong agricultural and natural resources base, as well as favourable climatic conditions for agricultural production, an estimated of about N1 billion is spent daily by Nigeria on the importation of rice (David, 2014).

Owing to world population growth, there is a tremendous increase in the demand for rice. The world rice production has doubled in past 30 years due to the introduction of superior varieties and better cultivation practices; it is still insufficient to reach the increasing global demands (Fischer *et al.,* 2000). It is estimated that the total demand for rice in the world would increase at about 1% per annum from 2001 to 2025, so the present average yield has to be increased considerably in order to meet up the rising needs (Maclean *et al*., 2002).

The agricultural land for crop production is decreasing annually due to urban growth and land degradation, hence, rice production needs to be increased from the same or even smaller amount of land. The effects of climatic change particularly through drought, heat, flooding, pests, and diseases are affecting rice production (Afiukwa *et al.,* 2016). Several reports from various rice breeding programs across the world have indicated narrow genetic diversity in the varieties developed and released to farmers (Adegbaju *et al*., 2015). It has also been noted that the primary gene pools of many crop plants are so depleted in genetic variability that breeders are now exploring the potentials of wild relatives for sources of disease resistance and other traits (Langridge and Chalmer, 2004).

The diversity of these genetic resources is being lost to the need for higher yields and early maturity (Ogunbayo *et al.*, 2005). More than 90% of rice cultivation is being done using high yielding varieties only, obviously, landraces are disappearing past (Sinha and Mishra, 2013).

1.2 Justification of the Study

Nigeria has a potential land area of between 4.6 to 4.9 million hectares suitable for rice production, but only 1.7 million hectares is being cropped which is an indication that food sufficiency through rice production has not yet been fully achieved (Oluwaseyi *et al*., 2016). Importance of landraces can never be overemphasized in the agriculture system because the improvement in existing variety depends upon desirable genes which are possibly present in landraces and wild varieties only. Landraces offer a valuable gene pool for the future breeding program (Sinha and Mishra, 2013). Landraces are valuable as they possess a huge treasure of genetic materials which is priceless in future crop development and improvement programs (Sinha and Mishra, 2012). Also, assessment of genetic diversity is very important in rice breeding program because selection and conservation of different landraces varieties and proper utilization may usher a variety that can resist biotic and abiotic stresses (Parikh *et al.*, 2012) and become an advancement or better yield than the best variety available (Zhang *et al*., 2011).

The use of adapted rice landraces as the primary source of variation into which desired characters present in modern cultivars are introgressed may be an effective strategy for producing cultivars adapted to difficult production environments. According to Thalapati *et al.* (2014), several useful traits have been introgressed from wild species to cultivars. The submergence tolerance SUB1 QTL was identified from submergence tolerant rice

landrace FR13A. Its identification and characterization led to successful introgression of the QTL to rice mega-varieties. Specifically, QTLs for yield and related traits have been mapped from several wild species of rice, Recently, the *NAL1* allele that was identified from tropical *Japonica* rice landrace Daringan significantly increased the yield of modern rice cultivars (Swamy *et al.*, 2014). Also, candidate genes have been identified from wild species which could help improve rice yield (He *et al.*, 2006).

Landraces and older crop varieties preserve much of the lost diversity and comprise the genetic resources for breeding new crop varieties to cope with environmental and demographic changes, but our information about them is incomplete. The only way to ensure food security for future generations is to exploit the present day genetic diversity of different crops and to identify the promising one for the future breeding program (Muhammad *et al.,* 2015). Agro-morphological evaluation and DNA marker analysis could help the identification and differentiation of landraces with different genetic make-up. The information could enable maximized selection of diverse parents and assist in broadening the germplasm base of future rice breeding programs.

1.3 Aim of the Study

The aim of this study is to evaluate the agro-morphological characteristics of rice landraces and their genetic diversity in the savanna zones of Nigeria.

1.4 Objectives of the Study

The objectives of the study are to:

1. Characterize rice landraces in savanna zones of Nigeria based on their agro-morphological traits.
2. Determine the genetic diversity of rice landraces in savanna zones of Nigeria using Simple sequence repeat (SSR) markers.

1.5 Hypotheses

1. There is no significant difference in the agro-morphological traits of rice landraces in savanna zones of Nigeria.
2. There is no significant differences in the genetic diversity of rice landraces in savanna zones of Nigeria.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Rice Production in Nigeria

Amongst agricultural commodities, rice has the third –highest production in the world measured in metric tonnes at 741.5 million metric tonnes record behind only to maize at 1.0 billion metric tonnes as second highest and sugarcane at 1.9 billion metric tonnes, the agricultural commodity with the highest production. According to the United Nations Food and Agricultural Organization Statistics (FAOSTAT) the breakdown of rice production in the world by country puts China at the top position with 206.5 million metric tonnes, followed by India with 157.2 million metric tonnes at the second position, followed by Indonesia with 70.8 million metric tonnes, Bangladesh with 52.3 million metric tonnes, Vietnam with 45.0 million metric tonnes, Thailand with 32.6 million metric tonnes and Myanmar with 26.4 million metric tonnes. Nigeria is the highest importer of rice globally and the largest producer of rice in West Africa and the 17th major producer in the world and it accounts for about 20% of sub-Saharan Africa's rice imports (Omotola and Ikechukwu, 2006).

Before the advent of the Second World War, the predominant rice variety cultivated in Nigeria was the African originated red-grained species of the *Oryza glaberrima*. However, with the outbreak of World War II and its attendant, the greater requirement of food for fighting troops, rice cultivation (especially the exotic) experienced the introduction of Guyana varieties, of which BG 79 was the most widely cultivated. Since then, a lot of progress has been made in the development and releases of new rice

varieties, by a host of Research Institutes in the country especially the National Cereals Research Institute (NCRI) (Sanusi, 2014).

Rice is produced in all the six geo-political zones of Nigeria namely; North-West, North-East, North-Central, South-West, South-East, and South-South geopolitical zones. Rice production in Nigeria is mainly done during the rainy (wet) season. The production can also be done during the dry season, though not in all states. According to the work done by the United Kingdom's Department for International Development (DFID) on growth and employment in states, a report of which was made available in 2016, Kebbi state emerged as the top producer of rice with a production of 2.05 million metric tonnes in the wet season and 1.51 million metric tonnes in the dry season. Kebbi state is followed by Kano state with a production of 1.86 million metric tonnes in the wet season and 0.96 million metric tonnes in the dry season. In Ebonyi state which has more than 72,000 hectares of arable land for rice production, the state produces 1.2 million metric tonnes, Benue state produced 1.5 million metric tonnes. Annual rice production in Nigeria has increased from 5.5 million tonnes in 2015 to 5.8 million tonnes in 2017. In 2015, Nigerians spent not less than N1 billion on rice consumption, while spending had drastically reduced, consumption had increased because of increased in the local production of the commodity. The consumption rate is now 7.9 million tonnes and the production rate has increased to 5.8 tonnes per annum which were as a result of the CBN's Anchor Borrowers Programme with a total of 12 million rice producers and 4 million hectares of FADAMA rice land (Punch, 2017). According to the United Nations Food and Agriculture Organisation (FAO), the country imported 2.3 million tonnes in

2016 about half of the country's estimated requirements. The Federal government of Nigeria is targeting a production of 7 million metric tonnes of rice in 2018.

There are many challenges associated with rice farming in Nigeria; these include climatic factors such as flood, soil salinity, erosion, drought, and global warming. Land tenure and development of farmlands in Nigeria are so fragmented that the average farm holding is about 1-2 ha. This perhaps is due to the land tenure system that tends to hinder the ownership of land in the country. Potential land suitable for rice irrigation is still untapped. Most of our rice farmers are illiterates, unorganized with low-capital base and employed the use of simple and crude tools with little farm mechanization equipment usage. Weeds, pests, and diseases problems have a significant negative impact on production. The high cost of productive inputs such as seeds, fertilizers, and other agro-chemicals also affects productivity. Improper handling or management of soil and water resource, inadequate extension services which resulted to the low ratio of extension worker to farmers, non-availability or inadequate credit facility to farmers are hampering the success of rice production. Others include; lack of good roads in the rural areas, irregular and fluctuating prices of rice grains due to seasonal variation and lack of good linkage between research institutes and farmers (Sanusi, 2014).

2.2 Origin and Diversity of Cultivated Rice Species

The major rice growing regions are found in Asia, Latin America, and Africa. African rice has been cultivated for 3500 years. Between 1500 and 800 BC, *Oryza glaberrima* propagated from its original center, the Niger River delta and extended to Senegal. However, it never developed far from its original region. Its cultivation even declined in favour of the Asian species, which was introduced to East Africa early in the

common era and spread westward. African rice helped Africa conquer its famine of 1203. African rice is locally called *Jatau* (red) throughout Hausa land and the Chad Basin and *Hakorin Montol* (literally, the tooth of Montol people because of its grain size) in the Plateau and Nasarawa area (Longtau, 2003). Asian rice is thought to be introduced to Nigeria by Portuguese traders, through Trans-Saharan trade or by missionary activities and after about hundred years later replaced the African rice and became the major rice type grown in most rice growing environments in Nigeria. Its spread by natural means results in a popular variety called *Kilaki* "prostitute" in the Hausa language. Asian rice replaced the African rice after about a hundred years of its introduction to Nigeria by Portuguese traders and became the major rice type grown in most rice growing environments (Longtau, 2003).

The rice genus *Oryza* contains 25 known species, 23 are wild species and the remaining two are *Oryza sativa* the Asian rice and *Oryza glaberrima* the African rice. The Asian rice species, *Oryza sativa* is more consumed, present in several countries, especially Asia and Africa and more diverse than *Oryza glaberrima* (Sarla and Swamy, 2005). Based on morphological and physiological characteristics, *Oryza sativa* is divided into subgroups: indica, japonica and javanica. The ancestry of the *Oryza sativa* are *Oryza rufipogon* and *Oryza nivara*, while *Oryza longistaminata* and *Oryza barthii* are the progenitors of *Oryza glaberrima* (Ishi *et al*., 2001; Ibrahim, 2015).

2.3 Rice Biology

Rice is a monocot, it is normally grown as an annual plant, although in tropical areas it can survive as a perennial and can produce a ratoon crop for up to 30 years. When rice is harvested it is called 'Paddy'. A paddy is a complete seed of rice and one grain of paddy

contains one rice kernel. Each paddy has many layers, the outermost layer is the husk. The husk consists of 2 interlocked half shells. Each protects one half of the paddy. The husk is composed of silica and cellulose. The next layers are bran layers. Each layer is a very thin film of bran. Bran is mainly composed of fibre, Vitamin B complexes, protein and fat, it is the most nutritious part. At the base of each grain is an embryo, which will grow into a new plant if planted. The inner part of the grain is the rice kernel, which is composed of mainly starch. Rice starch is composed of mainly two types of starches, amylose, and amylopectin. The exact mixture of these determines the cooking texture of the rice (Haward, 2009).

Rice plant growth is mainly divided into three different stages: vegetative, reproductive and grain filling or ripening stages (Counce *et al*., 2000). Germination, emergence leaf production, seedling establishment, and tiller production occur in the vegetative stage of the plant life cycle. The reproductive stage includes culm elongation, the emergence of the flag leaves, booting, heading, and flowering. The ripening stage of rice is defined as grain filling or hardening of the grains. The whole rice plant is divided into three vegetative parts: root, culm, and leaf (Tandekar and Koshta, 2014).

The root system is fibrous, Soon after sowing, rice seed gives out seminal roots out of the radical. These are temporary in nature. The real functional roots are secondary adventitious roots that are produced from the lower nodes of the culm. The rice stem known as culm is hollow and is made up of nodes and internodes. Each node bears a leaf and bud, which may grow into a shoot or tiller. Each node of the culm bears a leaf. Each leaf consists of Leaf sheath (It originates from the node of culm), Leaf blade (It is the upper expanded part of leaf and begins at node, where it is joined with leaf sheath. At the

joint there is a thick collar), Auricles (These are hairy appendages at the base of the leaf blade), Ligules (It is a thin papery structure just above the auricles. Different parts of leaf are of importance in identifying the varieties), Flag leaf (It is the uppermost leaf just below the panicle. It is generally shorter in length and remains erect at an angle), Panicle (The inflorescence of rice plant is born on terminal shoot and is known as panicle. It is determinate type and at maturity it is droopy in nature. Panicle bears the spikelets), Spikelet (A spikelet is the floral unit and consists of two sterile lemmas, a lemma, a palea, and the flower), Lemma (It is a 5 nerved hardened bract with a filiform extension known as awn. Rice varieties may or may not have an awn), Palea (It is a three nerved bract slightly narrower than lemma), Flower (It consists of six (6) stamens with two-celled anthers and a pistle with one ovary and two stigmas. The pistil consists of one ovule. Rice grain is the ripened ovary with lemma and palea firmly adhered to it, the lemma and palea with other smaller components from the hull are removed in shelling rice for consumption. The rice fruit is a caryopsis in which single seed is fused with the wall of the ovary (pericarp). The seed consists of endosperm and an embryo. The embryo is very small and is found on the ventral side of the caryopsis. It contains plumule (embryonic leaves) and radicle (root). On submergence in water or on sowing the radicle grows as root and plumule grow as shoot (Haward, 2009).

2.4 Rice Landraces

A landrace is a local variety of domesticated rice plants species which has developed largely by natural processes, by adaptation to the natural and cultural environment in which it lives (Kamarouthu, 2013). Rice landraces are the groups of lineages that originated and evolved in the field over millennia through selective breeding by

generations of farmers, who chose random mutants and gene combinations in domesticated rice, for better yield, grain size, and other agronomic values. Landraces of rice can contain some valuable alleles not common in modern germplasm (Ahmed *et al.*, 2016). They have been shown to be excellent sources of genes for novel alleles and precious genetic resources because they contain huge genetic variability which can be used to complement and broaden the gene pool of advanced genotypes (Loresto *et al*., 2000).

Rice landraces maintained through traditional farming practices possess high genetic diversity and specific traits such as disease resistance, environmental constraint tolerance and nutritional qualities which are often used in crop improvements. (Camachovilla *et al.,* 2005). Their adaptations to local agro-environmental conditions contribute to yield stability and hence, they continue playing an important role in traditional and subsistence farming. Thus, the landraces of rice play a very important role in local food security and sustainable development in agriculture (Tang *et al.,* 2002).

2.5 Genetic Diversity

Genetic diversity reflects the amount of genetic variability amongst individuals or populations within a variety or species. Genetic variability measures the tendency of individuals to vary from one another based on morphometrics or molecular markers (Raazak *et al.,* 2016). Genetic diversity arises primarily because of variation in the linear sequence of nucleotides in DNA. Mutations generally happen in the coding region of genes, or the spacer regions within and among genes, in the number of gene copies, the linkage relationship between several genes or indeed in the whole chromosomes (Ibrahim, 2015). According to Brown (2008), a small portion of these changes translates

into protein variation, characters, into marker polymorphisms, morphological and physiological variation in agronomic characters and ultimately genotypes given different names by scientists and farmers. The extent of genetic diversity in a crop population depends on recombination, mutation, selection, and random genetic drift. Mutation and recombination bring new variations to a population, whereas selection and genetic drift remove some alleles, often from agronomically important lines (Pervaiz *et al*., 2010).

The amount of genetic diversity within a species is essential for the survival of species and other adaptation to changing environment, including new emerging biotic (pests and diseases) and abiotic stresses such as global warming (Gao, 2003). The large scale cultivation of genetically uniform cultivars has increased the vulnerability of many crops. This genetic diversity is essential to decrease crop vulnerability to biotic and abiotic stress, ensure long-term selection gain in genetic improvement and promote rational use of the genetic resource. Knowledge of the genetic diversity is important for identifying new genes, further improvement of the germplasm (Thomson *et al.,* 2007), germplasm conservation, variety identification and for studying the evolutionary ecology of the plant (Duran *et al.,* 2009)

Evaluating the amount of genetic diversity present in a crop species is a precondition for initiating an effective breeding program, as it offers the basis for tailoring desirable genotypes. Information on the nature and degree of genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. Genetically diverse parents are likely to segregate and or to produce higher heterotic genotypes. The more diverse parental lines are the greater the chances of attaining higher heterotic F1s and broad spectrum of variability within

segregating generations. Hybridization program involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature and promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents (Sarwar *et al*., 2015). Different genetic markers (morphological, biochemical and molecular) methods could be used to assess genetic diversity in crop plants (Fisseha, 2014).

2.6 Morphological Markers

Morphological markers are usually visually characterized phenotypic characters used during the early history of plant breeding. These include flower colour, seed shape, growth habits or pigmentation (Sumarani *et al.,* 2004). Morphological characters have been routinely used to analyze genetic diversity but did not have the resolution power for revealing polymorphisms in genetic analyses and/or for differentiating between closely related genotypes (Emmanuel, 2014). Studying of morpho-agronomic diversity among genotypes is the traditional way of assessing genetic variability for plant breeders. For many species, especially crops like rice, it is still the only method used by the majority of breeders (Ibrahim, 2015).

The major disadvantages associated with it are labour-intensive, time-consuming and limited number of traits to characterize, highly heritable traits show no variation over much of the material studied and largely influenced environmental conditions and cultural practices (Adegbaju *et al*., 2015). Consequently, special breeding programs and experimental designs are needed to distinguish genotypic from phenotypic variation (Fisseha., 2014). Many of these markers are not associated with economic traits (yield and quality) and even have an undesirable effect on the development and growth of the

plant. As a result, different plant genotypes cannot always be distinguished. However, despite all these limitations, these markers are still important in genetic diversity studies. A number of works have been reported by using different morphological and agronomic traits in rice. Hien *et al*. (2007) determined genetic diversity and relationships among 36 aromatic rice cultivars using 22 morphological characters. Cluster analysis placed the cultivars into five cluster groups with great morphological similarity, the clusters did not necessarily include all the cultivars from the same origin. They reported that there was no association between morphological characters and geographical location. Sadia *et al*. (2012) investigated sixty-eight commercial and primitive cultivars and found a considerable level of polymorphism among the cultivars. Clustering of the cultivars did not show any pattern of association between the morphological characters and the origin of the cultivars. Instead, cultivar groups were associated with their morphological similarities. Sinha and Mishra (2013) characterized thirty-four landraces of rice based on twelve quantitative agro-morphological characters using multivariate statistical analysis and five cluster groups were obtained from the 12 agro-morphological characters. Nadia *et al*. (2014) studied twenty-six landraces and four high yielding rice accessions for fourteen morphological markers to observe genetic diversity and identification of superior genotypes for crop improvement program. A wide range of morphological diversity was found among the rice accessions tested and it was grouped into 4 clusters based on morphological markers uksing Unweighted Pair Group Method with Arithmetic Means (UPGMA) cluster analysis at a cut-off similarity coefficient 0.98%. Sharma *et al*. (2014) reported genetic diversity of 2142 accessions of rice based on the multivariate

analysis for 10 agro-morphological traits. In all, a total of 8 clusters were obtained based on the estimates of genetic diversity using the UPGMA.

The discriminators mostly used in morphological diversity study of rice genetic resources are those approved by the International Board for Plant Genetic Resources (IBPGR) and IRRI rice advisory committee on rice standard descriptors. These descriptors include both qualitative and quantitative; seedling height, leaf blade length, leaf blade width, ligules length, Culm length, Culm number after full heading, Culm diameter at flowering period, panicle length, 100 seed weight at maturity, grain length and grain width measured as quantitative characters, and later at the vegetative stage leaf blade pubescence, leaf blade colour, basal leaf sheath colour, leaf angle, flag leaf angle, ligule colour, ligule shape, collar colour, auricle colour, Culm angle after flowering, internodes colour after flowering, panicle type at near maturity, secondary branching, panicle exertions, seed coat colour at maturity (Emmanuel, 2014). A number of works have been reported by using different agronomic and morphological traits in rice.

2.6.1 Characterization based on morphological and agronomic traits

Ali *et al*. (2000) characterized rice genotypes and found a significant difference in 100-grain weight among the accessions studied. He also observed relative greater range in plant height than the other characters. Rao *et al*. (2001) characterized 123 native cultivars and landraces using morpho agronomic descriptors to estimate variability and found the majority of cultivars possessing green basal leaf sheath, green corolla and white stigma. Hussain *et al*. (2005) found out that planting and sowing methods, transplanting date and soil condition affect plant height in rice. Zahid *et al*. (2005) studied twelve (12) genotypes of coarse rice and reported highly significant variation for various morphological traits

including number of panicles per plant. Weiya *et al*. (2008) studied rice genotypes and observed variation in days to flowering of several genotypes and identified a regulatory gene responsible for variation in this physiological trait among rice genotypes. Patil *et al*. (2009) studied 100 genotypes of rice germplasm for 8 characters. They found significant variability for days to 50% flowering, flag leaf area, plant height, panicle length, number of filled grain per plant, 100 seed weight and grain yield per plant. Prakash *et al*. (2011) observed that Leaf area index, photoperiod, sink and source relationship, competition among plant population and plant density contribute to variation among genotypes for panicle per plant. Rahman *et al*. (2011) reported that tillers contribute a great portion of grain yield and the extent of contribution varies among genotype and planting density.

Parikh *et al*. (2012) characterized seventy-one aromatic rice accessions for twelve morphological characters and found a wide range of variability for all the morphological traits studied. Out of twelve morphological characters, basal leaf sheath colour, leaf blade colour, ligule colour, plant habit, apiculus colour and awning showed high variation among the accessions and the rest of the six characters found in each of two classes among different accessions. A majority of genotypes were found to have green basal leaf sheath colour, green leaf blade colour, green tip colour, green leaf margin colour, green collar colour, white ligule colour, light green auricle colour, white apiculus colour, white stigma colour and white sterile glume colour. On the basis of awning character, most of the genotypes were found to be awnless followed by awned and tipped awn. Ekka *et al*. (2013) characterized rice based on eighteen qualitative characters and found that the absolute frequency was very high for the intermediate type of leaf pubescence, while ligule colour, cleft type of ligule shape, pale green auricle colour, green internode colour,

absent type of awning and straw sterile lemma colour. Manik (2013) evaluated the performance of 32 exotic early maturing rice (*Oryza sativa* L.) lines for their yield and yield contributing characters at phenotypic level and found significant variation among the genotypes for days to flowering, days to maturity, plant height, total tillers per hill, effective tillers per hill, panicle length, filled grains per panicle, unfilled grains panicle per panicle, 1000 seed weight and yield per plant. Mazid *et al.* (2013) evaluated forty-one rice genotypes for 13 morphological traits, almost all the traits exhibited highly significant variation.

Sarawgi *et al.* (2013) characterized seven hundred eighty-two rice germplasm accessions on the basis of twenty-nine morphological and eight agronomical traits. A majority of accessions were found to possess green basal leaf sheath colour, light purple auricles, white ligule colour, white stigma colour, and white grain colour. Emmanuel (2014) determine the extent of genetic diversity and relationship among 79 rice (*Oryza sativa* L.) landraces and its wild relative and found considerable diversity range based on fourteen quantitative morphological characters analysed. Sarawgi *et al*. (2014) on the basis of frequency distribution for eighteen qualitative traits of 408 rice germplasm accessions reported that majority of genotypes possessed green basal leaf sheath colour (87.25 %), green leaf blade colour (89.70 %), pubescent leaf (48.03 %), well panicle exsertion (57.10 %), white stigma colour (65.93 %), straw apiculus colour (78.18 %), compact panicle type (55.63 %), awnless (88.48 %), white seed coat (82.84 %), straw hull colour (70.34 %), intermediate threshability (47.30 %), erect flag leaf angle (57.59 %), medium leaf senescence (67.15 %) and straw sterile lemma (97.05 %). Tandekar and Koshta (2014) classified 100 genotypes into 26 groups on the basis of pigmentation on 12

plant parts, three groups were also made on the basis of awning character. Ibrahim (2015) used 87 rice accessions from six countries to determine the genotypic variation among rice accessions using phenotypic traits and SSR markers and the relationship between phenotypic traits and yield of rice accessions. He observed highly significant ($P < 0.001$) differences among the accessions for all the quantitative traits. Differences were also observed among the accessions regarding the 11 qualitative traits. The accessions from six countries were grouped into seven clusters based on the morphological traits at 21 % similarity coefficient.

Judith (2015) evaluated the genetic diversity of 191 rice germplasms collected from Eastern and Southern Africa based on morphological, molecular and quality traits and found most variation among the genotypes for basal leaf sheath colour, leaf blade colour, apiculus colour, lemma or palea colour, awning, number of days to 50% flowering, panicle length, plant height and spikelet fertility. Singh *et al*. (2015) assessed the genetic diversity of 76 rice accession using microsatellite markers and found a significant genetic variation for all the characters analysed. Kumar (2016) evaluated 64 aromatic rice germplasm and found wide variation among the germplasm for most of the studied traits. Purple colour of auricles and ligule was found in only one genotype, while light purple colour of auricles was recorded in four genotypes. White colour of stigma was recorded in 57 accessions, whereas purple stigma was observed in six accessions and awns present in 31 accessions. Kumar *et al*. (2016) established the distinctness among 64 aromatic rice germplasm by using 35 agro-morphological and quality traits. Wide variation was observed among the aromatic rice germplasm for most of the traits studied. Rashid *et al.* (2017) evaluated the performance of rice landraces under salinity stress and found

significant ($p<0.01$) variation among the genotypes. Sahu *et al.* (2018) studied the genetic behaviour of awning character in rice genotypes on the basis of morphological characteristics. They observed that the expression of long and fully awned trait was due to the presence of two independent genes, one dominant and another one recessive in the accession of wild species (*Oryza* officinalis). Partially awned character was governed by trigenic gene interaction.

2.6.2 Genetic variability parameters

Variability analysis in any diverse population provides valuable information about the selection of individuals plant having a distinct character which may further be utilized in various breeding strategies to improve the population. Genotypic coefficient of variation (GCV) measures the range of variability in crop and also enables to compare the amount of variability present in different traits. Higher GCVs indicate that worthwhile improvement could be achieved for traits through simple selection because environmental influences on the expression of the traits were minor. The success of rice improvement programmes depends on the amount of genetic variability and the degree to which the desirable traits are heritable. Although GCV provides information on the genetic variability present in various quantitative traits, it is not possible to determine the amount of the variation that is heritable from only the GCV (Singh *et al*., 2016). The estimates of heritability act as a predictive instrument in expressing the reliability of phenotypic value (Prasad *et al.*, 2013). Heritability estimate provides information regarding the amount of transmissible genetic variation to total variation and determines genetic improvement and response to selection. A number of works have been reported based on rice genetic variability.

Mishra *et al*. (2003) evaluated 88 rice genotypes to obtain information on genetic variability, heritability, genetic gain and interrelationship of some grain quality, grain yield and its attributes. The mean square due to genotypes was significant for most of the characters indicating the presence of a considerable amount of variability among the genotypes. The high genotypic variances were observed for biological yield and grain yield per plant. Das *et al.* (2005) assessed 22 semi deep-water rice genotypes for genetic variability, heritability in a broad sense was observed to be high for all the traits under study. Okelola *et al*. (2007) assessed the genotypic and phenotypic variability for seed vigour traits and seed yield in 24 genotypes of West African rice genotypes and found that phenotypic coefficient of variation was generally higher than the genotypic coefficient of variation for most of the traits. Ahmed *et al.* (2010) studied rice genotypes and found high heritability estimates for plant height. Khalid *et al*. (2012) studied rice genotypes and found high heritability (>85%) for plant height, number of tillers per plant and 100-grain weight. Parikh *et al*. (2012) studied rice genotypes and found high heritability estimates for plant height, panicle length, grain yield per plant and hundred seed weight.

Roy *et al*. (2012) studied the variation in agro-morphological and grain quality traits among traditional and Basmati-type aromatic quality rice to investigate plausible relationships between the traits. A set of 12 cultivars, comprising ten traditional and two Basmati types were studied. Highest variation was observed for grains per panicle followed by grain yield per plant. Dutta *et al.* (2013) estimated variability and genetic parameters of sixty-eight rice genotypes for twelve agronomically important characters, high genotypic and phenotypic coefficients of variations, high heritability (broad sense)

and high genetic advance as percentage of mean were shown by tillers per plant, days to 50% flowering, panicles per plant and grain yield. Thus these characters were under the influence of additive gene action and a satisfactory selection programme for agronomic improvement on the basis of these characters is possible. Manik (2013) evaluated the performance of 32 exotic early maturing rice (*Oryza sativa* L.) lines and found highest PCV and GCV values for a number of unfilled grains per panicle, followed by grain yield per plant(g) and the lowest PCV and GCV values were recorded for days to maturity. Estimates of heritability in a broad sense were high for days of 50% flowering, days to maturity, plant height, 1000 seed weight (g) and yield per plant (g) and was 75.62, 92.95, 78.74, 99.78 and 70.82%, respectively.

Mazid *et al*. (2013) evaluated forty-one rice genotypes for 13 morphological traits. Among the genotypes, almost all the traits exhibited highly significant variation. The higher extent of genotypic (GCV), as well as phenotypic coefficients of variation (PCV), were noticed for a number of tillers per hill, total number of spikelets per panicle, number of filled grains per panicle and yield per hill. High heritability together with high genetic advance was observed for total number of spikelets per panicle, number of filled grains per panicle and yield per hill indicating a dominant role of additive gene action in the expression of these traits. Vanisree *et al*. (2013) evaluated 21 rice genotypes for 12 yield and quality traits. High estimates of GCV were recorded for plant height, number of filled grains per panicle and grain yield per plant. Khare *et al.* (2014) estimated high heritability coupled with high to moderate phenotypic and genotypic coefficient of variation for grain yield per plant, plant height and total grains per panicle. Kumar (2016) categorized PCV and GCV values as <10% to be low, 10-20% moderate and >20% high. For heritability

estimates, <30% means low, 31-60% moderate and <60% high. Fathelrahman *et al*. (2017) investigated genetic variability of rice for yield and yield component under semi-arid zone and observed phenotypic coefficients of variation (PCV) to be higher than genotypic coefficients of variation (GCV) estimates for all the studied characters in all genotypes displaying the influence of environmental effect on the studied characters.

2.6.3 Correlation

Pearson's correlation is a measure of strength of linear relationship between two traits. Through correlation, we could easily assume the relationship between groups of characters or which character is directly associated with other characters. It assists plant breeders at the time of selection and provides valuable information about yield and yield-related traits (Ibrahim, 2015). The higher the coefficients, the more effective will be in discriminating between germplasms, regardless of the positive or negative sign (Nachimuthu *et al*., 2014). Rice grain yield improvement is the major character of economic interest. Therefore, its correlation with other character is most desirable. For traits with significant positive correlation with grain yield, it means that any increase in these traits caused an increase in the grain yield and would be ideal for selection to improve rice grain yield. Ekka *et al*. (2011) on the basis of association analysis reported that grain yield per plant had positive significant correlation with leaf width, days to 50 % flowering, plant height, panicle length, number of filled grains per panicle, 100 seed weight and paddy grain length.

Ashfaq *et al*. (2012) associated various morphological traits with yield, a strong association was revealed between the plant yield and panicle length, number of seeds per panicle, productive tillers per plant and seed weight per panicle.

Sadia *et al*. (2012) investigated sixty-eight commercial and primitive cultivars and found a considerable level of polymorphism among the cultivars. some of the characters exhibited positive correlations, while others showed negative associations with one another. Days to flowering was highly significant positively associated with days to maturity (r = 0.92) and straw yield per plant (r = 0.79). Plant height had a positive association with panicle length (r = 0.65) and had a negative correlation with grain yield per plant.

Manik (2013) evaluated the performance of 32 exotic early maturing rice (*Oryza sativa* L.) lines and found that grain yield per plant showed a non-significant positive association with days to 50% flowering, days to maturity, total number of tillers, effective number of tillers per hill, number of filled grains per panicle, number of unfilled grains per panicle and weight of 1000 seeds. Days to 50% flowering showed a significant positive correlation with 1000 seed weight and yield per plant. Days to 50% flowering showed a significant negative correlation with a number of unfilled grains per panicle. Plant height showed a significant positive association with panicle length and filled grains per panicle, Number of filled grains per panicle showed positive and significant association with yield per plant.

Emmanuel (2014) determined the extent of genetic diversity and relationship among 79 rice (*Oryza sativa* L.) landraces and its wild relative and found significant and positive association of grain length (r = 0.360), flag leaf width (r = 0.511) and one hundred seed weight (r = 0.319) with grain yield per plant.

Sarawgi *et al*. (2015) reported that the leaf length, leaf width, days to 50% flowering, effective tiller, plant height, panicle length and days to maturity had a positive direct effect on grain yield per plant. These characters could be used as a direct selection criterion for higher grain yield.

Kumar (2016) evaluated 64 aromatic rice germplasm, and found highly significant positive correlations between thousand grain weight and grain length (r = 0.436), thousand grain weight exhibited highly significant and negative correlation with days to 50 % flowering (r = -0.329), number of spikelets per panicle (r = -0.233) and plant height (r = -0.219), higher value of positive and significant correlation of grain yield per plant with number of filled spikelets per panicle (r = 0.572), days to 50 % flowering (r = 0.267), grain breadth (r = 0.258) and plant height (r = 0.161) He revealed that grain yield is under direct influence as it tends to increase along with increasing of these traits.

2.7 Molecular Markers

DNA markers are fragment of DNA revealing mutations or variation which can be used to detect polymorphisms between different genotypes or alleles of a gene in a population or gene pool. DNA markers can cover the whole genome and therefore, is much larger in quantity. Ideal DNA marker must have some desirable properties such as high polymorphism and reproducibility, selective neutral behaviours, it should be easy and fast to detect, co-dominant inheritance and numerous occurrences in genome (Sharma *et al*., 2008; Fisseha, 2014). The DNA based markers are more reliable, less labour input and remain unaffected across different seasons, growth stages, agronomic practices and locations (Ren *et al*., 2003). Information regarding genetic diversity at the molecular

level could be used to aid, identify and develop genetically unique genotype that compliments existing cultivars (Ni *et al*., 2002).

DNA markers may be broadly divided into three classes based on the method of their detection: (1) hybridization-based; (2) PCR based and (3) DNA sequence-based; depending upon how the polymorphism is revealed. In hybridization based markers, DNA profiles are visualized by hybridizing restriction endonuclease digested DNA fragment to a labelled probe while PCR based markers involve in vitro amplification of particular DNA sequences with the help of primers and a DNA polymerase enzymes (Sharma *et al.,* 2008).

DNA markers may reveal genetic differences that can be visualized by using a technique called gel electrophoresis and staining with ethidium bromide or silver nitrate or detection with radioactive or colourimetric probes. They are called polymorphic markers when they reveal differences between individuals of the same or different species markers, whereas markers that do not discriminate between genotypes are called monomorphic markers. DNA markers are widely accepted as potentially valuable tools for crop improvement in rice (Mackill *et al.,* 1999).

2.8 Molecular Markers for Genetic Studies

As a result of advancement in plant genetics and molecular biology, Many types of molecular markers have been developed to characterize germplasm with each method differing in principle, application, type, and amount of polymorphism detected, cost, and requirement. These include restriction fragment length polymorphisms (RFLPs), random amplification of polymorphic DNAs (RAPDs), amplified fragment length polymorphisms

(AFLPs), Microsatellites or simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs) (Rabbani *et al.,* 2008).

2.9 Simple Sequence Repeat Markers

These are PCR markers that are also known as the microsatellites and or sequence-tagged microsatellite sites (STMS), are simple tandemly repeated, di- to tetra-nucleotide sequence motifs such as $(GT)_{n,}$ $(ATT)_n$ and $(GATA)_n$ flanked by unique sequences and widely distributed throughout the genomes of plants (Adegbaju *et al*., 2015). The copy numbers of these repeats vary between genotypes and is a source of polymorphism in plants and are referred to as variable number of tandem repeats (VNTRs) or hypervariable regions (Mittal and Dubey, 2009).

SSR markers are actually non-coding regions which remained conserved during the course of evolution and are ideal for DNA fingerprinting and varietal identification. Any variation in the DNA sequence of priming sites and repeat number may help in diversity analysis among genotypes. The SSR markers reveal polymorphism due to variations in the length of microsatellite at particular loci among different genotypes. They have the advantage of being abundant, evenly distributed over the genome and are easily assayed by PCR (Gour *et al.,* 2017), hypervariable, multiallelic, co-dominant in nature, reproducibility, locus-specific, high throughput genotyping and can be automated (Singh *et al*., 2016). They provide a valuable source of polymorphism, making them an important class of genetic markers (Varshney *et al*., 2005).

The multifold nature of these markers make them widely applied in genetic diversity analysis, gene mapping (Ma *et al*., 2011), construction of fingerprints (Xiao *et al*., 2006; Ma *et al*., 2011), genetic purity test (Peng *et al.,* 2003), analysis of germplasm diversity

(Zhou *et al.*, 2003; Jin *et al.*, 2010) and identification of closely related species. Microsatellite markers are considered to be appropriate for assessment of genetic diversity, phylogenetic relationship and varietal identification because of their ability to detect large numbers of discrete alleles repeatedly, accurately and efficiently. Furthermore, it has been stated that the data produced by SSR markers analysis was helpful in providing a simple, fast and safe mean of genome assay in rice (Upadhyay *et al*., 2011). The success of these molecular markers in characterizing and analyzing genetic diversity in rice has been demonstrated by a number of studies.

Siwach *et al*. (2004) analysed allelic diversity among 24 basmati and non- basmati long grain indica rice varieties using 50 SSR markers and observed maximum number of alleles in the cases of RM markers with GA, AT, ATT and CTT repeat motifs. Claudio *et al*. (2006) characterized the allelic diversity of 192 traditional varieties of Brazilian rice using 12 simple sequence repeat markers. They revealed identical accessions with the same name, few with different names and a mixture of pure lines, indicating that SSR markers are fundamental in determining the genetic relationship between landraces. Pervaiz *et al*. (2010) analysed genetic diversity of seventy-five rice landraces using thirty-five microsatellite markers and detected 142 alleles, the number of alleles identified by each marker ranged from 2 to 13 with a mean of 4.4.

Rahman *et al*. (2011) used 34 SSR markers to study a set of 21 rice varieties composed of 20 BRRI developed modern rice varieties and one local variety to detect their genetic variation, five clusters were revealed at 50% genetic similarity coefficient. Kumar *et al*. (2012) determined the genetic diversity of 64 rice genotypes using 20 SSR primers on chromosome number 7-12, they found a number of alleles per locus ranged from 2 to 11,

with an average of 4.18 alleles across 34 loci. A total of 57 rare alleles were detected at 24 loci, whereas 42 unique alleles were detected at 20 loci. Polymorphic Information Content (PIC) values ranged from 0.157 to 0.838, with an average of 0.488. Rahman *et al*. (2012) studied thirty-four microsatellite markers across 21 types of rice to characterize and discriminate among different varieties.

Sajib *et al*. (2012) used a total of 24 SSR markers across 12 elite aromatic rice genotypes for their characterization and discrimination. Among these 24 markers, 9 microsatellite markers were showed to be polymorphic. They found the number of alleles per locus ranged from 2 alleles to 6 alleles with an average of 3.33 alleles The polymorphic information content values ranged from 0.14 (RM510) to 0.71 (RM163) with an average of 0.48. The frequency of most common allele at each locus ranged from 41 % to 91 %. Das *et al*. (2013) assessed genetic diversity in 91 accessions using 23 previously mapped SSR markers to examine population structure and found 182 alleles including 51 rare and 27 null alleles. Manik (2013) used three microsatellites (SSRs) marker to determine the relationship and diversity among 32 exotic early maturing rice (*Oryza sativa* L.) lines and found number of allele per locus ranged from 8 to 14 and the frequency of SSR allele ranged from 0.031 to 0.187. Positive correlations were found between gene diversity, number of alleles, the allele size range and the maximum number of repeats. Polymorphic information content (PIC) ranged from 0.7891 to 0.8964 and the primer RM215 was found to be the most polymorphic. Meti *et al*. (2013) used microsatellite or simple sequence repeat (SSR) markers to determine the allelic diversity and relationship among 48 traditional indigenous aromatic rice germplasm grown under the Eastern part of India. Out of 30 primers, 12 primers showed DNA amplification and polymorphism among 48

aromatic rice genotypes. A total of 28 bands appeared by using 12 SSR primers in 48 aromatic rice landraces. Out of 28 bands, 25 bands were polymorphic and 3 were monomorphic bands. The results reveal that all the tested primers showed distinct polymorphism among the landraces indicating the robust nature of SSR markers.

Nadia *et al*. (2014) reported genetic diversity among twenty-six landraces and four high yielding rice accessions using a set of 27 SSR markers which generated 321 polymorphic alleles. Genetic similarity analysis using UPGMA grouped the accessions into 6 clusters based on SSR marker's data at a cut-off similarity coefficient of 0.17%. Adegbaju *et al*. (2015) determined the genetic diversity and phylogenetic relationship of 6 improved African lowland rice varieties, using 129 SSR primers on the twelve chromosomes of rice. The result reveals that six varieties produced a total of 492 alleles and the average number of alleles per locus was 3.8. The polymorphic Information Content (PIC) values range from 0.0 to 0.375 and gene diversity ranges from 0.0 to 4.4. Ibrahim (2015) used 12 SSR markers to determine the genetic diversity of 87 rice accessions. He found the number of alleles ranged from 2-9 with an average of 6.83 while PIC ranged from 0.34-0.79 with an average of 0.55. The cluster dendrogram generated based on the 6 SSR markers grouped the accessions into 4 clusters at 41 % similarity coefficient. Judith (2015) used 18 SSR's markers to evaluate the genetic diversity of 191 rice germplasm. A total of 121 alleles were obtained on polymorphic SSR with an average of 7.56 allele per marker and the number of alleles ranged from 2 to 20 while Polymorphic Information Content (PIC) values ranged from 0.01 to 0.89 with an average value of 0.49. Singh *et al*. (2015) evaluated the genetic polymorphism and identification of diverse parents among the 76 rice accessions using SSR markers. The accessions showed significant phenotypic

variation for all the characters analyzed. The SSR markers were highly polymorphic across all accessions and altogether 79 alleles were detected. The overall Polymorphic information content (PIC) value ranged from 0.26 to 0.65 with an average of 2.82 per locus indicating a high level of genetic variation. The cluster analysis showed the rice germplasm accessions can be grouped into two major groups and 14 subgroups.

Singh *et al*. (2015) assessed the genetic variation and relationships among 32 rice genotypes of diverse origin using 19 SSR primers. Among 19 SSRs primers, 17 showed 100% polymorphism. The number of alleles ranged from 2 to 10 with an average value of 4.37 per locus. Polymorphic information content (PIC) values of the primers ranged from 0.79(RM 167) to 0.99(RM 47 and RM 10) with an average of 0.84. Cluster analysis based on SSR banding pattern grouped the rice genotypes into 2 major clusters with additional sub-clusters.

Kumar (2016) evaluated 64 aromatic rice germplasm and detected 61 alleles for 25 polymorphic SSR loci varied from 2 to 4 alleles with an average of 2.44 alleles and polymorphism information content (PIC) values ranged from 0.278 to 0.642 with an average of 0.465. A dendrogram based on the cluster analysis by microsatellite polymorphism grouped 24 promising aromatic rice genotypes into three major clusters at a 40% level of similarity. Singh *et al*. (2016) genotyped a set of 729 Indian rice varieties using 36 SSR markers to assess the genetic diversity and genetic relationship. A total of 112 alleles were amplified with an average of 3.11 alleles per locus with mean Polymorphic Information Content (PIC) value of 0.29. Vu *et al*. (2016) studied the genetic diversity in a set of 40 Vietnamese lowland rice varieties using 30 simple sequence repeat (SSR) markers covering all rice chromosomes. A total of 111 alleles

were detected, with a mean of 3.7 alleles per locus. The number of polymorphic alleles detected by each SSR marker ranged from 2 to 6. The fragment size of a given SSR locus varied between 85 and 650 bp and the frequency of a major allele at each locus ranged from 32.5% to 76.9%. Polymorphism information content value varied from 0.355 to 0.774 with an average of 0.594. Gour *et al.* (2017) analysed 83 indigenous rice germplasm using different yield and quality traits. On the basis of trait differences in the materials for quality aspect, 19 rice lines were selected for molecular analysis. A total of 12 SSR markers were applied from which only nine markers were found polymorphic. The average percentage of major allele frequency ranged between 42.11 % (RM256) to 100.00% (RM341).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Study Area

The morphological and agronomic evaluations of the rice landraces were conducted at the Botanical garden of the Department of Botany, Ahmadu Bello University, Zaria (Latitude 11°, 9' N and Longitude 67°, 39' E).

The genetic diversity analysis of the rice landraces was analysed at Bioscience laboratory, International Institute of Tropical Agriculture (IITA) Ibadan (Latitude 3° 54' N and Longitude 7° 30' E), Nigeria.

3.2 Sources of Materials

Seventy rice landraces were collected from local farmers in the 18 northern states; that constitutes the Savanna zones of Nigeria. The seeds were identified by the farmers with their local names (Table 1).

3.3 Experimental Design

The experiment was laid out in a complete randomized design (CRD) with three replications. Five seeds of each landrace were sown per hole at a depth not more than 1cm in labelled polythene (35 x 57cm) bags containing 8kg of loamy soil. A uniform spacing of 20 cm x 20 cm was adopted between rows and column. The seedlings were thinned to three seedlings per bag after two weeks of germination and watered daily, weeds were controlled by a combination of hoeing and hand weeding (Akinwale *et al*., 2012). Fertilizer was applied at 50 N, 25 P and 25 K mg/kg of soil before the seeds were planted (Wazed, 2014).

Table 3.1: Collection Locality and Species of Rice Landraces used for the Study

S/n	Rice Landrace	Location	State	Species	Ecosystem
1	2bc	Funtua	Katsina	*O. sativa*	Upland
2	Ba Ingila	Rabah	Sokoto	*O. sativa*	Upland
3	Bakin Iri – Borno	Borno	Borno	*O. glaberrima*	Upland
4	Bakin Iri Kebbi	Birnin Kebbi	Kebbi	*O. glaberrima*	Lowland
5	Bakin Yar China Bau	Bauchi	Bauchi	*O. sativa*	Upland
6	Bayawure	Argungu/Bunza	Kebbi	*O. glaberrima*	Lowland
7	Biruwa	Doma	Nasarawa	*O. sativa*	Lowland
8	Bolaga	Funtua	Katsina	*O. sativa*	Upland
9	Cdi	Vandekya/Zakibien	Benue	*O. sativa*	Upland
10	Chaina	Gombe	Gombe	*O. sativa*	Upland
11	Cp Gombe	Gombe	Gombe	*O. sativa*	Lowland
12	Dan Kaushi	Yobe	Yobe	*O. glaberrima*	Upland
13	Dan Koydo	Borno	Borno	*O. glaberrima*	Upland
14	Dantudu	Lapai	Niger	*O. glaberrima*	Upland
15	Doguwar Carolea	Giwa	Kaduna	*O. sativa*	Upland
16	Doguwar Jamila	Giwa	Kaduna	*O. sativa*	Upland
17	Farar Ja	Funtua	Katsina	*O. sativa*	Lowland
18	Farar Jana	Wudil	Kano	*O. sativa*	Upland
19	Farar Jellof	Zaria	Kaduna	*O. sativa*	Upland
20	Fijo	Zaria	Kaduna	*O. sativa*	Upland
21	Frajalam	Giwa	Kaduna	*O. sativa*	Upland
22	Gajere Carolea	Giwa	Kaduna	*O. sativa*	Upland
23	Iresi Tsarigi	Kwara	Kwara	*O. sativa*	Upland
24	Jaka	Funtua	Katsina	*O. glaberrima*	Upland
25	Jamila Plt	Plateau	Plateau	*O. sativa*	Upland
26	Jamila-Bauchi	Bauchi	Bauchi	*O. sativa*	Upland
27	Jamila-Gombe	Gombe	Gombe	*O. sativa*	Upland
28	Jamila-Jigawa	Kyawa/Shuwarin	Jigawa	*O. sativa*	Upland
29	Jamila Katsina	Funtua	Katsina	*O. sativa*	Upland
30	Jamila-Niger	Egabi	Niger	*O. sativa*	Upland
31	Jamila-Yola	Yola	Adamawa	*O. sativa*	Upland
32	Jamila-Zaria	Zaria	Kaduna	*O. sativa*	Upland
33	Jan Iri – Borno	Borno	Borno	*O. glaberrima*	Upland
34	Jan Iri Kebbi	Birnin Kebbi/Yauri	Kebbi	*O. glaberrima*	Lowland
35	Jap	Jibia	Katsina	*O. sativa*	Upland

Table 3.1 (Continued): Collection Locality and Species of Rice Landraces used for the Study

	Rice Landrace	Location	State	Species	Ecosystem
36	Jaton Mini	Yobe	Yobe	*O. glaberrima*	Upland
37	Koro-Koro	Iga/Basa	Nasarawa	*O. glaberrima*	Upland
38	Lete/Viu	Bgoko	Benue	*O. sativa*	Upland
39	Mai Adda/Kilaki	Zaria	Kaduna	*O. sativa*	Lowland
40	Mai Allura	Zaria	Kaduna	*O. sativa*	Lowland
41	Mai Madara	Bauchi	Bauchi	*O. sativa*	Upland
42	Mai Zabuwa Giwa	Giwa	Kaduna	*O. sativa*	Upland
43	Mai Zabuwa/Biro	Zaria	Kaduna	*O. sativa*	Upland
44	Mass/Osi	Vandekya/Zakibien	Benue	*O. sativa*	Upland
45	Miruwa	Akwara/Aledi	Benue	*O. sativa*	Lowland
46	O-Tu	Jalingo	Taraba	*O. sativa*	Lowland
47	Santana (Yar Ruwa)	Dutsinma	Katsina	*O. glaberrima*	Lowland
48	Shatika	Funtua	Katsina	*O. glaberrima*	Upland
49	Sipi-Niger	Tufa	Niger	*O. sativa*	Upland
50	Sipi Nasarawa	Asakto	Nasarawa	*O. sativa*	Upland
51	Soppi	Bayango	Benue	*O. sativa*	Lowland
52	Tasama	Bauchi	Bauchi	*O. glaberrima*	Upland
53	Wacot	Funtua	Katsina	*O. sativa*	Upland
54	Water Proof	Awe	Nasarawa	*O. sativa*	Lowland
55	Wati	Suleja	Niger	*O. sativa*	Lowland
56	Yar China Kebbi	Jega/Yauri	Kebbi	*O. sativa*	Upland
57	Yar Dan Hassan	Zaria	Kaduna	*O. sativa*	Upland
58	Yar Das	Birnin Kudu	Jigawa	*O. glaberrima*	Upland
59	Yar Dashe	Giwa	Kaduna	*O. glaberrima*	Upland
60	Yar Dirya	Kaura	Zamfara	*O. sativa*	Upland
61	Yar Gidan Yarima	Funtua	Katsina	*O. sativa*	Upland
62	Yar Kabori	Wurno	Sokoto	*O. sativa*	Upland
63	Yar Kalage	Jega	Kebbi	*O. glaberrima*	Upland
64	Yar Kura	Giwa	Kaduna	*O. sativa*	Upland
65	Yar Maaji	Funtua	Katsina	*O. sativa*	Upland
66	Yar Mamman	Birnin Kebbi/Argungu	Kebbi	*O. glaberrima*	Lowland
67	Yar Nupawa	Zaria	Kaduna	*O. sativa*	Upland
68	Yar Telak	Zaria	Kaduna	*O. sativa*	Upland
69	Yar Yiginaye	Giwa	Kaduna	*O. sativa*	Upland
70	Yar Zaiti	Rabah	Sokoto	*O. sativa*	Upland

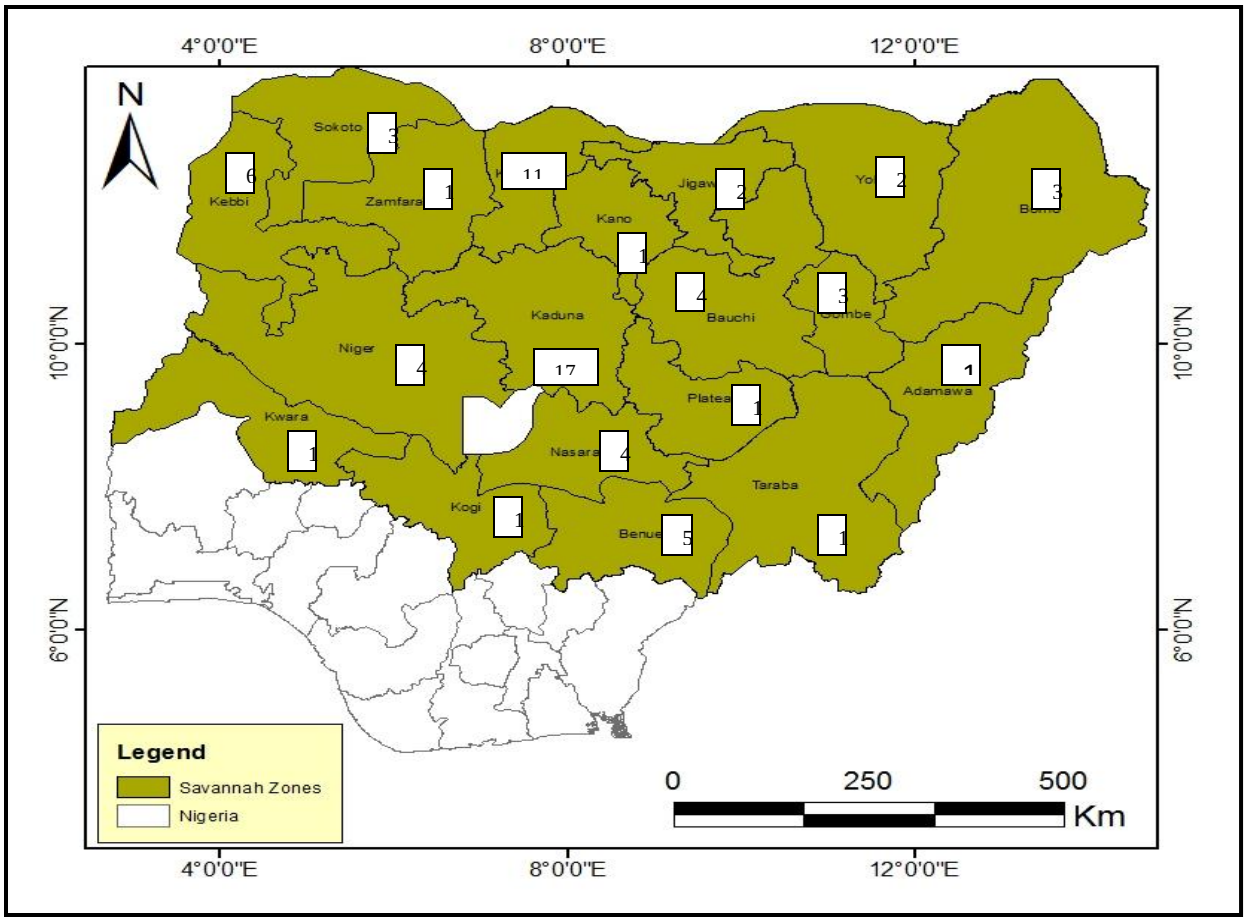

Figure 1: Location of landraces used for the study

Source: Adapted and Modified from Administrative Map of Nigeria

3.4 Collection of Data

Agro-morphological data were collected for both qualitative and quantitative traits at different stages of the plant development based on the International Rice Research Institute Standard evaluation system (IRRI, 2013).

3.4.1 Qualitative morphological traits

The qualitative morphological traits evaluated were; Basal leaf sheath colour (BLS), Leaf blade colour (LBC), Leaf tip colour (LTC), Leaf margin colour (LMC), Junctura Colour (JC), Ligule colour (LC), Auricle colour (AC), Internode colour (IC), Node colour (NC), Stigma colour (SC), Apiculus colour (APC), Awning (AW), Sterile glume colour (SGC), Chalkiness of endosperm (CE) and Seed colour (SDC).

3.4.2 Phenotypic evaluations of the agronomic traits

Agronomic traits evaluations were done using the Standard Evaluation Score for Rice (IRRI, 2013) as follows;

i. Days to Germination was evaluated as the average number of days from seeding to germination and averaged over three plants.
ii. Days to 50% flowering was evaluated as the average number of days from seeding until 50% of the plants have flowered and averaged over three plants.
iii. Number of tillers per plant was measured as the average number of tillers per plant for three plants at maximum tillering.
iv. Number of leaves per plant was measured as the average number of leaves per plant for three plants at maximum tillering .

v. Plant height (cm) was measured as the average height in centimeters of three plants from the base of the shoot to the tip of the tallest panicle (awn excluded) when about 80% of the seeds have ripened.

vi. Panicle length (cm) was measured as the average number of all panicles for three plants in centimeters from the base to the tip of the panicle near maturity.

vii. The number of panicles per plant was measured as the average number of panicles per plant for three plants at maturity.

viii. The number of filled grains per panicle was measured as the average number of filled grains per plant calculated for three plants when about 80% of the seeds have ripened.

ix. The number of unfilled grains per panicle was measured as the average number of unfilled grains per plant calculated for three plants when about 80% of the seeds have ripened.

x. The number of total grains per panicle was measured as the average number of filled and unfilled grains per plant calculated for three plants when about 80% of the seeds have ripened.

xi. One hundred seed weight (g) was measured as the average weight of 100 filled grains in grams for three plants.

xii. Grain yield per plant (g) was measured as the average weight of all filled grains in grams for three plants.

3.5 Estimation of Genetic Parameters

The various genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability were calculated according to the method described by Burton (1952), Singh and Chaudhary (1985).

Genotypic co-efficient of variation is computed using the formula below;

$$GCV = \frac{\delta^2 g}{X} \text{ x } 100$$

Where;

$\delta^2{}_g$ = Genotypic variance; and

x = Population mean

Phenotypic coefficient of variation is computed using the formula below;

$$PCV = \frac{\delta^2{}_P}{X} \text{ x } 100$$

Where;

$\delta^2{}_P$` = Phenotypic variance; and

x = Population mean

Broad-sense heritability is computed using the formula below;

$$h^2b = \frac{\delta^2 g}{\delta^2{}_P} \text{ x } 100$$

Where ;

$\delta^2{}_g$ = Genotypic variance; and

$\delta^2{}_P$ = Phenotypic variance

3.6 Evaluation of the Molecular Diversity of Rice Landraces using SSR Markers

Twenty-one polymorphic primer pairs were selected for the genetic diversity analysis on the basis of published rice microsatellite framework map (Temnykh *et al*., 2001).

3.6.1 Isolation of rice DNA for PCR array

Genomic DNA of the selected landraces were isolated separately. DNA was extracted from young plant leaves collected from at least 2-3 seedlings in each landrace according to the method described by Doyle and Doyle (1990) as modified by Aliyu *et al*. (2013). Healthy fresh leaf (5mg tissue was used) samples were collected from young seedling with sterilized scissors, lyophilized and taken to the laboratory. The sample was ground in a geno-grinder. Sodium hydroxide (100 µl) and 400 µl 100 mM Tris were added. It was shaken by inversion for 5 minutes and centrifuged at a maximum speed of 13000 revolutions per minute (rpm) for 10 minutes. The supernatant was transferred into new Eppendorf and 20µl TE-RNase solution added, then incubated for 20 minutes at 37ºC. 300µl Sodium hydroxide and 300 µl isopropanol were added and spun down at 13000 rpm for 10 minutes. It was decanted to get pellet and was then rinsed in 200 µl 70 % ethanol. It was again decanted and air dried for 20 minutes and then suspended in 100µl low salt TE.

3.6.2 DNA Quantification

The concentration of DNA was measured using an ND-1000 Spectrophotometer. The purity of all genotypes was accessed by obtaining the absorbance ratio $A_{260/280}$ using the Nanodrop Spectrophotometer.

3.6.3 Polymerase chain reaction array (PCR)

DNA samples from each genotype were subjected to PCR amplification with SSR markers using Perkin-Elmer thermocycler using the Genomic DNA of the rice as described by Gregorio *et al*. (1997). The reaction mixture in a 0.5ml Eppendorf tube consisted of the 50µl reaction mixture containing DNA (1µg), 200µM of each dNTPs. 1 µM of each forward and reverse primer, 1 unit Taq DNA polymerase, 200mM $MgCl_2$ and 1 x Taq buffer. The genomic DNA template was denatured at 95ºC for 5 minutes. PCR was performed with 30 cycles of denaturing at 95ºC for 45 seconds, annealing at 65ºC for 45 seconds and extension at 72ºC for 60 seconds. Final extension incubation was done at 72ºC for 15 minutes. After electrophoresis, the ethidium bromide-stained bands were viewed under UV light in a gel documentation system.

3.6.4 Gel electrophoresis

The amplification product was subjected to electrophoresis in 2% agarose gel in a 1xTBE buffer at 70-80 volts for 2-3 hours for good separation. About 3g of agarose was poured into a 150ml 0.5 TBE buffer in a conical flask. The mixture was heated in a microwave for 2 minutes. The conical flask was placed on a magnetic stirrer and allowed to cool for 5minutes. The warm gel was poured in a gel clamped casting stand and allowed to polymerize, the combs and clamps were removed. The gel was placed on a gel tank and 1xTBE buffer was poured into the tank to cover the gel. The gel was loaded with DNA samples and run for 2-3hours at 70-80 volts for good separation. The gel was removed from the electrophoresis system and placed carefully in an ethidium bromide staining solution, stained for 5minutes and viewed under an ultraviolet transilluminator.

A 1kb DNA ladder was used as a size marker to compare the molecular weight of the amplified products which was viewed under ultraviolet light.

3.6.5 Allelic scoring

For each marker, an allelic band was scored based on a 1 (present) and 0 (absent) binary code. Only prominent and unambiguous bands were scored for data reliability.

3.7 Data Analyses

3.7.1 Agro morphological analysis

Agronomic quantitative data obtained were subjected to analysis of variance (ANOVA) using SAS 2007 (version 9.0). Least Significant Difference (LSD) Test at 5 % was used to separate the means where significant. Pearson's correlation was used to determine the interrelationship between the agronomic quantitative data. Frequency distribution was used to classify the landraces into groups based on the qualitative morphological traits. A dendrogram was drawn by unweighted pair group method of average linkage (UPGMA) using Multivariate Analysis System Statistical Software for cluster analysis based on morphological traits and agronomic traits.

3.7.2 Molecular data analysis

Polymorphic information content (PIC) value for each SSR was calculated using the formula proposed by Anderson *et al.* (1993).

$$PIC = 1 - \sum_{j=1}^{n} p^2 ij$$

Where n is the number of marker alleles for a marker (i) and P*ij* is the frequency of the *jth* allele for marker (i).

Major allele frequency (MAF), number of alleles (NA) and gene diversity were calculated using genetic analysis package Power Marker V3.25 (Liu and Muse, 2005).

A neighbour-joining tree was constructed using the Darwin software version 6.0.015 to depict the relationship between the rice landraces.

CHAPTER FOUR

4.0 RESULTS

4.1 Characterization of Qualitative Traits of Rice Landraces

Significant variability was observed among the landraces for basal leaf sheath colour, leaf blade colour, leaf tip colour, leaf margin colour, junctura colour, ligule colour, auricle colour, internode colour, node colour, apiculus colour, stigma colour, sterile glume colour, awning, seed colour and chalkiness of endosperm. Frequency distributions for these fifteen qualitative traits are presented in Table 4.1. Forty-seven landraces (67.14%) were observed to have green basal leaf sheath colour, 9 (12.86%) landraces had purple lines colour, 4 (5.71%) had light purple colour and 10 (14.29%) had purple basal leaf sheath. Based on leaf blade colour, the landraces were differentiated into green 65 (92.86%), dark green 3 (4.29%) and 2 (2.86%) purple blotch. Purple leaf tip colour was observed in 20 (28.57%) of the landraces and the remaining 50 (71.43%) landraces had green leaf tip colour. Fifty-four (77.14%) landraces had green leaf margin colour and 16 (22.86%) landraces had purple margin colour.

Based on junctura colour, sixty-five (92.86%) had a light green colour and 5 (7.14%) landraces had a green colour. Sixty-seven (95.71%) landraces had white ligules while 3 (4.29%) had white with purple lines ligules colour. Majority of the landraces had light green auricles 67 (95.71%) while the rest 3 (4.29%) had purple auricles. Fifty-three (75.71%) of the landraces evaluated had green internode, 15 (21.43%) had purple lines and only 2 (2.86%) had purple internode colour. Green node colour was observed in 68 (97.14%) landraces while the remaining 2 (2.86%) had purple node colour. White apiculus colour was observed in 47 (67.14%) of the landraces, 15 (21.43%) had purple

apiculus, 6 (8.57%%) had red, and 2 (2.86%) had purple apex apiculus. White stigma colour was observed in 47 (67.14%) of the landraces studied, whereas 18 (25.71%) had purple and 5 (7.14%) had light purple stigma colour. Sterile glume is the flowerless bract at the base of spikelet. Sixty-eight 68 (97.14%) were observed to have white sterile glume colour while 2 (2.86%) landraces had purple sterile glume colour. Awn was observed in 36 (51.43%) of the landraces, 27 (38.57%) landraces were awnless while the remaining 7 (10%) had tipped awn. Seed coat of 33 (47.14%) of the landraces evaluated were white colour, red colour was observed in 18 (25.71%) landraces, 17 (24.29%) had a light brown colour and 2 (2.86%) had brown sterile glume colour. None chalky endosperm was observed in 26 (37.14%) of the landraces, twenty-four (34.29%) were observed to have less than 10% of a chalky texture, 8 (11.43%) had medium chalkiness (10-20%) and 12 (17.14%) landraces had large (>20%) chalkiness.

Table 4.1: Frequency Distribution for Qualitative Traits of Seventy Rice Landraces

Morphological Traits	Colour / Pattern type	Frequency	Percentage
Basal leaf sheath colour (BLSC)	Green	47	67.1
	Purple	10	14.3
	Green with Purple lines	9	12.9
	Light purple	4	5.7
Leaf blade colour (LBC)	Green	65	92.9
	Dark green	3	4.3
	Purple blotch	2	2.9
Leaf tip colour (LTC)	Green	50	71.4
	Purple	20	28.6
Leaf margin colour (LMC)	Green	54	77.1
	Purple	16	22.9
Junctura colour (JC)	Light green	65	92.9
	Green	5	7.1
Ligule colour (LC)	White	67	95.7
	Purple lines	3	4.3
Auricle colour (AC)	Light green	67	95.7
	Purple	3	4.3
Internode colour (IC)	Green	53	75.7
	Purple	2	2.9
	Purple lines	15	21.4
Node colour (NC)	Green	68	97.1
	Purple	2	2.9
Apiculus colour (APC)	White	47	67.1
	Red	6	8.6
	Purple apex	2	2.9
	Purple	15	21.4
Stigma colour (SC)	White	47	67.1
	Purple	18	25.7
	Light purple	5	7.1
Sterile glume colour (SGC)	White	68	97.1
	Purple	2	2.9
Awning (AW)	Awnless	27	38.6
	Awn	36	51.4
	Tipped awn	7	10.0
Seed colour (SDC)	White	33	47.1
	Light brown	17	24.3
	Brown	2	2.9
	Red	18	25.7
Chalkiness of endosperm (CE)	None	26	37.1
	Less	24	34.3
	Medium	8	11.4
	Large	12	17.1

4.2 Clustering of Rice Landraces based on Qualitative Traits

Qualitative traits were used to construct a dendrogram, the seventy rice landraces were grouped into five clusters group using Euclidean distance following Ward's method, the genotypes were grouped into distinct clusters (Figure 4.1).

Cluster group I contained landraces from Kaduna, Katsina, Adamawa, Bauchi, Gombe, Jigawa, Niger, Kwara, Nasarawa, Sokoto, Kano, Plateau and Benue. These are landraces with none to the less chalky endosperm. Cluster group II had landraces from Kaduna, Bauchi, Gombe, Jigawa, Niger, Kebbi, Taraba, Zamfara, Nasarawa and Benue. They are landraces with medium to large chalky endosperm. Cluster group III contained landraces from Benue and Borno, they are landraces with purple lines basal leaf sheath colour, purple and red apiculus colour, purple to light purple stigma, white and red seed coat colour. Cluster group IV contained landraces from Kaduna, they had purple blotch leaf blade colour, purple apex apiculus, awnless and light brown seed coat colour. Cluster group V contained landraces from Kaduna, Katsina, Kebbi, Yobe, Bauchi and Nasarawa. These are landraces with purple and red apiculus colour, purple and light purple stigma. The clustering pattern of most of the landraces under this study did not follow any clear distinction based on the qualitative traits evaluated at a similarity coefficient of 60%. The distribution of the landraces to different clusters is presented in Table 4.2.

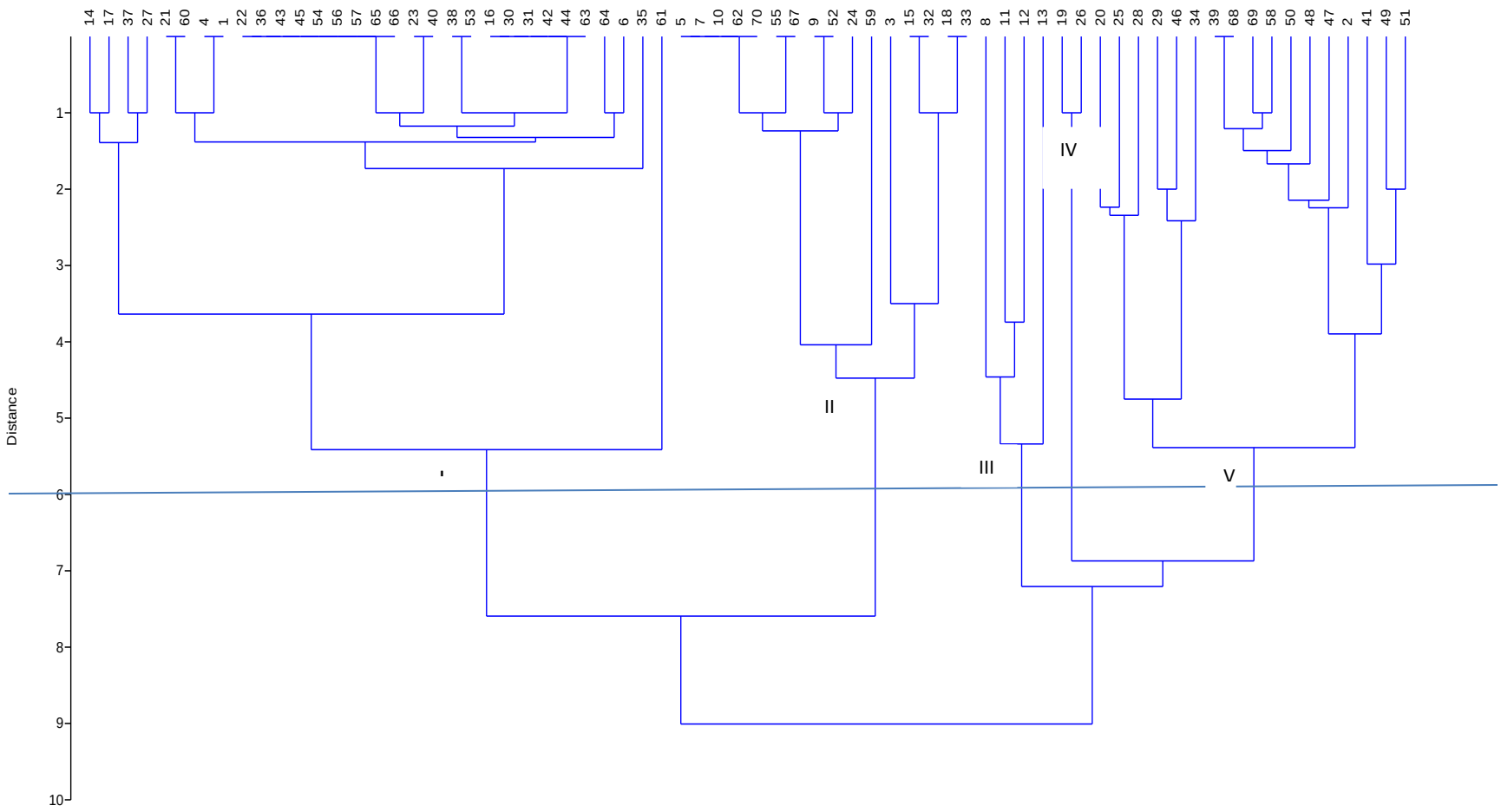

Figure 4.1: Dendrogram showing Relationships of Rice Landraces based on Qualitative Traits

Table 4.2: Distribution of Rice Landraces to Five Cluster Groups based on Unweighted Pair Group Method

Cluster groups	I	II	III	IV	V
Landraces	Ba ingila, Biruwa, Bolaga, Cp-Gb, Farar-ja, Farar-jana, Fara-rjellof, Iresi-Tsagiri, Jamila-Plt, Jamila-Ba, Jamila-Gb, Jamila-Kt, Jamila-Yl, Jamila-Zrx, Jap, Lete/Viu, Mai allura, Santana, Sipi ng, Wacot, Water proof, Wati, Yar Das-Gb, Yar Dashe, Yar gidan yarima, Yar Kabori, Yar kura, Yar maaji, Yar nupawa, Yar yiginaye, Yar zaiti	Mai madara, Mass/osi, Cdi, Jamila-Ng, Yar Dirya, Sipi-nsw, Soppi, Otu, (Yar china-kb, Frajalam, Dantudu, Chaina-Gb, Tasama, Doguwar-jamila, Jamila-jg, Fijo	Bakin iri-Bn, Miruwa, Jan iri-bn, Dan koydo	Mai zabuwa-Gw, Mai zabuwa/biro	Mai adda/kilaki, Doguwar-carolea, Gajere-Carolea, Yar telak, 2bc, Yar Dan Hassan, Jaka, Jaton mini, Dan kaushi, Koro-koro, Bakin iri-Kb, Yar mamman, Yar kalage, Bakin yar china-Ba, Shatika, Jan Iri-kb, Bayawure

4.3 Agro-morphological Characterization based on Agronomic Traits

Highly significant (P< 0.01) differences were observed among the various agronomic traits evaluated (Table 4.3.1).

Days to germination ranged from 4 days to 6.67 days with a mean of 5.29 days. Lower days to germination was observed in YAR NUPAWA while the longer days to germination value were observed in IRESI TSARIGI and JATON MINI. Plant height ranged from 43.67 to 93.33cm (FARAR JANA and DOGUWAR CAROLEA respectively) with a mean height of 70.99cm. A Mean of 22.33 cm panicle length was obtained and a ranged from 14.94 cm to 34.50cm as observed in MAI ZABUWA/BIRO and BIRUWA respectively. The number of leaves per plant ranged from 11.67 to 31.67 as observed in DAN KAUSHI and MAI MADARA respectively with a mean value of 17.55. Average tiller number of 5.46 was obtained and ranged from 4 in FARAR JA, MIRUWA and YAR MAAJI to 7.33 in YAR KALAGE.

Days to 50 % flowering ranged from 63 days in YAR KALAGE to 126.33 days in 2BC with a mean of 97.79. Panicle number per plant ranged from 3 in YAR MAMMAN to 9.89 inYAR KALAGE with a mean of 5.41. A Mean of 16.54 was obtained for a number of filled grain per panicle and a ranged from 2.00 in 2BC, JAKA and YAR MAMMAN to 63.56 in YAR CHINA-KB. The number of unfilled grain per panicle ranged from 12.50 in FARAR JELLOF to 74.45 in OTU with a mean of 34.20. The mean number of grains per panicle of 50.77 was obtained and a range from 25.44 to 86.45 as obtained in YAR MAMMAN and YAR CHINA-KB respectively. One hundred seed weight ranged from 1.97g to 3.1g in YAR CHINA-KB and MASS/OSI respectively with a mean of

2.55g. A Mean of 2.35g of grain yield per plant was obtained and ranged from 0.16g to 9.24g in YAR MAMMAN and WACOT respectively (Table 4.3.2).

Table 4.3.1: Mean square Values of the Agronomic Traits of Rice Landraces

Source of Variation	DF	DG	PHT	PAN	NLP	NTP	DFF	NPP	NFG	NUG	NTG	HSW	GYP
Rep	3	2.16	119.85	3.10	4.15	1.13	244.01	1.55	94.68	66.85	46.01	0.27	1.42
Landraces	69	1.13**	488.99**	44.67**	47.80**	2.30**	704.09**	6.48**	509.36**	406.65**	482.66**	147.24**	10.70**
Error	138	0.47	22.37	10.712	9.10	0.59	127.90	0.31	27.55	41.03	35.48	0.00	0.67

** highly significant at $P < 0.01$

NOTE: DG-Days to Germination, PHT-Plant Height, PNL-Panicle Length, NLP-Number of Leaves per plant, NTP- Number of Tillers per plant, DFF-Days to 50% Flowering, NPP- Number of Panicles per plant, NFG- Number of Filled grains per panicle, NUG- Number of unfilled grains per panicle , NTG- Number of Total grains, HSW-Hundred Seed Weight, GYP-Grain Yield per plant

Table 4.3.2: Mean ± Standard error, Standard deviation, Minimum and Maximum values of the Agronomic Traits of Rice Landraces

Traits	Mean ± S.E	Standard Deviation	Minimum	Maximum
DG	5.28±0.33	0.61	4.00	6.67
PHT	70.99±2.46	12.77	43.67	93.33
PNL	22.32±2.72	3.86	14.94	34.50
NLP	17.55±1.37	3.99	11.67	31.67
NTP	5.46±0.33	0.88	4.00	7.33
DFF	97.79±5.53	15.32	63.00	126.33
NPP	5.41±0.23	1.47	3.00	9.89
NFG	16.54±2.25	13.03	2.00	63.56
NUF	34.20±2.95	11.64	12.50	74.45
NTG	50.77±2.87	12.68	25.44	86.45
HSW	2.55±0.01	0.25	1.97	3.10
GYP	2.35±0.33	1.89	0.16	9.24

NOTE: DG-Days to Germination, PHT-Plant Height, PNL-Panicle Length, NLP-Number of Leaves per plant, NTP- Number of Tillers per plant, DFF-Days to 50% Flowering, NPP- Number of Panicles per plant, NFG- Number of Filled grains per panicle, NUG- Number of unfilled grains per panicle , NTG- Number of Total grains, HSW-Hundred Seed Weight, GYP-Grain Yield per plant

4.4 Estimation of Genetic Parameters of Rice Landraces

Genotypic variances, phenotypic variances, genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %) and broad sense heritability (H_B %) for all the quantitative traits are presented in Table 4.4.

4.4.1 Variability parameters

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits evaluated. Among the traits, PCV and GCV values were recorded for grain yield per plant (80.37 and 77.83), number of filled grains per panicle (78.78 and 76.62), number of unfilled grains per panicle (34.04 and 32.28), number of panicles per plant (27.18 and 26.51) number of total grains (24.98 and 24.05), number of leaves per plant (22.74 and 20.46), plant height (17.98 and 17.57), panicle length (17.28 and 15.07), number of tillers per plant (16.04 and 13.84), days to 50% flowering (15.66 and 14.17), hundred seed weight (9.72 and 9.69) and days to germination (11.62 and 8.90) respectively (Table 4.4).

4.4.2 Estimate of heritability

High heritability estimates (> 60%) were observed for all the traits studied except for days to germination which showed medium heritability (31-60%) (Table 4.4).

Table 4.4: Genetic Variation and heritability of the Agronomic Traits of Rice Landraces

Traits	Genotypic variance	GCV (%)	Phenotypic variance	PCV (%)	H^2b (%)
DG	0.22	8.91	0.38	11.62	58.85
PHT	155.54	17.57	163	17.98	95.42
PNL	11.32	15.07	14.89	17.28	76.01
NLP	12.9	20.46	15.93	22.74	80.96
NTP	0.57	13.84	0.77	16.04	74.47
DFF	192.06	14.17	234.7	15.66	81.83
NPP	2.06	26.51	2.16	27.18	95.19
NFG	160.6	76.62	169.79	78.78	94.59
NUF	121.87	32.28	135.55	34.04	89.91
NTG	149.06	24.05	160.89	24.98	92.65
HSW	0.06	9.69	0.06	9.72	99.32
GYP	3.35	77.83	3.57	80.37	93.78

NOTE: DG-Days to Germination, PHT-Plant Height, PNL-Panicle Length, NLP-Number of Leaves per plant, NTP- Number of Tillers per plant, DFF-Days to 50% Flowering, NPP- Number of Panicles per plant, NFG- Number of Filled grains per panicle, NUG- Number of unfilled grains per panicle , NTG- Number of Total grains, HSW-Hundred Seed Weight, GYP-Grain Yield per plant, GCV-Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, h^2b-Broad-sense heritability

4.5 Desirable Landraces for the Important Yield and Yield Related Traits

The potential donor landraces for yield and yield related traits are listed in Table 4.5. Biruwa had the highest panicle length, followed by Jamila-JG and Jap. For Number of tillers, Yar ma' aji had the maximum tillers no, followed by Dan kaushi and Jamila-BA. Yar china-KB had the highest number of filled spikelets, then Wacot and Bolaga. Hundred seed weight was highest in Mass/osi followed by Doguwar Jamila and Wati. For the Grain yield per plant Wacot was the highest, followed by Yar china-KB and Jamila-PLT.

Table 4.5: Desirable Landraces for the Important Yield and Yield Related Traits

Traits	Landraces	Values
Panicle length (cm)	Biruwa	34.50
	Jamila-JG	31.89
Number of tillers	Yar Kalage	7.33
	Jan iri-BN	7.00
Number of filled grains/panicle	Yar china-KB	63.56
	Wacot	51.33
Hundred seed weight (g)	Mass/osi	3.10
	D/Jamila	3.00
Grain yield per plant (g)	Wacot	9.24
	Yar china-K	8.26
Days to 50% flowering (days)	Farar ja	70.00
	Yar Kalage	63.00

4.6 Correlation Analysis for Agronomic Traits

Correlation analyses for the twelve (12) agronomic traits studied are presented in Table 4.6. Significant positive correlations were obtained in: Panicle length and plant height (r= 0.48), Number of tillers per plant and number of leaves per plant (r= 0.29), Number of panicles per plant and number of tillers per plant (r= 0.43), Number of total grain per panicle and number of filled grain per panicle (r= 0.60), Grain yield per plant and filled grain per panicle (r= 0.94). Significant negative correlations were obtained in a number of panicles per plant and days to 50% flowering (r= -0.44), Number of unfilled grain per panicle and number of filled grain per panicle (r= -0.49).

Table 4.6: Correlation Co-efficient Analysis for Agronomic Traits of Rice Landraces

variables	DG	PHT	PNL	NLP	NTP	DFF	NPP	NFG	NUF	NTG	HSW	GYP
DG												
PHT	-0.07											
PNL	-0.07	0.48**										
NLP	-0.17	-0.10	-0.17									
NTP	0.01	-0.06	0.02	0.29*								
DFF	-0.12	0.12	0.03	0.22	-0.17							
NPP	0.13	-0.16	-0.04	-0.03	0.43*	-0.44*						
NFG	0.12	-0.15	-0.09	0.05	-0.22	-0.06	-0.03					
NUG	-0.06	0.10	0.23	0.07	0.10	0.02	-0.07	-0.49**				
NTG	0.07	-0.07	0.12	0.12	-0.14	-0.04	-0.09	0.60**	0.41*			
HSW	-0.12	0.13	-0.08	-0.23	-0.06	0.05	-0.04	-0.01	-0.20	0.20		
GYP	0.09	-0.17	-0.09	0.10	-0.12	-0.15	0.19	0.94**	-0.49**	0.53**	0.08	

*significant at P < 0.05, ** highly significant at P < 0.01

NOTE: DG-Days to Germination, PHT-Plant Height, PNL-Panicle Length, NLP-Number of Leaves per plant, NTP- Number of Tillers per plant, DFF-Days to 50% Flowering, NPP- Number of Panicles per plant, NFG- Number of Filled grains per panicle, NUG- Number of unfilled grains per panicle , NTG- Number of Total grains, HSW-Hundred Seed Weight, GYP-Grain Yield per plant, GCV-Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, $\mathbf{h^2b}$-Broad-sense heritability

4.7 Cluster Analysis based on Agronomic Traits

Relationship revealed by agronomic traits using similarity coefficients based on the unweighted pair group method with arithmetic mean (UPGMA) is shown in Figure 4.2. The seventy rice landraces were clustered into three major cluster groups at a similarity coefficient of 91.2%. Cluster group I contained only 1 landrace YAR CHINA –KB from Kebbi state. This landrace was characterized by the highest number of leaves per panicle, number of panicles per plant, number of filled grains, number of total grains and grain yield per plant while lowest mean values for plant height and days to 50% flowering. Cluster II had 19 landraces from eleven (11) states, these landraces had highest mean values for hundred seed weight. Cluster group III contained 50 landraces from sixteen states, these landraces exhibited highest mean values for plant height and panicle length (4.9). The mixed accessions in these clusters may indicate that they constitute a heterogeneous group of accessions with different origins. The clustering pattern of some genotypes under this study did not follow zonal distribution because landraces from different states were found in similar clusters.

Table 4.7: Mean values of Agronomic Traits obtained for Cluster Groups of Rice Landraces

Characters	Cluster I	Cluster II	Cluster III
DG	5.33	5.47	5.21
PHT	54.00	69.33	71.96
PANL	20.29	21.15	22.82
NLPPAN	20.33	17.11	17.67
NTPPAN	4.67	5.14	5.59
DFF	86.00	96.28	98.61
NPPLT	6.22	5.33	5.43
NFG	63.56	31.31	9.98
NUFG	19.56	24.65	38.12
NTG	86.45	55.96	48.09
HSW	1.97	2.61	2.54
GYPLT	8.26	4.38	1.46

NOTE: DG-Days to Germination, PHT-Plant Height, PNL-Panicle Length, NLP-Number of Leaves per plant, NTP- Number of Tillers per plant, DFF-Days to 50% Flowering, NPP- Number of Panicles per plant, NFG- Number of Filled grains per panicle, NUG- Number of unfilled grains per panicle , NTG- Number of Total grains, HSW-Hundred Seed Weight, GYP-Grain Yield per plant.

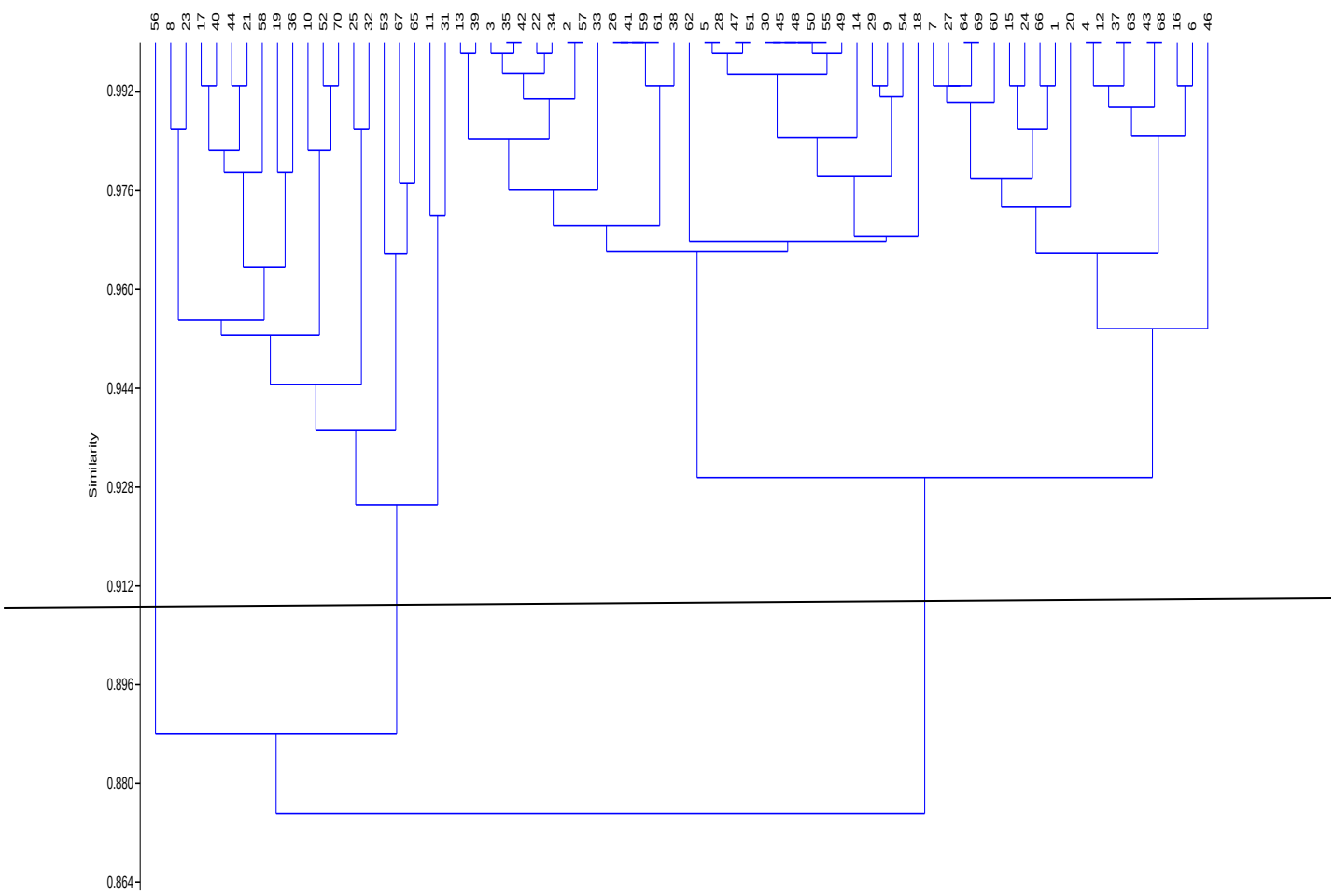

Figure 4.2: Dendrogram of the Relationships of Rice Landraces based on Agronomic Traits.

2bc(1), Ba ingila(2), Bakin iri Bn(3), Bakin iri-Kb(4), Bakin yar china-Ba(5), Bayawure(6), Biruwa(7),Bolaga(8), Cdi(9), Chaina-Gb(10), Cp Gb(11), Dan kaushi(12), Dan koydo(13), Dantudu(14), Doguwar-carolea(15), Doguwar-jamila(16), Farar-ja(17), Fararjana(18), Fararjellof(19), Fijo(20), Frajalam(21), GajereCarolea(22), IresiTsagiri(23), Jaka(24), Jamila-Plt(25), Jamila-Ba(26), Jamila-Gb(27), Jamila-jg(28), Jamila-Kt(29), Jamila-Ng(30), JamilaYl(31), JamilaZrx(32), Jan iri-bn(33), Jan Iri-kb(34), Jap(35), Jaton mini(36), Koro-koro(37), Lete/Viu(38), Mai adda/kilaki(39), Mai allura(40), Mai madara(41), Mai zabuwa Gw(42), Mai zabuwa/biro(43), Mass/osi(44), Miruwa(45), Otu(46), Santana(47), Shatika(48), Sipi ng(49), Sipi-nsw(50), Soppi(51), Tasama(52), Wacot(53), Water proof(54), Wati(55), Yar china-kb(56), Yar Dan Hassan(57), Yar Das-Gb(58), Yar Dashe(59), Yar Dirya(60), Yar gidan yarima(61), Yar Kabori(62), Yar kalage(63), Yar kura(64), Yar maaji(65), Yar mamman(66), Yar nupawa(67), Yar telak(68), Yar yiginaye(69), Yar zaiti(70)

4.8 Genetic Diversity Assessment of Rice Landraces using SSR Markers

A total of 36 SSR primers were used to detect polymorphism across 72 rice landraces. Among the 36 SSR primers used in this study, 21 yielded scorable amplification products . A total of 84 alleles were obtained on polymorphic SSR with an average of 4 alleles per primer. The number of alleles per locus ranged from 3 [R228M, RM 228, RM 223 and R223M] to 6 [R518M and RM 236]. Major allele frequency at each locus ranged from 0.29 to 0.86 with an average of 0.62. The Polymorphic Information Content (PIC) was calculated for each marker as a relative measure of informativeness. It ranged from 0.23 (R 223M) to 0.73 (RM 236) with an average value of 0.45. The primer RM 236 was most informative since it had the highest level of polymorphism with PIC value of 0.73 and gene diversity value of 0.77. The average genetic diversity obtained was 0.50 (Table 4.8).

4.9 Genetic Diversity of the Rice Landraces

The genetic similarity index of the rice landraces is presented in Figure 4.3. The NJ-tree revealed four clusters. Cluster group I and III contained 19 and 15 landraces with 3 and 2 sub clusters respectively. Cluster group II had the least number of landraces of 13 divided into 2 sub clusters. Cluster IV was the largest containing 25 landraces and was divided into 5 sub clusters. The distribution pattern of the landraces did not follow any distinctive pattern due to region of collection. Landraces from similar states clustered in all the groups.

Table 4.8: Allele Number, Major Allele Frequency, Gene Diversity and Polymorphic Information Content (PIC) values Generated from twenty one SSR Primers for the Rice Landraces

Marker	Chromosome No	Major Allele Frequency	Allele No	Gene Diversity	PIC
R462M	1	0.63	4.00	0.51	0.44
R490M	1	0.85	4.00	0.27	0.26
RM236	2	0.29	6.00	0.77	0.73
RM555	2	0.57	4.00	0.60	0.55
R132M	3	0.78	4.00	0.37	0.33
R518M	4	0.50	6.00	0.60	0.53
R574M	5	0.70	4.00	0.51	0.46
R589M	6	0.75	4.00	0.41	0.39
R314M	6	0.72	4.00	0.45	0.42
R432M	7	0.79	4.00	0.35	0.33
R346M	7	0.79	4.00	0.35	0.32
RM515	8	0.47	4.00	0.66	0.60
RM223	8	0.72	3.00	0.43	0.39
R223M	8	0.86	3.00	0.25	0.23
RM566	9	0.39	4.00	0.68	0.62
R216M	10	0.57	4.00	0.59	0.53
R228M	10	0.78	3.00	0.37	0.33
RM228	10	0.72	3.00	0.43	0.38
R332M	11	0.33	4.00	0.70	0.65
R17M	12	0.49	4.00	0.54	0.43
RM235	12	0.43	4.00	0.64	0.57
Mean		**0.62**	**4.00**	**0.50**	**0.45**

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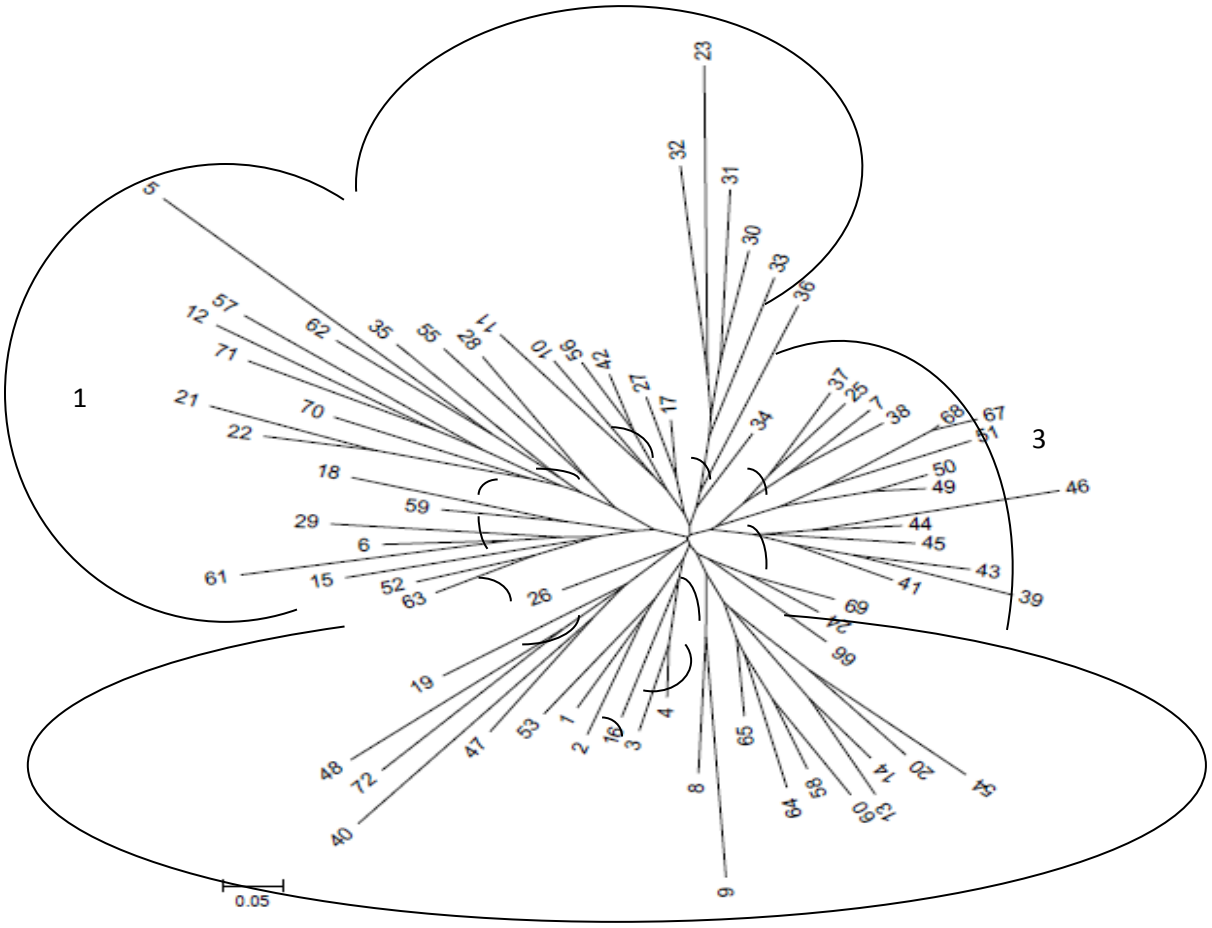

Figure 4.3: Neighbor-Joining (NJ) Tree of Genetic Diversity of Rice Landraces using 21 SSR Primer

CHAPTER FIVE

5.0 DISCUSSION

Characterization of crop germplasm through different morphological traits is an important step for assessment of its genetic potential. The success of a crop improvement programme depends on the magnitude of genetic variability and the extent to which the desirable traits are heritable. Analysis of genetic variability in landraces can help in identifying diverse parental combinations for further selection and help in introgressing desirable genes into crop plants.

5.1 Characterization of Qualitative Traits in Rice Landraces

Qualitative traits are considered as the most important characters to describe a particular plant variety. Qualitative traits are mostly genetically controlled thus they are less independent to the environmental response. According to Hien *et al*. (2007), qualitative traits are mainly influenced by natural selection, socio-economic scenarios and consumer preference. wide variation among the qualitative morphological traits indicated wide variation in the landraces and may be utilized for selection purposes in plant breeding. The different pigmentation observed does not appear to be related to crop development, pest resistance or grain yield but it has been found useful in recognizing, removing off-types and maintaining the genetic purity of seed. However, it will not be reliable for identification of cultivars, because the intensity of green colour of many cultivars gets bleached when the plant is left in the field to dry in sun or as a result of the influence of fertilizers and environmental conditions. This is supported by Tandekar and Koshta (2014), they classified 100 genotypes into 26 groups on the basis of pigmentation on 12 plant parts, They found out that certain plant parts such as apiculus and stigma were more

frequently pigmented than others whereas, leaf blade was found pigmented for only a few accessions and reported that both linkage and pleiotropy are responsible for simultaneous occurrence of anthocyanin in different plant parts. Rao *et al*. (2001) who studied 123 native cultivars and landraces based on frequency distribution for eleven morphological characters, found majority of the cultivars possessing green basal leaf sheath and white stigma. Parikh *et al*. (2012) also supported this result when they characterized seventy-one aromatic rice germplasm and found variation among the germplasm based on anthocyanin pigmentation. Sarawgi *et al.* (2013) characterized seven hundred and eighty-two rice germplasm accessions on the basis of twenty-nine morphological and eight agronomical traits, the majority of the accessions were found to possess green basal leaf sheath colour, light purple auricles and white stigma colour. Sarawgi *et al*. (2014) characterized dwarf and medium duration rice germplasm accessions on the basis of eighteen morphological and seven agronomical traits and majority of genotypes were found to have green basal leaf sheath colour (87.25%), green leaf blade colour (89.70%), white stigma colour (65.93%), awnless (88.48%), white seed coat (82.84%) and straw hull colour (70.34). Sahu *et al*. (2018) reported that the presence of awns is controlled by a single dominant gene. Sarawgi *et al*. (2013) reported similar qualitative traits variation in rice genotypes. Chalkiness observed might be due to malformed starch granules with air spaces between them. Quantification of chalkiness is important because of its apparent tie to milling quality which could help in the development of cultivars that are resistant to kernel chalk formation. This result is in agreement with the work of Judith (2015).

5.2 Clustering of Rice Landraces based on Qualitative Traits

Cluster analysis is very useful in revealing complex relationships among populations of diverse origins in a more simplified manner. It is also effective in indicating accessions

with useful traits belonging to different clusters for hybridization. The cluster analysis for the morphological traits using the Euclidean distance classified the landraces into five groups. The dendrogram revealed that the landraces that are derivatives of genetically similar type clustered together. Clusters were grouped according to their morphological differences. This result is in agreement with Sadia *et al*. (2012) who reported that in cluster analysis, cultivars grouped together with greater morphological similarities, but cluster did not essentially include all the cultivars collected from the same origin.

The inter-cluster distance was found to be highest between cluster I and IV while the lowest inter-cluster distance was found between cluster III and V. The inter-cluster distances were higher than the intracluster distance in all cases reflecting wider diversity among the breeding lines of the distant group. For higher variability in plant breeding, the parent should be selected based on wider inter-cluster distances as also suggested by Mishra *et al.* (2003). The variation observed among the accessions suggests that morphological traits can reveal diversity existing among rice accessions as supported by Efisue *et al.* (2014).

5.3 Agro-morphological Characterization based on Agronomic traits

Analysis of variance revealed highly significant ($p< 0.01$) variations among the landraces for all the observed traits indicating the presence of high variability among the landraces. Thus genetic improvement through selection could be promising. This variation is very important for plant breeders because selection is effective when the magnitude of variability in the breeding population is too high.

The highly significant ($p< 0.01$) variance for days to 50 % flowering among the landraces might be due to the different genetic makeup of the landraces or genotypic environmental

interactions. The availability of early flowering could lead to early maturing genotypes which could be selected for areas with short rain seasons to avoid drought condition and in areas where farmers grow a second crop to take advantage of residual water after harvesting the early rice crop. This result is similar to those previously reported by Weiya *et al*. (2008), they observed variation in days to 50% flowering of several genotypes and identified a regulatory gene responsible for variation in this physiological trait among rice landraces. Too few tillers result in too few panicles as they are directly associated. The highly significant differences for this trait is supported by Rahman *et al*. (2011).

Panicle length and number of panicle per plant directly control the yield of a particular variety (Ashfaq *et al.,* 2012). The panicle number with filled grain determines the yield outcome of the crop. Zahid *et al*. (2005) studied twelve (12) genotypes of coarse rice and reported highly significant variation for a number of panicles per plant. Similar findings were also made by Hassan *et al*. (2003), they concluded that genetic variation was responsible for the significant differences for these traits. Prakash *et al*. (2011) reported that photoperiod, competition among plant population and plant density, exposure to an unfavourable environmental condition, time of planting along interrelationship with various traits also contributes to variation in panicle length among the rice landraces. Plant height is of paramount importance as the reduction of it may develop their resistance to lodging and reduce substantial yield losses associated with this trait. Planting and sowing methods, transplanting date and soil condition could lead to a variation of plant height in rice. This result is in conformity with that of Rashid *et al.* (2017) and Hussain *et al*. (2005). Fathelrahman *et al.* (2015) also found significant differences in plant height. The difference in 100-grain weight among the landraces

studied could be due to grain size and shape. Grain weight provides information about the size and density of the grain. IRRI (2009) reported that longer grains are lighter in weight than medium or bold. This result was in conformity with Judith (2015). The yield of the plant is related to the number of filled grains per panicle. Less number of unfilled grains per panicle is a positive attribute towards higher yield. Significant variation for these traits was also observed by Rashid *et al*. (2017). The highly significant difference ($P < 0.01$) variation for grain yield per plant is supported by Ali *et al*. (2000)**.** Highly significant ($p < 0.01$) variation for the number of filled grain per panicle and number of total grain per panicle is supported by Patil *et al.* (2009) and Singh *et al*. (2015).

5.4 Estimation of Genetic Parameters of Rice Landraces

Greater variability in the initial breeding material ensures better chances of producing desired types of a crop plant (Manik, 2013). The genotypic coefficient of variation (GCV) measures the range of variability in crop and also enables to compare the amount of variability present in different traits (Fathelrahman *et al*, 2015). A wide range of variation was observed for all the agronomic traits. The magnitude of the phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation for all the agronomic traits, this could be due to a higher degree of interaction of genotypes with the environment (Parikh *et al*., 2012). This suggests that environmental effects constitute a major portion of the total phenotypic variation. Thus, the selection of superior genotypes based on such traits would not be effective (Okelola *et al*., 2007). This trend was observed by Kumar *et al*. (2016) and Sarawgi *et al*. (2014).

The highest magnitude of genotypic and phenotypic coefficient of variation observed for grain yield per plant, number of filled grains per panicle, number of unfilled grains per

panicle, number of total grains per panicle, number of panicles per plant and number of leaves per plant indicates that environmental influences on the expression of these traits were minor, therefore, selection can be applied to these traits to isolate more promising line. Higher GCVs indicate that worthwhile improvement could be achieved for such traits through simple selection because environmental influences on the expression of the traits were minor. Similar findings for high estimates of genotypic coefficient of variation and phenotypic coefficient of variation for number of filled grains per panicle and number of total grains per panicle has been reported by Roy *et al*. (2012), Vanisree *et al.* (2013) evaluated 21 rice genotypes for 12 yield and quality traits and found high estimates of GCV for number of filled grains per panicle and grain yield per plant. Mazid *et al.* (2013) evaluated forty-one rice genotypes for 13 morphological traits and observed higher genotypic as well as phenotypic coefficients of variation for a number of filled grains panicles. Similar findings for grain yield was also obtained by Khare *et al.* (2014) and Dutta *et al.* (2013).

Moderate PCV and GCV observed for plant height, panicle length, number of tillers per plant and days to 50% flowering suggests that these traits can be improved by vigorous selection. This result is in conformity with the report of Kumar *et al*. (2016). Moderate estimates of PCV and GCV of plant height and number of tillers per plant have been reported by Tandekar and Koshta (2014) and Parikh *et al*. (2012). The low PCV and GCV exhibited by Days to germination indicates that this trait is less amenable to improvement by selection. Therefore, breeders should go for a source of high variability for these traits to make an improvement.

The high heritability in broad sense observed for all the agronomic traits studied except days to germination indicated that environmental factors did not greatly affect phenotypic variation for these traits; rather a genetic constitution of the landraces was responsible for the variation. This means that these traits are controlled by additive gene effect and response to selection can be predicted. The high heritability estimates for plant height, panicle length, grain yield per plant and hundred seed weight were in confirmation with the previous report of Parikh *et al*. (2012). The finding of high heritability estimates for days to 50% flowering is in accordance with the finding of Khare *et al.* (2014). Similar results of high heritability for plant height were observed by Ahmed *et al.* (2010). Khalid *et al*. (2012) estimated high heritability (>85%) for plant height, number of tillers per plant and 100-grain weight. High heritability in days to 50% flowering was also reported by Das *et al.* (2005) who assessed 22 semi deep-water rice genotypes for genetic variability, heritability and genetic advance.

5.5 Pearson's Correlation Co-efficient Analysis of the Agronomic Traits

Traits with significant positive correlation with grain yield means that any increase in these traits could result in an increase in the grain yield and would be ideal for selection to improve rice grain yield. The positive and significant correlation of grain yield per plant with number of filled grains per panicle and number of total grains per panicles revealed that they could be used to predict grain yield and selection for these traits will be useful in improving grain yield, this finding is in agreement with the results of Ekka *et al*. (2011) who reported that grain yield per plant had positive significant correlation with number of filled grains per panicle. Khare *et al.* (2014) observed a positive and significant correlation of total grains per panicle with grain yield per plant. Manik (2013)

also revealed the positive and significant correlation of grain yield per plant with the number of filled grains per panicle and number of total grains per panicles when evaluating the performance of 32 exotic early maturing rice.

Plant height had a positive correlation with panicle length showing the importance of plant height in improving panicle length in rice. This result was in agreement with Chakravorty and Ghosh (2012) whose correlation analysis indicated that plant height had a positive and significant correlation with panicle length and grain weight. This is also supported by Sadia *et al*. (2012), Emanuel (2014) and Kumar *et al*. (2016). They all reported that plant height had a highly significant and positive correlation with panicle length.

5.6 Genetic Relationship based on Agronomic Descriptors

The reason for the high level of similarity coefficient among the landraces could be due to intra-specific variation in the germplasm used. Siwach *et al*. (2004) reported a high coefficient of similarity ranging from 0.67 to 0.91 in rice. According to Abubakar *et al.* (2011), high heterosis could be achieved by crossing between landraces with low similarity coefficient. Maximum heterosis is expected when genotypes from distant clusters are crossed.

The dendrogram reveals that the genotypes that are genetically similar cluster more together. The independent grouping of Yar china-KB indicated that it is genetically different from other landraces. This landrace had desirable agronomic traits and could serve as a source of genes to bring genetic diversity for rice improvement. The lowest mean value for plant height, days to 50% flowering and days to maturity indicated that landraces in this cluster could be used as parents for developing short duration varieties.

Cluster III comprised of the genotypes with highest mean values for panicle length and 100 grain, Thus the landraces in these clusters are good for improving yield contributing traits. The distribution pattern of landraces did not show any distinctive clustering pattern which could be due to the admixture of landraces over time.

5.7 Genetic Diversity Studies of Rice using SSR Markers

Molecular characterization is the alternative strategy to overcome the several limitations of morpho-agronomic traits characterization of genetic materials. The average number of alleles per locus (4.00) obtained in the present study were comparable with the earlier reports by Pervaiz *et al.* (2010) who reported an average of 4.4 alleles using 32 microsatellite markers in Pakistani rice landraces and Rahman *et al.* (2012) reported an average 4.18 alleles per locus. The number of alleles detected in the present study was higher than those observed by Meti *et al*. (2013) who detected 2.08 alleles per locus using 48 traditional indigenous aromatic rice germplasm. Singh *et al*. (2016) reported 3.11 alleles per locus with SSR markers during characterization of 729 rice varieties. The mean alleles were lower than that of Claudio *et al*. (2006) who reported a range of 6-22 numbers of alleles per primer with an average of 14.7 alleles per locus. Das *et al*. (2013) reported 7.9 alleles per locus using Indian landraces comprising different cultivar group. The discrepancy in the number of alleles might be due to the difference in the sets of germplasms, the number of genotypes used and distribution of SSR loci and methods of gel electrophoretic detection in different studies. The low number of alleles was usually obtained from a collection of breeding lines and closely related cultivars. A high number of alleles was expected to be found when a large number of landraces from a wide range of geographic origins are included in the study.

The average genetic diversity of 0.50 obtained was comparable to 0.55 previously reported by Sajib *et al*. (2012), who used 9 SSR markers to study genetic diversity among 12 aromatic landraces of rice. Nachimuthu *et al*. (2015) also reported an average of 0.52. The gene diversity obtained in the present study was quite low as compared to Gour *et al*. (2017) who reported genetic diversity range of 0.00 to 0.66 with an average of 0.39 with SSR markers. Sajib *et al*. (2012) also found a moderate level of diversity exists among 9 loci studied across 12 rice accessions, ranged from 0.15 to 0.75 with an average of 0.54. Islam *et al*. (2015) observed that the gene diversity at each SSR locus was significantly correlated with the number of alleles detected, number of repeat motif and with the allele size range.

The range of 0.29 to 0.86 with an average of 0.62 for major allele frequency is in agreement with the work of Judith (2015) who reported major allele frequency of 0.63 and Gour *et al*. (2017) reported an average major allele frequency of 0.67. Kumar (2016) also reported a comparable average of major allele frequency of 0.63. Vu *et al.* (2016) studied the genetic diversity in a set of 40 lowland rice varieties using 30 simple sequence repeat (SSR) markers covering all rice chromosomes and found major allele frequency at each locus ranged from 0.33 to 0.7.

The PIC range and average observed in this study are similar to those reported earlier by Kumar *et al*. (2016) they reported PIC value ranged from 0.28 to 0.64 with a mean of 0.47. The mean PIC value was also supported by Judith (2015) who characterize 191 landraces of rice using 16 markers and found average PIC of 0.49. Pervaiz *et al.* (2010) reported a PIC range of 0.12 to 0.84 with an average of 0.57. Nadia *et al*. (2014) assessed genetic diversity of twenty-six landraces rice and four high yielding rice accessions on

the basis of twenty-seven simple sequence repeat (SSR) markers which generated 321 polymorphic alleles. Polymorphic information content (PIC) values ranged between 0.68 (RM 11) and 0.94 (RM 474) with an average of 0.84. Vu *et al.* (2016) studied the genetic diversity in a set of 40 lowland rice varieties using 30 simple sequence repeat (SSR) and found Polymorphic information content value varied from 0.36 to 0.77 with an average of 0.59. The difference in PIC mean value might be linked with the selection of different markers and a more diverse set of varieties. According to Kumar *et al*. (2012), the markers with a PIC value of 0.5 or higher indicate that they are highly informative and extremely useful in distinguishing the polymorphism rate of a marker at a specific locus. The highest PIC value was obtained for RM 236 marker and was considered as the best marker. However, 8 SSR markers showed PIC values of 0.5 or more which indicated they were highly informative. Higher values of PIC might be the result of diverse genotypes and lower values may be the result of closely related genotypes (Ibrahim, 2015).

Four major cluster groups based on the genetic diversity of rice landraces was unable to categorise the landraces based on the state of the collection because landraces from the same state were found in different clusters as well as in the same cluster. This indicates that although genetic diversity is generally associated with geographical diversity, factors other than geographical separation are also responsible for divergence, which might be due to selection, genetic drift and frequent exchange of genetic materials among breeders and farmers of different locations for cultivation. A similar observation was also reported by Judith (2015) and Chakma *et al.* (2012).

CHAPTER SIX

6.0 SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

6.1 SUMMARY

The study was carried out to evaluate the agro-morphological characteristics and genetic diversity of rice landraces in savanna zones of Nigeria. A total of seventy rice landraces were used. They were evaluated for 15 qualitative morphological (Basal leaf sheath colour, Leaf blade colour, Leaf tip colour, Leaf margin colour, Junctura Colour, Ligule colour, Auricle colour, Internode colour, Node colour, Stigma colour, Apiculus colour, Awning, Sterile glume colour, Chalkiness of endosperm and Seed colour) and 12 quantitative agronomic traits (Days to Germination, Days to 50% flowering, Number of tillers per plant, Number of leaves per plant, Plant height (cm), Panicle length (cm), Number of panicles per plant, Number of filled grains per panicle, Number of unfilled grains per panicle, Number of total grains per panicle, One hundred seed weight (g) and Grain yield per plant) using standard evaluation system for rice. Molecular characterization was also carried out using 2k1 SSR markers.

The result of agro-morphological traits showed significant ($p < 0.01$) variability for all the traits while the result of molecular markers showed seven markers (R518M, R216M, RM235, RM236, RM566, RM555, RM515 and RM332) to be highly informative. The genetic diversity revealed close clustering patterns of the landraces at a similarity coefficient of 95%.

6.2 CONCLUSIONS

1. Highly significant ($p < 0.01$) variability was obtained in all qualitative and quantitative traits evaluated. Mean values for yield-related agronomic traits are thus presented: Number of tillers per plant (5.46), days to 50% flowering (97.79), number of total grains (50.77) and grain yield per plant (2.35g). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was highest for grain yield per plant (80.37% and 77.83%). Broad-sense heritability estimates were highest in hundred seed weight (99.32%). A positive correlation for a number of filled grain per panicle ($r = 0.94$) and total grain per panicle ($r = 0.53$) with grain yield was obtained. The high yielding landraces were WACOT (9600kg/ha), Yar china-KB (858.18kg/ha), Jamila PLT (589.09kg/ha) and Yar Zaiti (560kg/ha). The qualitative and quantitative agro-morphological traits of the rice landraces from Nigeria savanna region at a similarity coefficient of 60% and 91% respectively showed distinct variation in morphology.
2. Seven markers (R518M, R216M, RM235, RM236, RM566, RM555, RM515 and RM332) were highly informative for genetic evaluation of rice landraces in Northern Nigeria. PIC values ranged from 0.53 - 0.73. The landraces showed close clustering patterns at a similarity coefficient of 95%.

6.3 RECOMMENDATIONS

1. Rice landraces with highest genetic dissimilarity and traits of interest could be selected and used in breeding programs.

2. The high yielding landraces WACOT (9600kg/ha), Yar china-KB (858.18kg/ha), Jamila PLT (589.09kg/ha) and Yar Zaiti (560kg/ha) could be incorporated in rice breeding program.

3. R518M, R216M, RM235, RM236, RM566, RM555, RM515 and RM332 could be used in determining the genetic diversity of rice landraces.

4. These landraces could be further evaluated for both biotic and abiotic stresses.

Plate I. Rice Landraces

a: At Seedling Stage

b: Showing Green Basal Leaf Sheath

b: Showing purple basal leaf sheath

d: At Maturity Stage

REFERENCES

Abubakar, B. Y. M., Wusirika, R., Muazu, S., Khan, A. U. and Adamu, A. K. (2011). Detection of Genetic Variability using Random Polymorphic DNA Markers in Some Accessions of *Moringa oleifera* Lam. from Northern Nigeria. *International Journal of Botany*, 7(3): 237-242.

Acquaah, G. (2007). *Principles of Plant Genetics and Breeding*. Blackwell publishing Ltd. UK. 569p.

Adegbaju, M. S., Akinyele, B. O., Akinwale, M. G., Igwe, D. and Osekita, O. S. (2015). Molecular Characterization and Genetic Diversity Analysis of Elite African Lowland Rice Varieties using SSR Marker System. *International Journal of Research Studies in Biosciences*, 3(10): 54-65, *www.arcjournals.org.*

Afiukwa, C. A., Faluyi, J. O., Atkinson, C. J., Ubi, B. E., Igwe, D. O. and Akinwale, R. O. (2016). Screening of Some Rice Varieties and Landraces Cultivated in Nigeria for Drought Tolerance based on Phenotypic Traits and their Association with SSR Polymorphisms. *African Journal of Agricultural Research*, 11(29): 2599-2615. doi: 10.5897/AJAR2016.11239.

Ahmad, H., Razvi, S. M., Ashraf, B. A., Najeeb, S., Wani, N., Habib, M., Mir, M. R. and Gupta, B. B. (2010). Genetic Variability and Genetic Divergence of Important Rice (*Oryza sativa* L.) Varieties. *International Journal of Current Resources*, 4: 033-037.

Ahmad, N. S. (2013). Genetic Analysis of Plant Morphology in Bambara Groundnut (*Vigna subterranea*(L.) Verd c.). PhD thesis, University of Nottingham. http://eprints.nottingham.ac.uk/13150/1/thesis for_Nariman Ahmadpdf.

Ahmad, F., Hanafi, M. M., Hakim, M. A., Rafii, M. Y., Arolu, I. W. and Akmar, A. S. N. (2015). Genetic Divergence and Heritability of 42 Coloured Upland Rice Genotypes (*Oryza sativa*) as revealed by Microsatellites Marker and Agro-Morphological Traits.
Plos One, 10(9). doi:10.1371/journal.pone.0138246

Ahmed, M. S., Bashar, M. K. and Shamsuddin, A. K. M. (2016). Study of Qualitative Characters of Balam Rice (*Oryza sativa* L.) Landraces of Bangladesh. *Rice Genomics and Genetics*, 7(1): 1-8. doi: 10.5376/rgg.2016.07.0001.

Akinwale. M. G., Akinyele, B. O., Odiyi, A. C., Nwilene, G. and Oyetunji, O. E. (2012). Phenotypic Screening of Nigeria Rain fed Lowland Mega Rice Varieties for Submergence Tolerance, In: *proceedings of the World Congress on engineering,* Vol. 1 WCE 2012, London, UK. ISBN: 978-988-19251-3-8.

Akpokodje, G., Lanco, F. and Erentein, O. (2001). The Nigerian Rice Economy in a Competitive World: Constraints, Opportunities and Strategic Choices. Nigeria's Rice Economy: State of the Art. WARDA, Bouake, Cote d Ivoire. November, 2001, pp. 12 7-38.

Ali, S. S., Jafri, S. J. H., Khan, T. Z., Mahmood, A. and Butt, M. A. (2000). Heritability of Yield and Yield Components of Rice. *Pakistan Journal of Agricultural Resources*, 16: 89-91.

Aliyu, R. E., Wasiu, A. A., Dangora, D. B., Ademola, J. O. and Adamu, A. K. (2013). Comparative Study of Genomic DNA Extraction Protocol in Rice species. *International Journal of Advancement in Research and Technology*, 2(2): 1-3.

Anderson, J. A., Churchill, G. A., Autrique, J. E., Tanksley, S. D. and Sorrels, M. E. (1993). Optimizing Parent Selection for Genetic Linkage Maps. *Genome*, 36(1): 181-186.

Arif, M., Waheed, R., Muqaddasi, Q. H., Ahmed, Z. and Khalid, M. (2016). Use of Bulk Segregant Analysis for Varietal Identification and Genetic Diversity Estimation in Pakistani Basmati and Non-basmati Rice Cultivars through Molecular Markers. *Advanced Crop Science Technology*, 4: 227. doi:10.4172/2329-8863.1000227.

Ashfaq, M., Khan, A. S., Khan, S. H. U. and Ahmad, R. (2012). Association of Various Morphological Traits with Yield and Genetic Divergence in Rice (*Oryza sativa* L.). *International Journal of Agricultural Biol*ogy, 14: 55-62.

Bachmann, K. (1994). Tansley review no. 63: Molecular markers in plant ecology. *New phytologist*, 126: 403-418.

Bakari, M. M. (2010). *Genetic Diversity of some Rice (Oryza sativa L.) Landraces Grown in Tanzania using Simple Sequence Repeat (SSR) Markers*. Dissertation for award of M. Sc. Degree at Sokoine University of Agriculture, Morogoro, Tanzania, p. 72.

Bashir, M. U., Akbar, N., Iqbal, A. and Zaman, H. (2010). Effect of Different Sowing Dates on Yield and Yield Components of Direct Seeded Coarse Rice (*Oryza sativa* L.*). Pakistan Journal of Agricultural Science*, 47: 361-365.

Belsnio, B. (1980). The Anatomy and Physical Properties of Rice Grain Towards Integrated Commodity and Pest Management in Grain Storage. FAO, Rome.

Bhadru, D., Rao, V. T., Mohan, Y. C. and Bharathi, D. (2012). Genetic Variability and Diversity Studies in Yield and its Component Traits in Rice (*Oryza sativa* L.). *Journal of Breeding and Genetics*, 44(1): 129-137.

Biswash, M. R., Sharmin, M., Rahman, N. M. F. and Siddique, M. A. (2016). Genetic Diversity in Modern T. Aman Rice Varieties of Bangladesh (*Oryza sativa* L.). *Sains Malaysiana*, 45(5): 709-716.

Brown, A. H. D. (2008). Indicators of Genetic Diversity, Genetic Erosion and Genetic Vulnerability for Plant Genetic Resources. Thematic Background Study, State of Worlds Plant Genetic Resources. Food and Agriculture Organization, Rome, Italy. 278-290.

Burton, G. W. (1952). Quantitative Inheritance in Grasses. *In proceedings of sixth International Grassland Congress Ames, Iowa*, USA, pp. 227-283.

.

Camachovilla, T. C., Maxted, N., Scholten, M. and Ford-lloyd, B. (2005). Defining and Identifying Crop Landraces. *Plant Genetic Resources*, 3: 373-384.

Chakma, S. P., Huq, H., Mahmud, F. and Husna, A. (2012). Genetic Diversity Analysis in Rice (*Oryza sativa L.*). *Bangladesh Journal of Plant Breeding and Genetics*, 25(1): 31-39.

Chakravorty, A. and Ghosh, P. D. (2012). Grain Dimension Studies in View of Kernel Weight Development in Traditional Rice of West Bengal. *International Journal of Biosciences*, 10(2): 95-102.

Chakravarthi, B. K. and Naravaneni, R. (2006). SSR Marker Based DNA Fingerprinting and Diversity Study in Rice (*Oryza sativa* L). *African Journal of Biotechnology*, 5(9): 684-688.

Claudio, B., Tereza, C. B., Paulo, H. R. and Rosana, P. B. (2006). Determination of Genetic Variability of Traditional Varieties of Brazilian Rice using Microsatellite Markers. *Genetics and Molecular Biology*, 29(4): 676-684.

Counce, P. A., Keisling, T. C. and Mitchell, A. J. (2000). A Uniform, Objective and Adaptive System for Expressing Rice Development. *Crop Science*, 40(2): 436-443.

Das, R., Borbora, T. K., Sharma, M. K. and Sharma, N. K. (2005). Genotypic Variability for Grain Yield and Flood Tolerance in Semi-deep Water Rice (*Oryza sativa* L.) of Assam. *Oryza*, 42(4): 313-314.

Das, B., Sengupta, S., Parida, S. K., Roy, B., Ghosh, M., Prasad, M. and Ghose, T. K. (2013). Genetic Diversity and Population Structure of Rice Landraces from Eastern and North Eastern States of India. *BMC Genetics*. 14: 71.

David, B. (2014). Yield Response of Rice in Nigeria: A Co-integration Analysis. *American Journal of Agriculture and Forestry*, 2(2): 15-24. doi:10.11648/j.ajaf.20140202.11.

DeWoody, J. A., Honeycutt, R. L. and Skow, L. C. (1995). Microsatellite Markers in White-Tailed Deer. *Journal of Heredity*. 86: 317-319.

Doyle, J. J. and Doyle, J. L. (1990). Isolation of Plant DNA from Fresh Tissue. *Focus*, 12(1): 13-15.

Duran, C., Appleby, N., Edwards, D. and Batley, J. (2009). Molecular Genetic Markers: Discovery, Applications, Data Storage and Visualisation. *Current Bioinformatics*, 4: 16-27.

Dutta, P., Dutta, P. N. and Borua, P. K. (2013). Morphological Traits as Selection Indices in Rice: *A Statistical View Universal Journal of Agricultural Research*, 1(3): 85-96.

Efisue, A. A., Umunna, B. C. and Orluchukwu, J. A. (2014). Effect of Yield Components on Yield Potential of some Lowland Rice (*Oryza sativa* L.) in Coastal Region of Southern Nigeria. *Journal of Plant Breeding and Crop Science*, 6(9): 119-127.

Ekka, R. E., Sarawgi, A. K. and Kanwar, R. R. (2011). Correlation and Path Analysis in Traditional Rice Accessions of Chhattisgarh. *Journal of Rice Research*, 4(1): 11-17.

Emmanuel, A. M. (2014). *Genetic Diversity of Rice (Oryza sativa L.) Landraces Conserved at the National Gene bank as Revealed by Simple Sequence Repeat (SSR) DNA Markers.* Dissertation for Award of M.Sc. Degree at Sokoine University of Agriculture, Morogoro, Tanzania.

FAO. (2000). Rice Information. Food and Agricultural Organization of the United Nations, Rome, Italy. 2: 20-27.

FAO (2011). Http://faostat.fao.org/.

Fathelrahman, S. A., Alsadig, A. I. and Dagash, Y. I. (2015). Genetic Variability in Rice Genotypes (*Oryza Sativa* L.) in Yield and Yield Component under Semi-Arid Zone (Sudan). *Journal of Forest Products and Industries*, 4(2): 21-32.

Fischer, K. S., Barton, J., Khush, G. S., Leung, H. and Cantrell, R. (2000). Collaborations in Rice. *Science*, 290: 279 - 280.

Fisseha, W. K. (2014). *Genetic Diversity in Rice based on SSR Markers, Morpho-agronomic Characters and Resistance to Brown Planthopper* (*Nilaparvata lugens* Stal). Thesis for award of Doctor of Philosophy at Kasetsart University.

Food and Agriculture Organization of the United Nations (FAO, 2016). Food Outlook: Biannual Report on Global Food Markets, ISSN: 0251-1959.

Gao, L. Z. (2003). The Conservation of Chinese Rice Biodiversity: Genetic Erosion, Ethnobotany and Prospects. *Genetic Resources of Crop Evolution*, 50: 17-32.

Gour, L., Koutu, G. K., Singh, S. K. and Mishra, D. K. (2017). Genetic Potency Identification of Indigenous Rice (*Oryza sativa* L.) Lines using Quality Assessment and SSR Marker Analysis. *International Journal of Chemical Studies*, 5(4): 97.

Gregorio, G. B., Senadhira, D. and Mendoza, R. D. (1997). Screening Rice for Salinity Tolerance. IRRI Discussion Paper series No. 22, PP. 1-31. International Rice Research Institute, Metro Manila, Philippines.

Hassan, G., Khan, N. U. and Khan, Q. N. (2003). Effect of Transplanting Date on the Yield and Yield Components of Different Rice Cultivars under High Temperature of Dera Ismail Khan. *Sci. Khy*. 16: 129-137.

Hassan, M. M., Shamsuddin, A. K. M., Islam M. M., Khatun, K. and Halder, J. (2012). Analysis of Genetic Diversity and Population Structure of some Bangladeshi Rice Landraces and High Yielding Varieties. *Journal of Science Resources*, 4 (3): 757-767. http://dxdoi.org/10.3329/jsr.v4i3.10416.

Haward, N. (2009). Botanical Classification of Rice. Agropedia http://agropedia .iitk.ac.in/content/botanical-classification-rice.

He, G. M., Luo, X. J. M., Tian, F., Li, K. J. G., Zhu, Z. F., Su, W., Qian, X. Y., Fu, Y. C., Wang, X. K., Sun, C. Q. and Yang, J. S. (2006). Haplotype Variation in Structure and Expression of a Gene Cluster associated with a Quantitative Trait Locus for Improved Yield in Rice. *Genome Resources.* 16(5): 618-626.

Herrera, T. H., Duque, D. P., Almeida, I. P., Nunez, G. T., Pieters, A. J., Martinez, C. P. and Tohme, J. M. (2008). Assessment of Genetic Diversity in Venezuelan Rice Cultivars using Simple Sequence Repeats Markers. *Electronic Journal of Biotechnology*, 11(5): 1-4. Doi:10.2225/vol11 issue5-full text-6.

Hien, N. L., Sarhadi, W. A., Hirata, Y. and Oikawa, Y. (2007). Genetic Diversity of Morphological Responses and the Relation among Asia Aromatic Rice (*Oryza sativa* L.) Cultivars. *Tropics*, 16: 343-355.

Hossain, M. M., Islam, M. M., Hosain, H., Ali, M. S., Teixeiradasilva, J. A., Komamine, A. and Prodhan, S. H. (2012). Genetic Diversity analysis of Aromatic Landraces of Rice (*Oryza sativa* L.) by Microsatellite Markers. *Genomics*, 6: 42-47.

Hoque, A., Begun, S. N. and Hassan, L. (2014). Genetic Diversity Assessment of Rice (*Oryza sativa* L.) Germplasm using SSR markers. *Research in Agriculture, livestock and fisheries,* 1(1): 37-46.

Hussain, S., Ramzan, M., Aslam, M., Zaheen, M. and Ehsan, S. M. (2005). Effect of Various Stand Establishment Method on Yield and Yield Components of Rice. *Proceedings of the International Seminar on Rice Crop*. October 23. Rice Research Institute, Kala Shah Kau, Pakistan. 212-220.

Ibrahim, S. (2015). *Genetic Diversity Analysis of Rice Germplasm (Oryza sativa, Oryza glaberrima) using Morphological and Molecular Markers*. Theses M. phil. Agronomy Kwame Nkrumah University of Sceince and Technology, Kumasi, Ghana.

International Rice Research Institute (IRRI, 2009). Introduction to Seed Management; Available at http//www.knowledgebank.irri.org/qualityseed. Accessed 18/12/09.

IRRI (2013). Annual Report for 2013. Los Banos, Laguna, Philippines. pp.525.

Ishi, T., Xu, Y. and Mccounch, S. R. (2001). Nuclear and Chloroplast Microsatellite Variation in A-Genome species of Rice. *Journal of Genome,* 44: 658-666.

Islam, S. N., Islam, M. M., Mohammad, A. U. and Alam, M. S. (2015). Molecular Characterization of Selected Landraces of Rice for Salt Tolerance using SSR Markers. *International Journal of Innovation and Scientific Research,* 17(1): 206-218. http://www.ijisr-journals.org/.

Jin, L., Lu, Y., Xiao, P., Sun, M., Corke, H. and Bao, J. (2010). Genetic Diversity and Population Structure of a Diverse Set of Rice Germplasm for Association Mapping. *Theoretical and Applied Genetic*s, 121: 475–487.

Jing, Q., Spiertz, J. H. J., Hengsdijk, H., Keulen, H. V., Cao, W. and Dai, T. (2010). Adaptation and Performance of Rice Genotypes in Tropical and Subtropical Environments NJAS Wageningen. *Journal of Life Sciences,* 57(2): 149-157.

Jones, D. B. and Synder, G. H. (1987). Seeding Rate and Row Spacing Effects on Yield and Yield Components of Drill Seeded Rice. *Agronomy Journal*, 9:623-626.

Judith, J. (2015). *Morphological, Molecular and Quality Characterization of Rice Varieties and Landraces from Eastern and Southern Africa*. Msc Thesis, University of Sokoine Agriculture. Morogoro, Tanzania.

Kamarouthu, D. (2013). Study of Genetic Diversity in Karnataka Rice (*Oryza sativa* L.) Landraces using Trait Specific Simple Sequence Repeat (SSR) Markers. *International Journal of Thesis Projects and Dissertations,* 1:45-70.

Khalid, A. O., Ahmed, M. M., Ali, F., Zheng, Y. and Fazhan, Q. (2012). Genetic Variability for Yield and Yield Related Attributes of Upland Rice Genotypes in Semi-arid Zone (Sudan). *African Journal of Agriculture,* 7(33): 4613-4619.

Khare, R., Singh, A. K., Eram, S. and Singh, P. K. (2014). Genetic Variability, Association and Diversity Analysis in Upland Rice (*Oryza sativa* L.), *SAARC Journal of Agriculture,* 12(2): 40-51.

Krupa, K. N., Shashidhar, H. E., Ningaraj, D., Mahendra, R. and Swamy, H. V. (2017). Molecular Marker based Genetic Diversity Analysis in Rice Genotypes (*Oryza sativa* L.) using SSR Markers. *International Journal of Pure and Applied Bioscience,* 5 (2): 668-674. DOI: http://dx.doi.org/10.18782/2320-7051.2892.

Kumar, V. (2016*). Characterization, Inheritance and Allelic Relationship Study of Gene(s) Governing Aroma and Quality Traits in Rice (Oryza sativa* L.*)* Ph. D. Thesis, Faculty of Agriculture Indira Gandhi Krishi Vishwavidyalaya Raipur (Chhattisgarh)

Kumar, V., Rastogi, N. K., Sarawgi, A. K., Chandraker, P., Singh, P. K. and Jena, B. K. (2016). Agro-morphological and Quality Characterization of Indigenous and Exotic Aromatic Rice (*Oryza sativa* L.) Germplasm. *Journal of Applied and Natural Science,* 8 (1) : 314 – 320.

Kura, M. U. (2009). Rice Production in Kano State: Current Status and Prospect. Paper Presented at the Stakeholders Workshop on Kano State Rice Development Policy, Kano. October, 2009. pp. 2-3.

Langridge, P. and Chalmer, K. (2004). Biotechnology in Agriculture and Forestry, Molecular Marker Systems (ed. By H. Lorz and G. Wenzel), pp. 38.

Linares, O. F. (2002). The History and Future of African Rice. www.jstor.org//stable 40175114. [Accessed 2015 January 10].

Liu, K. and Muse, S. V. (2005). Power Marker: Integrated Analysis Environment for Genetic Marker Data. *Bioinformatics,* 21: 2128-2129. http://dx.doi.org/10.1093/bioinformatics/bti

Longtau, S. R. (2003). Multi-Agency Partnerships in West African Agriculture: A review and Description of Rice Production Systems in Nigeria. Document Prepared by the Overseas Development Institute (ODI) London.

Loresto, G. C., Guevarra, E. and Jackson, M. T. (2000). Use of Conserved Rice Germplasm. *Plant Genetic Resources,* 124:51-56.

Ma, H., Yin, Y., Guo, Z. F., Cheng, L. J., Zhang, L., Zhong, M. and Shao, G. J. (2011). Establishment of DNA Fingerprinting of Liaojing Series of Japonica Rice. *Middle East Journal of Scientific Research,* 8(2): 384-392.

Mackill, D. J., Nguyen, H. T. and Zhan, J. (1999). Use of Molecular Markers in Plant Improvement Programs For Rainfed Lowland Rice. *Field Crop Resources*. 64: 177-185.

Maclean, J. L., Dawe, D. C., Hardy, B. and Hettel, G. P. (2002). Rice lmanae. Los Banos (Pilippines): International Rice Research Inistitute, Buake (Coted'lvorie): West Africa Rice Development Association, Cali (Colombia): International Centre for Tropical Agriculture, Rome (Italy): Food and Agriculture Organization, 253p.

Manik, S. (2013*). Morphological and Molecular Characterization of some Exotic Early Maturing Rice Lines*. M. Sc. Thesis Bangladesh Agricultural University Mymensingh- 2202.

Mazid, M. S., Rafii, M. Y., Hanafi, M. M., Rahim , H. A., Shabanimofrad, M. and Latif, M. A. (2013). Agro-Morphological Characterization and Assessment of Variability, Heritability, Genetic Advance and Divergence in Bacterial Blight Resistant Rice Genotypes. *South African Journal of Botany*, 86: 15–22.

McCouch, S. R., Chen, X., Panaud, O., Temnykh, S., Xu, Y., Chao, Y. G., Huang, N., Ishii, T. and Blair, M. (1997). Microsatellite Marker Development, Mapping and Applications in Rice Genetics and Breeding. *Plant Molecular Biology*, 35: 89-99.

McCouch, S. R., Kochert, G., Yu, Z. H., Wang, Z. Y. and Khush, G. S. (1998). Molecular Mapping of Rice Chromosomes. *Theoretical and Applied Genetics*, 76: 815 - 829.

Meti, N., Samal, K. C. Bastia, D. N. and Rout, G. R. (2013).Genetic Diversity Analysis in Aromatic Rice Genotypes using Microsatellite based Simple Sequence Repeats (SSR) Marker. *African Journal of Biotechnology*, 12(27): 4238-4250.

Meti, N., Samal, K. C., Bastia, D. N. and Rout, G. R. (2014). Genetic Diversity Analysis in Aromatic Rice Genotypes using Microsatellite based Simple Sequence Repeats (SSR) Marker. *African Journal of Biotechnology*, 12(27): 4238-4250.

Mishra, K. K., Vikram, P., Yadav, R. B., Swamy, B. P. M., Dixit, S., Stacrum, M. T. and Maturan, P. (2013). qDTY 12.1 : A Locus with a Consistent Effect on Grain Yield under Drought in Rice. *BMC Genetics*,12: 12.

Mishra, A., Kumar, P., Singh, R. S., Yadav, M. K., Kumar, M. and Chaudhary, P. C. R. (2017). Assessment of Quality based Diversity by using Morphological and Molecular Approaches of Selected Rice (*Oryza sativa* L.) Varieties. *Progress Agriculture*, 17 (1): 52-64. DOI : 10.5958/0976-4615.2017.00022.9.

Mittal, N. and Dubey, A. K. (2009). Microsatellite Markers- A New Practice of DNA based Markers in Molecular Genetics. *Pharmacognosy Review*, 3 (6): 235-246.

Muhammad, S., Khan, S. A., Khurshid, H., Iqbal, J. A., Muhammad, N. S. and Shah, S. M. A. (2015). Characterization of Rice (*Oryza sativa* L.) Germplasm through Various Agro-Morphological Traits. *Scientia Agriculturae,* 9(2): 83-88. doi:10.15192/PSCP.SA.2015.9.2 .8388.

Nachimuthu, V. V., Muthurajan, R., Duraialaguraja, S., Sivakami, R., Pandian, B. A. and Ponniah, G. (2015). Analysis of Population Structure and Genetic Diversity in Rice Germplasm using SSR Markers: An Initiative Towards Association Mapping of Agronomic Traits in *Oryza sativa*. *Rice*, 8: 30-54.

Nadia, I., Mohiuddin, A. K. M., Sultana, S. and Ferdous, J. (2014). Diversity Analysis of Indica Rice Accessions (*Oryza sativa* L.) using Morphological and SSR Markers. *Annals of Biological Research*, 5(11): 20-31.

Ni, J., Colowit, P. M. and Mackill, D. J. (2002). Evaluation of Genetic Diversity in Rice Sub Species using Microsatellite Markers. *Crop Science*, 42: 601-607.

Ogunbayo, S. A., Ojo, D. K., Guei, R. G., Oyelakin, O. O. and Sanni, K. A. (2005). Phylogenetic Diversity and Relationships among 40 Rice Accessions using Morphological and RAPDs Techniques. *African Journal of Biotechnology*, 4 (11): 1234-1244. http://www.academicjournals.org/AJB.

Okelola, F. S., Adebisi, M. A., Kehinde, O. B. and Ajala, M. O. (2007). Genotypic and Phenotypic Variability for Seed Vigour Traits and Seed Yield in West African Rice (*Oryza sativa* L.) Genotypes, *Journal of American Science*, 3(3): 34-41.

Oko, A. O., Ubi, B. E. and Efisue, A. A. (2012). A Comparative Study on Local and Newly Introduced Rice Varieties in Ebonyi State of Nigeria based on Selected Agronomic Characteristics. *International Journal of Agriculture and Forestry,* 2(1): 11-17. Doi:10.5923/j.ijaf.20120201.03.

Oluwaseyi, A. B., Nehemmiah, D. and Zuluqurineen, S. B. (2016). Genetic Improvement of Rice in Nigeria for Enhanced Yield and Grain Quality- A Review. *Asian Research Journal of Agriculture.* 1(3):1-18. Doi:10.9734/ARJA/2016/28675.

Omotola, K. A. and Ikechukwu, A. (2006). Rice Milling in Nigeria, Internet, http://www.ricenigeria.com.

Panda, D., Rao, D. N., Sharma, S. G., Strasser, R. J. and Sarkar, R. K. (2006). Submergence Effects on Rice Genotypes during Seedling Stage: Probing of Submergence driven Changes of Photosystem 2 by Chlorophyll a Fluorescence Induction O-JI-P Transients.

Parikh, M., Motiramani, N. K., Rastogi, N. K. and Sharma, B. (2011). Characterization and Assessment of variability in Aromatic Rice Germplasm. *Progress Agriculture,* 11(2): 343-347.

Parikh, M., Motiramani, N. K., Rastogi N. K. and Sharma, B. (2012). Agro-morphological Characterization and Assessment of Variability in Aromatic Rice Germplasm. *Bangladesh Journal of Agricultural Resources*, 37(1): 1-8.

Park, Y., Lee, J. K. and Kim, S. (2009). Simple Sequence Repeat Polymorphisms (SSRPs) for Evaluation of Molecular Diversity and Germplasm Classification of Minor Crops, *Molecules*, 14: 4546-4569. doi: 10.3390/molecules/4//4546.

Patil, S. G., Sahu, V. N. and Deokar, P. A. (2009). Study of Variability of Rice Germplasm Accessions used for Wild Rice Eradication. *International Journal of Plant Sciences Muzaffarnagar,* 4(2): 535-537.

Peng, S. B., Huang, J. L., Sheehy, I. E., Laza, R. C., Visperas, R. M., Zhong, X. H., Centeno, G. S., Khush, G. S. and Cassman, K. G. (2003). Rice Yields Decline with Higher Night Temperature from Global Warming. *Proceedings of the National Academy of Sciences of the United States of America,* 101(27): 9971-9975.

Pervaiz, Z. H., Ashiq, M. R., Ishtiaq, K., Stephen, R. P. and Salman, A. M. (2010). Genetic Diversity Associated with Agronomic Traits using Microsatellite Markers in Pakistani Rice Landraces. *Electronic Journal of Biotechnology,* 13(3): 0717-3458.

Prakash, M., Anandan, A. and Kumar, S. B. (2011). Varietal Variations in Flag Leaf Area and Yield in Mutant Lines of PY5 Rice. *Journal of Agricultural Scien*ce, 24 (4): 525-526.

Prasad, S. V., Sujatha, M., Rao, S. L. V. and Chaithanya, U. (2013). Studies on Variability, Heritability and Genetic Advance for Quantitative Characters in Rice (*Oryza sativa* L.). *Annals of Biological Research,* 4(6): 372-375.

Punch (2017). Rice production in Nigeria increases to 5.8m tonnes in 2017**.** https://punchng.com/rice-production-in-nigeria-increases-to-5-8m-tonnes-in-2017-rifan/.

Rabbani, M. A., Pervaiz, Z. H. and Masood, M. S. (2008). Genetic Diversity Analysis of Traditional and Improved Cultivars of Pakistani Rice (*Oryza sativa* L.) using RAPD Markers. *Electronic Journal of Biotechnology*, 11(3): 0717.

Rabbani, M. A., Masood, M. S., Shinwari, Z. K. and Yamaguchi, S. K. (2010). Genetic Analysis of Basmati and Non-basmati Pakistani Rice (*Oryza sativa* L.) Cultivars using Microsatellite Markers. *Pakistani Journal of Botany, 42*: 2551 - 2564.

Rahman, M. S., Sohag, M. K. H. and Rahman, L. (2010). Microsatellite based DNA Fingerprinting of 28 Local Rice (*Oryza sativa* L.) Varieties of Bangladesh. *Journal of Bangladesh Agriculture*, 8(1): 7 – 17.

Rahman, M. M., Hussain, A., Sayed, M. A., Ansari, A. and Mahmud, M. A. A. (2011). Comparison among Clustering in Multivariate Analysis of Rice using Morphological Traits, Physiological Traits and Simple Sequence Repeat Markers. *Journal of Agricultural and Environmental Sciences*, 11 (6): 876- 882.

Rahman, M. M., Rasaul, M. G., Hossain, M. A., Iftekharuddaula, K. M. and Hasegawa, H. (2012). Molecular Characterization and Genetic Diversity Analysis of Rice using SSR Markers. *Journal of Crop Improvement*, 26: 244-257.

Ram, P. C., Singh, B. B., Singh, A. K., Ram, P., Singh, P. N., Singh, H. P., Boamfa, I. and Singh, R. K. (2002). Submergence Tolerance in Rainfed Lowland Rice: Physiological bases and Prospects for Cultivar Improvement through Marker-aided Breeding. *Field Crops Research*, 76: 131-152.

Ram, T., Majumder, N. D., Krishnaveni, D. and Mishra, B. (2010). Jarava: A New High Yielding and Pest Resistant Rice Variety for Coastal Saline Areas. *International Rice Resource Notes*, 34: 1-4.

Rao, L. V. S., Prasad, G. S. V., Rao, U. P., Prasad, A. S. R., Acharyulu, T. L. and Ramakrishna, S. (2001). Collection, Characterization and Evaluation of Rice Germplasm. *Indian Journal of Plant Genetic Resources*, 14(2): 222-226.

Rao, S. A., Schiller, J. M., Bounphanousay, C. and Jackson, M. T. (2006). Diversity within the Traditional Rice Varieties of Laos. *In*: Schiller, J. M., Chanphengxay, M. B., Linquist, B. and Rao, S. A. (eds.) Rice in Laos, Los Baños, *Philippines*, *IRRI*, pp. 123–140.

Rao, L.V. S., Prasad, S. G., Chiranjivi, M., Chaitanya, U. and Surendhar, R. (2013). DUS Characterization for Farmer Varieties of Rice, OSR *Journal of Agriculture and Veterinary Science*, 4(5): 35-43. http://dx.doi.org/10.9790/2380-0453543.

Rashid, M., Nuruzzaman, M., Hassan, L. and Begum, S. (2017). Genetic Variability Analysis for Various Yield Attributing Traits in Rice Genotypes. *Journal of the Bangladesh Agricultural University*, *15*(1): 15-19. https://doi.org/10.3329/jbau.v15i1.33525.

Razak, S., Ismail, N. S., Jaafar, A., Muhammad, Y. M. F., Kamaruzaman, R. A., Nasir, K. H. and Abdullah, N. (2016). Genetic Diversity of Malaysian Rice Landraces Based on Single Nucleotide Polymorphism (SNP) Markers. *International Journal of Pure and Applied Bioscience*, 4 (1): 28-34. doi: http://dx.doi.org/10.18782/2320-7051.2194.

Ren, F., Lu, B. R., Li, S., Huang, J. and Zhu, Y. (2003). A Comparative Study of Genetic Relationships among the AA-genome *Oryza species* using RAPD and SSR Markers. *Theoretical and Applied Genetics*, 108 (1): 113-120.

Ren, Z. H., Gao, J. P., Li, L. G., Cai, X. L., Huang, W., Chao, D. Y., Zhu, M. Z., Wang, Z. Y., Luan, S. and Lin, H. X. (2005). A Rice Quantitative Trait Locus for Salt Tolerance encodes a Sodium Transporter. *Nature Genetics*, 37: 1141-1146.

Rosalin, S., Shibani, M., Pritesh, R., Swain, D., Singh, O. N., Meher, J., Dash, S. K., Rao, G. J. N. and Subudhi, H. N. (2017). Assessment of Genetic Diversity in Wild Rice of Eastern India using SSR Markers. *Thai Journal of Agricultural Science*, 9(6): 239-250. doi:10.5539/jas.v9n6p239**.**

Roy, S., Banerjee, A., Pattanayak, A., Roy, S. S., Rathi, R. S., Misra, A. K., Ngachan, S. V. and Bansal, K. C. (2013). *Chakhao* (delicious) Rice Landraces (*Oryza sativa* L.) of North-East India: Collection, Conservation and Characterization of Genetic Diversity. *Plant Genetic Resources*, 12: 264–272.

Roy, S., Banerjee, A., Senapati, B. K. and Sarkar, G. (2012). Comparative Analysis of Agro-morphology, Grain Quality and Aroma Traits of Traditional and Basmati Type Genotypes of Rice (*Oryza sativa* L.). *Plant Breeding*, 131(4): 486-492.

Sadia, T., Zahida, H. P., Yasin, M. M., Ashiq, M. R. and Shahid, M. M. (2012). Assessment of Phenotypic Variability in Rice (O*ryza sativa* L.) Cultivars using Multivariate Analysis. *Pakistan Journal of Botany*, 44(3): 999 – 1006.

Sahu, G. R., Burman, M., Nair, S. K., Sarawgi A. K. and Rao, R. K. (2018). Genetic Behaviour of Awning Character in Rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, 7(5): 490-493. https://doi.org/10.20546/ijcmas.2018.705.061.

Sajib, A. M., Musharaf, H., Mosnaz, A. T. J., Hossain, H., Islam, M., Ali, S. and Prodhan, S. H. (2012). SSR Marker-based Molecular Characterization and Genetic Diversity Analysis of Aromatic Landraces of Rice (*Oryza sativa* L.). *Journal of Bioscience and Biotechnology*, 1 (2): 107-116.

Sanusi, M. (2014) Rice Farming In Nigeria: Challenges, Opportunities and Prospects. A Paper Presentation at the 2nd Nigeria Rice Investment Forum (Nirif).

Sarawgi, A. K., Subba Rao, L. V., Parikh, M., Sharma, B. and Ojha, G. C. (2013). Assessment of Variability of Rice (*Oryza sativa* L.) Germplasm using Agro-morphological Characterization. *Journal of Rice Research*, 6(1): 15-28.

Sarawgi, A. K., Parikh, M., Sharma, B. and Sharma, D. (2014). Phenotypic Divergence for Agro-morphological Traits among Dwarf and Medium Duration Rice Germplasm and Inter-relationship between their Quantitative Traits. *The Bioscane an International Journal of Life Science*, 9(4): 1677-1681.

Sarwar, G., Rashid, M. H., Parveen, S. and Hossain, M. S. (2015). Evaluation of Genetic Diversity in Agro-morphological Traits of Forty Two Aman Rice Genotypes (*Oryza sativa* L.) using D2 Analysis. *American Journal of Experimental Agriculture.* 8(5): 280-288. DOI: 10.9734/AJEA/2015/17138.

Sarla, N. and Swamy, B. P. M. (2005). *Oryza glaberrima*: A source for Improving *Oryza sativa*. *Current Science*, 89(6): 955-963.

SAS Institute Inc. (2007). Version 9.0 developed by SAS Institute Inc., Cary. North Carolina. USA. http://www. Sas.com.

Semon, M., Nielsen, R., Jones, N. P. and McCouch, S. R. (2005). The Population Structure of African Cultivated Rice *Oryza glaberrima* (Steud.): Evidence for Elevated Levels of Linkage Disequilibrium caused by Admixture with *O. sativa* and Ecological Adaptation. *Genetics Society of America*, 169: 1639-1647.

Shahidullah, S. M., Hanafi, M. M., Ashrafuzzaman, M., Ismail, M. R. and Khair, A. (2009). Genetic Diversity in Grain Quality and Nutrition of Aromatic Rice. *African Journal of Biotechnology*, 8(7): 1238-1246.

Sharma, D. K., Richaria, A. K. and Agarwal, R. K. (2004). Characterization of Ahu Rices of Assam for Morphological and Agronomic Traits under Transplanted Conditions. *Oryza*, 41(1 & 2): 8-12.

Sharma, R. K., Gupta, P., Sharma, V., Sood, A., Mohapatra, T. and Ahuja, P. S. (2008). Evaluation of Rice and Sugarcane SSR Markers for Phylogenetic and Genetic Diversity Analyses in Bamboo. *Genome*, 51(2): 91–103.

Sharma, S. K., Singh, J., Chauhan, M. and Krishnamurthy, S. L. (2014). Multivariate Analysis of Phenotypic Diversity of Rice (*Oryza sativa*) Germplasm in North-West India. *Indian Journal of Agricultural Science*, 84(2): 295-299.

Singh, A., Saini, R., Singh, J., Arya, M., Ram, M., Mukul, P. and Singh, P. K. (2015). Genetic Diversity Studies in Rice (*Oryza sativa* L.) using Microsatellite Markers. *International Journal of Agriculture, Environment and Biotechnology*, 8(1): 143-152. Doi:10.5958/732X.2015.00019.4.

Singh, N., Choudhury, D. R., Tiwari, G., Singh, A. K., Kumar, S., Srinivasan, K., Tyagi, R. K., Sharma, A. D., Singh, N. K. and Singh, R. (2016). Genetic Diversity Trend in Indian Rice Varieties: An Analysis using SSR Markers. *BMC Genetics*, 17: 127. doi: 10.1186/s12863-016-0437-7.

Sinha, A. K. and Mishra, P. K. (2012). Rice Diversity of Bankura District of West Bengal (India). *Bioscience Discovery*, 3(3):284- 287.

Sinha, A. K. and Mishra, P. K. (2012). Agronomic Evalution of Landraces of Rice (*Oryza sativa*) of Bankura District of West Bengal. *Columban Journal of Life Science*, 13 : 35-38.

Sinha, A. K. and Mishra, P. K. (2013). Morphology based Multivariate Analysis of Phenotypic Diversity of Landraces of Rice (O*ryza sativa* L.) of Bankura District of West Bengal. *Journal of Crop and Weed,* 9(2): 115-121.

Sinha, A. K., Mallick, G. K. and Mishra, P. K. (2015). Diversity of Grain Morphology on Traditional Rice Varieties (*Oryza sativa* L.) of Lateritic Region of West Bengal. *World Journal of Agricultural Sciences,* 11(1): 48-54.

Siwach, P., Jain, S., Saini, N., Chowdhury, V. K. and Jain, R. K. (2004). Allelic Diversity among Basmati and Non-basmati Long Grain Indica Rice Varieties using Microsatellite Markers. *Journal of Plant Biochemistry and Biotechnology,* 13(4): 25-32.

Skroch, R. J., Ronning, C. M. and Knight, R. J. (1995). Qualitative and Quantitative Characterization of RAPD Variation among Snap Bean (*Phaseolus vulgaris*) Genotypes. *Theoretical and Applied Genetics,* 91: 1078-1085.

Sumarani, G. O., Pillai, S. V., Harisankar, P. and Sundaresan, S. (2004). Isozyme Analysis of Indigenous Cassava Germplasm for Identification of Duplicates. *Genetic Resources and Crop Development,* 51: 205-209.

Swamy, B. P. M., Kaladhar, K., Reddy, G. A., Viraktamath, B. C. and Sarla, N. (2014). Mapping and Introgression of QTLs for Yield and Related Traits in Two Backcross Populations Derived from *Oryza sativa* cv. Swarna and Two Accessions of *O. nivara*. *Journal of Genetics,* 93: 643-654.

Tandekar, K. and Koshta, N. (2014). To Study the Agro-morphological Variation and Genetic Variability in Rice Germplasm. *Middle-East Journal of Scientific Research,* 20 (2): 218- 224. doi: 10.5829/idosi.mejsr.2014.20.02.11441.

Tang, S. X., Jiang, Y. Z., Wei, X. H., Li, Z. C. and Yu, H. Y. (2002). Genetic Diversity of Isozymes of Cultivated Rice in China. *Acta Agronomy Sinica,* 28: 203-207.

Temnykh, S., DeClerck, G., Lukashova, A., Lipovich, L., Cartinhour, S. and McCouch, S. (2001). Computational and Experimental Analysis of Microsatellites in Rice (*Oryza sativa* L.): Frequency, Length variation, Transposon associations and Genetic Marker Potential. *Genome Research,* 11: 1441-1452.

Thalapati, S., Guttikonda , H., Nannapaneni, N. D., Adari, P. B., Reddy, C. S., Swamy, B. P. M., Batchu, A. K., Basava, R. K., Viraktamath, B. C. and Neelamraju, S. (2014). Heterosis and Combining Ability in Rice as Influenced by Introgressions from Wild Species *(Oryza rufipogon*) including qyld2.1 Sub-QTL into the Restorer Line KMR3. *Euphytica*, 202(1): 81–95.

Thomson, M. J., Septiningsih, E. M., Suwardjo, F., Santoso, T. J. and Silitonga, T. S. (2007). Genetic Diversity analysis of Traditional and Improved Indonesian Rice (*Oryza sativa* L.) Germplasm using Microsatellite Markers. *Theoretical and Applied Genetics*,114: 559–568. DOI: 10.1007/s00122-006-0457-1.

Upadhyay, P., Singh, V. K. and Neeraja, C. N. (2011). Identification of Genotype Specific Alleles and Molecular Diversity Assessment of Popular Rice (*Oryza sativa* L.) Varieties of India. *International Journal of Plant and Breeding Genetics*, 5(2): 130–40.

Vange, T. (2009). Biometrical Studies on Genetic Diversity of some Upland Rice (*Oryza sativa* L.) Accessions. *Nature and Science*, 7(1): 21-27. http://www.sciencepub.org.

Vanisree, S., Anjali, K., Raju, C. D., Raju, C. S. and Sreedhar, M. (2013). Variability, Heritability and Association Analysis in Scented Rice. *Journal of Biological Science Opinion,* 1 (4): 347-352.

Vanisree, S., Swapna, K., Raju, D., Raju, S. and Sreedhar, M. (2013). Genetic Variability and Selection Criteria in Rice. *Journal of Biological and Scientific Opinion*, 1(4): 341-346.

Varshney, R. K., Graner, A., Sorrells, M. E. (2005) Genic microsatellite markers in plants: Features and applications. *Trends Biotechnology*, 23: 48–55.

Vilayheuang, K., Machida-Hirano, R., Bounphanousay, C. and Watanabe, N. K. (2016). Genetic Diversity and Population Structure of 'Khao Kai Noi', a Lao Rice (*Oryza sativa* L.) Landrace, revealed by Microsatellite DNA Markers. *Breeding Science*, 66(2): 204–212. doi:10.1270/jsbbs.66.204.

Vos, P., Hogers, R., Bleeker, M., Reijans, M., Van, T., De Lee, M., Hornes, A., Freijters, J., Pot, A., Peleman, J., Kuiper, M. and Zabeau, M. (1995). AFLP: A New Technique for DNA Fingerprinting. *Nucleic Acids Res*ources, 23: 4407-4414.

Vu, H. T. T., Nguyen, H. T. T., Tran, K. D., Khuat T. H. and Nakamura, C. (2016) Genetic Diversity of Vietnamese Lowland Rice Germplasms as Revealed by SSR Markers in Relation to Seedling Vigour under Submergence. *Biotechnology and Biotechnological Equipment*, 30(1): 17-25.

Wang, G. L., Mackill, D. J., Bonman, J. M., McCouch, S. R. and Nelson, R. J. (1994). RFLP Mapping of Genes Conferring Complete and Partial Resistance to Blast in a Durably Resistant Rice cultivar. *Genetics,* 136: 1421-1434.

Wazed, M. (2014). *Genetic Diversity Analysis in some Rice Lines for Submergence Tolerant using SSR Marker at Reproductive Stage* (Master's Thesis). Department of Biotechnology, Bangladesh Agricultural University, Mymensingh-2202.

Weerasinghe, P. A., Wijayawardhana, H. C. D., Herath, H. M. V. and Herath, H. M. D. (2015). Genetic Diversity of Selected Sri Lankan Rice Accessions based on Agro-Morphological Characters. *International Research Symposium Rajarata University of Sri Lank,* p159.

Weiya, X., Yongzhong, X., Xiaoyu, W., Yu, Z., Weijiang, T., Lei, W. and Hongju, Z. (2008). Natural variation in Ghd7 an Important Regulator of Heading Date and Yield Potential in Rice. *Nature Genetics*, 40: 761-767.

Weising, K., Nybom, H., Wolf, K. and Kahl, G. (2005). DNA Fingerprinting in Plants. Principles, Methods and Applications. 2nd Edition. CRC Press, USA. 230-239.

Worldometers (2019). Nigeria Population (LIVE), Department of Economic and Social Affairs, Population Division. World Population Prospects : (www.worldometers.info//).

Xiao, X. Y., Wang, Y. P., Zhang, J. Y., Li, S. G. and Rong, T. Z. (2006). SSR Marker-based Genetic Diversity Fingerprinting of Hybrid Rice in Sichuan, China. *Chinese Journal of Rice Science*, 20(1): 1-7.

Xu, Q., Yuan, X., Wang, S., Feng, Y., Yu, H., Wang, Y., Yang, Y., Wei, X. and Li, X. (2016). The Genetic Diversity and Structure of Indica Rice in China as Detected by Single Nucleotide Polymorphism Analysis. *BMC Genetics*, 17:53. doi: 10.1186/s12863-016-0361-x.

Xue, D., Chen, M., Zhou, M., Chen, S., Mao, Y. and Zhang, G. (2008). QTL Analysis of Flag Leaf in Barley (*Hordeum vulgare*) for Morphological Traits and Chlorophyll Content. *Journal of Zhejiang University of Science*, 9 (12): 938-943.

Yadav, S., Singh, A., Singh, M. R., Goel, N., Vinod, K. K., Mohapatra, T. and Singh, A. K. (2013). Assessment of Genetic Diversity in Indian Rice Germplasm (*Oryza sativa* L.): Use of Random versus Trait-Linked Microsatellite Markers. *Journal of Genet*ics, 92: 104–117.

Yu, S. B., Xu, W. J., Vijayakumar, C. H. M., Ali, J., Fu, B. Y., Xu, J. L., Jiang, Y. Z., Marghirang, R., Domingo, J., Aquino, C., Virmami, S. S. and Li, Z. K. (2003). Molecular Diversity and Multilocus Organization of the Parental Lines used in the International Rice Molecular Breeding Program. *Theoretical and Applied Genetics,* 108: 131-140.

Yu, G. Q., Bao, Y., Shi, C. H., Dong, C. Q. and Ge, S. (2005). Genetic Diversity and Population Differentiation of Liaoning Weedy Rice Detected by RAPD and SSR Markers. *Biochemical Genetics,*.43: 261-270.

Zahid, A. M., Akhtar, M., Sabar, M., Anwar, M. and Mushtaq, A. (2005). Interrelation-ship among Yield and Economic Traits in Fine Grain Rice. *Procedings of the International Seminar on Rice Crop.* October 2-3.Rice Research Institute, Kala Shah Kau, Pakistan. 21-24.

Zhang, H., Zhang, D., Wang, M., Sun, J., Qi, Y., Li, Y., Wei, X., Hen, L., Qiu, Z., Tang, S. and Li, Z. (2011). A Core Collection and Mini Collection of *Oryza sativa* L., in China. *Theoretical and Applied Genetics*, 122: 49-61.

Zhang, Y., Tang, Q., Peng, S., Zou, Y., Chen, S., Shi, W., Qin, J., Rebecca, M. and Laza, C. (2013). Effect of High Night Temperature on Yield and Agronomic Traits of Irrigated Rice under Field Chamber System Condition. *Australian Journal of Crop Science*, 7(1): 7-13.

Zhou, H. F., Xie, Z. W. and Ge, S. (2003). Microsatellite analysis of Genetic Diversity and Population Genetic Structure of a Wild Rice (*Oryza rufipogon* Griff) in China. *Theoretical and Applied Genetics*, 107(2): 332-339.

Appendix I: Qualitative Traits Record of Rice Landraces used for the study

	RICE NAME	STATE	BLS	LBC	LTC	LMC	JC	LC	AC	IC	NC	APC	STC	AW	SGC	CE	S C
1	2BC	KATSINA	PL	G	P	P	LG	W	LG	PL	G	R	P	A	W	NONE	WHITE
2	BA INGILA	SOKOTO	G	G	G	G	LG	W	LG	G	G	W	W	A	W	LESS	WHITE
3	BAKIN IRI – BN	BORNO	PL	G	P	P	LG	W	LG	PL	G	P	P	A	W	MEDIUM	RED
4	BAKIN IRI-KB	KEBBI	P	G	P	P	LG	W	LG	PL	G	P	LP	P	W	NONE	RED
5	BAKIN YAR CHINA	BAUCHI	P	DG	P	P	G	W	LG	PL	G	P	P	P	W	NONE	BROWN
6	BAYAWURE	KEBBI	LP	G	P	G	LG	W	LG	G	G	P	LP	A	W	LESS	RED
7	BIRUWA-NSW	NASARAWA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	WHITE
8	BOLAGA	KATSINA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	WHITE
9	CDI	BENUE	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LARGE	WHITE
10	CHAINA-GB	GOMBE	G	G	G	G	LG	W	LG	G	G	W	W	P	W	MEDIUM	WHITE
11	CP-GB	GOMBE	G	G	G	G	LG	W	LG	G	G	W	W	P	W	NONE	WHITE
12	DAN KAUSHI	YOBE	P	G	P	P	LG	W	LG	PL	G	P	P	A	W	NONE	RED
13	DAN KOYDO	BORNO	PL	G	P	G	LG	W	LG	G	G	P	P	P	W	MEDIUM	RED
14	DANTUDU	NIGER	G	DG	G	G	G	W	LG	G	G	W	W	A	W	LARGE	RED
15	D/ CAROLEA	KADUNA	PL	G	G	G	LG	W	LG	G	G	P	P	TA	W	NONE	L B
16	D/ JAMILA	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	MEDIUM	WHITE
17	FARAR JA	KATSINA	G	G	G	G	LG	W	LG	G	G	W	W	A	W	NONE	WHITE
18	FARAR JANA	KANO	G	G	G	G	LG	W	LG	G	G	W	W	A	W	NONE	WHITE
19	FARAR JELLOF	KADUNA	G	DG	G	G	G	W	LG	G	G	W	W	P	W	NONE	WHITE
20	FIJO	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	MEDIUM	L B
21	FRAJALAM	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LARGE	L B
22	GAJERE CAROLEA	KADUNA	LP	G	G	G	LG	W	LG	G	G	R	P	TA	W	NONE	WHITE
23	IRESI TSARIGI	KWARA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	WHITE
24	JAKA	KATSINA	P	G	P	P	LG	W	LG	PL	G	P	P	P	W	LESS	RED
25	JAMILA KT	KATSINA	G	G	G	G	LG	W	LG	G	G	W	W	TA	W	NONE	WHITE

Appendix I Cont'd: Qualitative Traits Record of Rice Landraces used for the study

SN	RICE NAME	STATE	BLS	LBC	LTC	LMC	JC	LC	AC	IC	NC	APC	STC	AW	SGC	CE	S C
26	JAMILA PLT	PLATEAU	G	G	G	G	LG	W	LG	G	G	W	W	P	W	NONE	WHITE
27	JAMILA-BA	BAUCHI	G	G	G	G	LG	W	LG	G	G	W	W	P	W	NONE	L B
28	JAMILA-GB	GOMBE	G	G	G	G	LG	W	LG	G	G	W	W	A	W	NONE	BROWN
29	JAMILA-JG	JIGAWA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	MEDIUM	L B
30	JAMILA-NG	NIGER	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LARGE	WHITE
31	JAMILA-YL	ADAMAWA	G	G	G	G	LG	W	LG	G	G	W	W	TA	W	NONE	L B
32	JAMILA-ZRX	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	A	W	NONE	L B
33	JAN IRI – BN	BORNO	PL	G	P	G	LG	W	LG	G	G	P	LP	P	W	LARGE	RED
34	JAN IRI-KB	KEBBI	LP	G	P	G	LG	W	LG	PL	G	P	LP	A	W	LESS	RED
35	JAP	KATSINA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	WHITE
36	JATON MINI	YOBE	P	G	P	P	LG	W	LG	PL	G	P	P	P	W	LESS	RED
37	KORO-KORO	NASARAWA	P	G	P	P	LG	W	LG	PL	G	P	P	A	W	LESS	RED
38	LETE/VIU	BENUE	G	G	G	G	LG	W	LG	G	G	W	W	A	W	LESS	L B
39	MAI ADDA/KILAKI	KADUNA	G	G	G	G	LG	W	LG	G	G	R	P	P	W	NONE	L B
40	MAI ALLURA	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	WHITE
41	MAI MADARA	BAUCHI	G	G	G	G	LG	W	LG	G	G	W	W	TA	W	LARGE	WHITE
42	MAI ZABUWA GIWA	KADUNA	P	P B	P	P	G	PL	P	P	P	P A	P	A	P	LESS	L B
43	MAI ZABUWA/BIRO	KADUNA	P	P B	P	P	G	PL	P	P	P	P A	P	A	P	NONE	L B
44	MASS/OSI	BENUE	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LARGE	WHITE
45	MIRUWA	BENUE	PL	G	P	P	LG	W	LG	G	G	R	P	A	W	MEDIUM	L B
46	O-TU	TARABA	G	G	G	G	LG	W	LG	G	G	W	W	A	W	LARGE	WHITE
47	SANTANA	KATSINA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	RED
48	SHATIKA	KATSINA	PL	G	G	G	LG	W	LG	PL	G	P	P	A	W	NONE	RED
49	SIPI-NG	NIGER	G	G	G	G	LG	W	LG	G	G	W	W	A	W	NONE	L B
50	SIPI-NSW	NASARAWA	G	G	G	G	LG	W	LG	G	G	W	W	A	W	LARGE	WHITE

Appendix I Cont'd: Qualitative Traits Record of Rice Landraces used for the study

SN	RICE NAME	STATE	BLS	LBC	LTC	LMC	JC	LC	AC	IC	NC	APC	STC	AW	SGC	CE	S C
51	**SOPPI**	**BENUE**	**G**	**G**	**G**	**G**	**LG**	**W**	**LG**	**G**	**G**	**W**	**W**	**A**	**W**	**LARGE**	**L B**
52	TASAMA	BAUCHI	G	G	G	G	LG	W	LG	G	G	W	W	P	W	MEDIUM	RED
53	WACOT	KATSINA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	WHITE
54	WATER PROOF	NASARAWA	G	G	G	G	LG	W	LG	G	G	W	W	A	W	LESS	WHITE
55	WATI	NIGER	P	G	P	P	LG	W	LG	PL	G	W	W	A	W	LESS	WHITE
56	YAR CHINA-KB	KEBBI	G	G	G	G	LG	W	LG	G	G	W	W	A	W	LARGE	L B
57	Y/ DAN HASSAN	KADUNA	PL	G	P	P	LG	PL	P	PL	G	R	P	P	W	LESS	WHITE
58	YAR DASHE	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	NONE	RED
59	YAR DAS-JG	JIGAWA	G	G	G	G	LG	W	LG	G	G	W	W	A	W	NONE	RED
60	YAR DIRYA	ZAMFARA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LARGE	WHITE
61	Y GIDAN YARIMA	KATSINA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	NONE	WHITE
62	YAR KABORI	SOKOTO	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	WHITE
63	YAR KALAGE	KEBBI	LP	G	P	P	LG	W	LG	PL	G	P	LP	A	W	LESS	RED
64	YAR KURA	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	NONE	WHITE
65	YAR MAAJI	KATSINA	G	G	G	G	LG	W	LG	G	G	W	W	TA	W	LESS	L B
66	YAR MAMMAN	KEBBI	PL	G	P	P	LG	W	LG	PL	G	P	P	P	W	LESS	RED
67	YAR NUPAWA	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	L B
68	YAR TELAK	KADUNA	P	G	P	P	LG	W	LG	PL	G	R	P	A	W	NONE	WHITE
69	YAR YIGINAYE	KADUNA	G	G	G	G	LG	W	LG	G	G	W	W	TA	W	NONE	WHITE
70	YAR ZAITI	SOKOTO	G	G	G	G	LG	W	LG	G	G	W	W	P	W	LESS	WHITE

BLS-Basal leaf sheath colour, LBC-Leaf blade colour, LTC-leaf tip colour, LMC-Leaf margin colour, JC-Junctura colour, AC-Auricle colour, IC- Internode colour, NC-Node colour, APC- Apiculus colour, SGC-Stigma colour, AW- Awning, SGC-Sterile glume colour, CE- Chalkiness of endosperm, SC- Seed coloueDG-Dark Green, G-Green, LG-Light green, P-Purple, LP-Light purple, PL-Purple line, P B- Purple blutch, PA- Purple apex, W-White, R-Red, A-Absent , TA- tipped Awn, L B-Light brown

Appendix II: Mean Performance of the Agronomic Traits of Rice Landraces used for the study

S/no	Rice Names	DG	PHT	PNL	NLP	NTP	DFF	NPP	NFG	NUG	NTG	HSW	GYP
1	2bc	4.33	79.00	16.67	22.00	6.33	126.33	3.67	2.00	49.00	51.00	2.70	0.22
2	Ba Ingila	5.67	76.33	24.94	19.00	5.33	80.00	6.89	16.11	40.11	56.22	2.30	2.84
3	Bakin Iri – Bn	5.67	88.67	28.48	14.00	5.33	88.67	7.44	11.00	30.00	41.00	2.70	2.18
4	Bakin Iri-Kb	4.67	64.00	17.67	12.67	5.00	98.67	6.67	4.22	33.78	38.00	2.80	0.79
5	Bakin Yar China-Ba	5.33	54.67	20.65	14.67	6.33	94.00	3.78	12.56	38.00	50.55	2.77	1.41
6	Bayawure	5.00	63.67	22.16	12.00	5.67	85.67	8.78	5.22	31.67	36.56	2.60	1.27
7	Biruwa	4.67	88.67	34.5	16.67	4.67	125.33	4.67	3.33	57.33	60.67	2.00	0.30
8	Bolaga	5.67	76.67	20.94	14.00	5.00	96.00	3.45	42.00	42.78	84.78	2.80	4.32
9	Cdi	4.67	79.33	24.00	20.00	5.33	123.33	3.67	21.00	33.00	54.00	2.70	2.27
10	Chaina-Gb	5.00	61.33	21.42	22.33	6.00	87.67	5.67	30.33	22.67	53.00	2.80	5.08
11	Cp-Gb	5.00	46.67	18.80	22.67	6.00	101.33	6.11	23.56	15.00	38.56	2.60	3.88
12	Dan Kaushi	6.00	74.00	24.12	11.67	7.00	83.67	7.22	3.67	35.78	39.45	2.57	0.72
13	Dan Koydo	6.00	69.33	25.58	12.67	6.00	75.33	6.11	17.56	34.78	52.31	2.60	3.00
14	Dantudu	5.67	69.33	20.50	14.00	5.00	115.00	3.67	5.00	29.22	34.22	2.47	0.49
15	Doguwar Carolea	4.33	93.33	25.62	19.00	5.00	76.00	3.89	2.50	44.00	46.50	2.47	0.25
16	Doguwar Jamila	4.67	69.33	22.61	14.67	6.67	92.00	5.33	4.75	39.75	44.5	3.00	0.76
17	Farar Ja	6.00	74.33	16.47	15.00	4.00	69.67	4.56	26.33	22.00	48.34	2.60	3.20
18	Farar Jana	5.00	43.67	24.00	14.00	5.00	81.00	4.11	15.33	60.00	75.33	2.40	1.59
19	Farar Jellof	5.00	64.00	19.45	12.00	4.00	85.33	3.33	30.33	12.50	42.83	2.60	2.37
20	Fijo	5.00	69.00	19.13	21.67	6.33	84.00	3.45	4.00	31.00	35.00	2.40	0.64
21	Frajalam	5.67	85.00	24.95	18.33	4.33	88.33	4.67	32.67	49.00	81.67	2.30	3.51
22	Gajere Carolea	4.67	84.00	24.41	17.67	4.67	109.33	5.33	7.22	48.55	55.78	2.60	1.00
23	Iresi Tsarigi	6.67	56.00	18.30	20.00	6.00	105.67	4.67	28.78	32.33	61.11	2.40	3.22
24	Jaka	5.33	85.00	21.13	14.00	6.00	77.67	5.00	2.00	43.33	45.33	2.50	0.27

Appendix II Cont'd: Mean Performance of the Agronomic Traits of Rice Landraces used for the study

S/no	Rice Names	DG	PHT	PNL	NLP	NTP	DFF	NPP	NFG	NUG	NTG	HSW	GYP
25	Jamila Plt	6.33	84.67	27.02	17.00	5.33	82.67	4.56	39.67	27.67	67.33	2.70	5.67
26	Jamila-Ba	4.33	77.00	18.62	25.67	7.00	111.33	6.22	16.33	30.67	46.89	2.70	2.90
27	Jamila-Gb	6.00	86.33	27.62	19.33	5.33	104.33	5.67	4.89	41.33	46.22	2.50	0.61
28	Jamila-Jg	4.33	73.00	31.89	19	6.67	104.33	4.22	13.78	41.78	55.55	2.80	1.77
29	Jamila-Kt	5.00	71.33	28.00	15.00	6.00	97.33	4.78	26.78	31.00	57.78	2.50	3.57
30	Jamila-Ng	6.00	86.33	30.01	13.33	4.33	118.67	4.00	9.89	36.22	46.11	2.90	1.15
31	Jamila-Yl	4.67	74.67	22.53	22.67	6.33	106.67	5.00	20.89	13.89	34.78	2.60	2.89
32	Jamila-Zrx	5.33	76.67	25.20	13.67	5.00	116.67	4.44	39.78	22.67	62.45	2.70	5.01
33	Jan Iri – Bn	4.67	75.67	23.27	16.67	7.00	74.33	9.89	7.45	36.00	43.45	2.60	2.26
34	Jan Iri-Kb	4.33	72.33	30.67	16.00	5.00	89.33	5.89	7.78	32.56	40.33	2.50	1.23
35	Jap	5.00	57.33	21.68	15.00	4.67	75.33	5.45	9.56	39.67	49.22	2.17	1.55
36	Jaton Mini	6.67	71.00	21.71	13.67	6.00	107.33	7.78	23.00	14.78	37.78	2.40	2.20
37	Koro-Koro	5.33	88.33	20.57	13.00	6.67	72.00	6.89	2.50	56.83	59.33	2.30	0.40
38	Lete/Viu	5.67	80.67	26.90	22.00	6.67	103.00	5.89	20.66	40.56	61.22	2.80	3.52
39	Mai Adda/Kilaki	4.67	65.33	23.06	16.00	5.00	96.33	5.33	22.89	34.11	57.00	2.80	3.37
40	Mai Allura	5.67	57.67	20.47	18.00	4.67	97.00	5.45	33.45	23.89	57.34	2.40	4.55
41	Mai Madara	5.00	57.00	18.69	31.67	7.00	104.00	6.89	13.33	41.78	55.11	2.40	2.41
42	Mai Zabuwa Giwa	4.67	56.00	18.58	15.00	4.33	107.00	5.33	12.78	42.67	55.45	2.60	1.77
43	Mai Zabuwa/Biro	5.33	48.67	14.94	17.33	6.33	108.33	7.89	4.89	43.22	48.11	2.80	1.09
44	Mass/Osi	5.33	85.00	24.14	13.67	4.33	115.33	5.22	22.89	31.00	53.89	3.10	3.85
45	Miruwa	5.33	84.00	20.67	20.00	4.00	109.33	3.22	15.00	28.00	43.00	2.80	1.54
46	O-Tu	5.33	64.33	20.94	17.00	4.67	115.00	4.56	2.50	74.45	76.61	2.40	0.28
47	Santana(Yar Ruwa)	4.67	89.67	23.84	22.00	4.67	112.00	3.67	9.00	40.56	49.56	2.67	0.89
48	Shatika	5.33	87.67	18.33	15.33	4.67	98.67	4.00	7.00	35.00	42.00	2.50	0.77
49	Sipi-Ng	5.67	57.67	21.67	18.33	5.00	122.00	5.00	16.78	30.33	47.11	2.00	1.68
50	Sipi-Nsw	6.00	54.33	21.04	15.00	5.33	119.67	4.67	9.78	33.00	42.78	2.40	1.10

Appendix II Cont'd: Mean Performance of the Agronomic Traits of Rice Landraces used for the study

S/no	Rice Name	DG	PHT	PNL	NLP	NTP	DFF	NPP	NFG	NUG	NTG	HSW	GYP
51	Soppi	5.67	89.33	24.04	21.67	5.67	115.00	5.33	12.33	32.00	44.33	2.20	1.44
52	Tasama	5.33	54.00	19.10	14.67	6.00	84.33	5.44	26.56	21.00	47.55	2.30	3.86
53	Wacot	5.33	83.00	21.36	19.67	5.33	99.33	6.67	51.33	27.00	78.33	2.70	9.24
54	Water Proof	4.33	75.33	23.33	18.33	5.67	106.67	5.11	18.56	27.00	45.56	2.27	2.27
55	Wati	5.67	83.33	17.00	14.67	4.33	122.33	3.33	8.34	20.00	28.34	3.00	0.80
56	Yar China-Kb	5.33	54.00	20.29	20.33	4.67	86.00	6.22	63.56	19.56	86.45	1.97	8.26
57	Yar Dan Hassan	5.00	51.67	21.12	15.33	4.67	75.33	7.45	12.89	29.00	41.89	2.80	3.13
58	Yar Das-Gb	5.00	68.00	20.73	20.00	4.67	101.00	6.00	31.22	34.33	65.55	2.20	4.89
59	Yar Dashe	5.00	71.67	22.15	22.33	6.67	105.33	6.00	20.89	36.00	56.89	2.13	3.03
60	Yar Dirya	6.00	64.67	17.96	25.33	5.33	96.33	5.33	4.78	39.67	44.44	2.23	0.57
61	Yar Gidan Yarima	5.67	57.67	18.80	20.67	6.33	93.33	6.00	18.00	22.78	40.78	2.40	2.59
62	Yar Kabori	6.33	53.00	18.91	21.00	5.33	88.67	6.00	15.00	46.89	61.89	2.73	2.48
63	Yar Kalage	6.33	88.33	25.51	12.00	7.33	63.00	9.33	4.33	33.00	37.33	2.60	1.30
64	Yar Kura	6.33	55.00	22.51	19.33	6.00	107.00	4.00	2.50	49.22	51.72	2.30	0.23
65	Yar Maaji	5.67	55.00	16.33	15.00	4.00	87.67	7.00	24.00	15.00	39.00	3.00	5.28
66	Yar Mamman	4.67	83.67	23.18	15.00	5.00	121.33	3.00	2.00	23.44	25.44	2.60	0.16
67	Yar Nupawa	4.00	71.67	19.67	16.67	4.67	99.33	5.00	35.78	15.44	51.22	2.90	4.85
68	Yar Telak	5.00	61.00	21.15	27.00	6.33	83.33	6.67	4.50	41.89	46.39	2.50	0.75
69	Yar Yiginaye	5.33	79.00	28.00	17.67	5.00	94.33	4.67	4.00	36.00	40.00	2.50	0.47
70	Yar Zaiti	5.67	72.00	23.27	16.00	6.00	98.00	6.22	32.33	25.33	57.66	2.50	5.39

NOTE: DG-Days to Germination, PHT-Plant Height, PNL-Panicle Length, NLP-Number of Leaves per plant, NTP- Number of Tillers per plant, DFF-Days to 50% Flowering, NPP- Number of Panicles per plant, NFG- Number of Filled grains per panicle, NUG- Number of unfilled grains per panicle , NTG- Number of Total grains, HSW-Hundred Seed Weight, GYP-Grain Yield per plant.

Appendix III: Distribution of Rice Landraces to Different Clusters based on SSR Analysis

CLUSTER TYPE	LANDRACE	STATE
1	BA INGILA	SOKOTO
1	IRESI TSARIGI	KWARA
1	CP	GOMBE
1	JAMILA PLT	PLATEAU
1	MASS/OSI	BENUE
1	YAR YIGINAYE	KADUNA
1	WATI	NIGER
1	MAI ZABUWA/BIRO	KADUNA
1	YAR NUPAWA	KADUNA
1	MAI ALLURA	KADUNA
1	YAR DIRYA	ZAMFARA
1	FUTIA 12	LINE
1	JAN IRI – BN	BORNO
1	DANTUDU	NIGER
1	FARO PLT	PLATEAU
1	LETE/VIU	BENUE
1	JAP	KATSINA
1	BIRUWA	NASARAWA
1	YAR TELAK	KADUNA
2	BAKIN IRI – BN	BORNO
2	DAN KOYDO	BORNO
2	KORO-KORO	NASARAWA
2	BOLAGA	KATSINA
2	GAJERE CAROLEA	KADUNA
2	JAMILA-JG	JIGAWA
2	FIJO	KADUNA
2	FRAJALAM	KADUNA
2	DOGUWAR JAMILA	KADUNA
2	YAR KURA	KADUNA
2	YAR DANHASSAN	KADUNA
2	SANTANA(Y RUWA)	KATSINA
3	FARAR JELLOF	KADUNA
3	FARAR JA	KATSINA
3	MAI ZABUWA	KADUNA
3	MIRUWA	BENUE
3	JAKA	KATSINA
3	JATON MINI	YOBE
3	O-TU	TARABA
3	YAR CHINA	KEBBI

Appendix III Cont'd: Distribution of Rice Landraces to Different Clusters based on SSR Analysis

CLUSTER TYPE	LANDRACE	STATE
3	BAYAWURE	KEBBI
3	BAKIN IRI	KEBBI
3	YAR MAMMAN	KEBBI
3	WACOT	KATSINA
3	2BC	KATSINA
3	JAMILA	KATSINA
3	YAR MAAJI	KATSINA
4	YAR GIDAN YARIMA	KATSINA
4	DAN KAUSHI	YOBE
4	DOGUWAR CAROLEA	KADUNA
4	FARO-JLG	TARABA
4	WATER PROOF	NASARAWA
4	JAMILA-ZRX	KADUNA
4	CHAINA	GOMBE
4	JAMILA-GB	GOMBE
4	JAMILA-NG	NIGER
4	SIPI-NG	NIGER
4	YAR ZAITI	SOKOTO
4	YAR KABORI	SOKOTO
4	CDI	BENUE
4	SOPPI	BENUE
4	JAMILA-BA	BAUCHI
4	TASAMA	BAUCHI
4	YAR DAS	JIGAWA
4	BAKIN YAR CHINA	BAUCHI
4	JAMILA-YL	ADAMAWA
4	SIPI	NASARAWA
4	YAR KALAGE	KEBBI
4	SHATIKA	KATSINA
4	FARAR JANA	KANO
4	JAN IRI	KEBBI
4	MAI ADDA/KILAKI	KADUNA
4	YAR DASHE	KADUNA