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Lectures Series
Volume 1

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Preface

An inaugural lecture, even from its very beginning at the University of Oxford, England where it originated as far back as 1623 (Omole as cited in Folorunso 2016:9), is meant to serve, at least, three major but purely academic purposes: (1) an account of the professor's stewardship in the academia and to inform the audience of the essence of his/her work to date, including current research, (2) stating his/her future plans especially the scheme of research which the professor proposes to do while occupying the chair, and (3) to talk about the state of the discipline; charting its progress, discussing its current health and problems, as well as examining its intellectual outputs which justify its inclusion in the university academic curriculum.

In line with the tradition, an inaugural lecture is a public presentation at which the professor is expected to tell the world what he/she professes in a language that is devoid of professional jargons and esoteric registers. The simplicity of language is important because an inaugural lecture provides the professor with the opportunity to address three blocks of audience simultaneously: his/her professional colleagues, the entire university community and the general public. With eighteen (18) of such lectures in a series in our university, one can attest or speak of an established tradition of inaugural lectures in Nasarawa State University, Keffi. The contribution(s) of each of the lectures is clear but the decision to edit into volumes (ten lectures in one volume), is informed by the desire to preserve the pieces of information contained in the lectures in one piece for unity of purpose, uniformity of preservation format and best practices. It is to allow the pieces of information to hang together rather than hanging separately; the more the merrier.

Of the eighteen (18) inaugural lectures presented so far in the series, this volume contains the first ten lectures in the series comprising three from the Faculty of Agriculture, two from Arts, another two from the Faculty of Natural and Applied Sciences, and one each from the faculties of Administration, Environmental Science and Social Sciences. These are inaugural lectures presented from 26th March, 2008 when the first of such lectures in the university entitled 'Soil Husbandry: Lifeline for National Food Security and Economic Empowerment' was presented by Prof. Olusola O. Agbede of the Faculty of Agriculture to 18th November, 2015 when the tenth Inaugural Lecture was presented by Prof. Folorunso A. Ajayi of the same faculty.

Agbede's lecture which is the first both in the series and in this volume, concerns itself with how our soils must be carefully and wisely used to attain food security in Nigeria. The second in the series and in the volume was presented by Prof. Obaje of the Faculty of Natural and Applied Sciences. Obaje's lecture entitled 'Geology and Mineral Resources of Nigeria: Development Options for Economic Growth and Social Transformation' (13th August, 2008) presents options that will enhance optimal exploitation of the mineral resource wealth of the nation for its economic growth and socio-political transformation. 'Before we Set the House Ablaze: Let Us Consult Our Oracle (History)' presented by Prof. Olayemi Akinwumi of the Faculty of Arts on 11th December, 2009 is

the third in the series. It was an eye-opener to the fact that if Nigeria is to be truly a great nation, we must go back to our sense of history; for the nation suffers which has no sense of history. This was followed by the fourth, 'Farm Production Efficiency: The Scale of Success in Agriculture' by Prof. Abdul Rahman of the Faculty of Agriculture presented on 26th June, 2013. Its major preoccupation was to describe farm as a system that produces agricultural commodities under certain restrictions as well as the interrelated factors that determine success in the entire agricultural sector of the national economy. The fifth in the series and in this maiden edition was MAINOMA (Most Acceptable Index Needed of Measuring Accountability) presented by Prof. Mainoma of the Faculty of Administration on 8th January, 2014. It seeks to provide the most acceptable model or index for measuring accountability.

'Researching Criminal Justice and Security Administration in Nigeria: Issues, Challenges and Opportunities' is the sixth in the series. It was presented on the 12th March, 2014 by Prof. Sam O. Smah of the Faculty of Social Sciences. The focus of the lecture was to draw attention to the fact that inaccuracy of available data due to lack of expertise by statistical officers, weak or poorly framed information gathering techniques and instruments, poor documentation attitude, inadequate analysis and storage are the banes of effective and efficient criminal justice and security administration in Nigeria. The seventh and eighth in the series were presented by Prof. Kwon-Ndung of Natural and Applied Sciences and Prof. Zaynab Alkali of the Faculty of Arts on the 17th September, 2014 and 17th December, 2014 respectively. Whereas the former shows how the presenter's research works in Plant Genetics and Breeding have contributed in the search for national and global food security, the latter dwells on the relevance of Gender Studies in Nigeria's Higher Institutions of Learning. The ninth Inaugural Lecture entitled 'Habitats and our Habits, Ecological Community and Common Unity' was presented by Prof. H. K. Ayuba on the 22nd April, 2015. It draws attention to the manifestations of unfolding economic, social and environmental catastrophes, which were largely due to pressures from human activities and economic necessities. It suggests a paradigm shift towards sustainable environmental management. The tenth in the series and the last in this volume was presented on 18th November, 2015 by Prof. Ajayi of the Faculty of Agriculture. The lecture entitled 'Insects, Plants and Humanity: The Organic Agriculture and Stored Products Protection Axis' is essentially an overview of the interplay between man and insects, highlighting that much of the crop harvests are lost to obnoxious insect pests during storage. It enunciates the factors that can enhance food security through better management of postharvest losses, propagating the use of traditional plant products as a means of protecting stored produce. In all, the divergent views and the varying thematic preoccupations of the lectures notwithstanding, one is left with the impression that though celebrations may vary from one place to another, true politeness is everywhere the same. In other words, methodology and approaches may vary but truly good scientific research is so recognized in every discipline.

Editing inaugural lectures which appear somewhat like finished products from seasoned professors who are authorities in their own rights was a daunting task. What we did was more of language editing to minimise grammatical and typo errors wherever found.

Even as it is, we do not guarantee uniformity in styles of content presentation and referencing but we have done the best that is possible given the circumstance in which we have found ourselves. I wish to thank all who had assisted in one way or the other in the editing and/or proofreading of the manuscripts.

I wish to use this medium to thank the Vice-Chancellor of our great university, Prof. M. A. Mainoma, and his Management Team for the all-round support and encouragement we have received from them since we came on board as the University Inaugural Lecture Committee, especially the provision of the fund for this publication. I thank the Inaugural Lecturers whose lectures have been published in this maiden edition of the NSUK Inaugural Lectures Series for the permission to do so. Congratulations! I thank the Information and Protocol Unit under the leadership of Abraham Ekpo who had been very helpful in organizing the University Inaugural Lectures Series. Thank you all.

Prof. G. S. Omachonu, PhD, FAvH, FICSHER
Editor/Chairman, Inaugural Lectures Committee
Keffi, 3rd July, 2018.

Foreword

Nasarawa State University, Keffi is known for upholding core University Academic Traditions, one of which is the Inaugural Lectures series. As many of us are aware, inaugural lecture provides an academic an opportunity to tell the world what he professes. It is a moment to celebrate excellence and breakthroughs with family, friends and colleagues. It is a testimony of one's contribution to the body of knowledge and his identification of his own building blocks in the system. It also affords the larger society opportunity to know researches that were carried out, those ongoing and the future plans. It also provides an opportunity to share with the audience how he/she used the knowledge of his/her chosen profession to advance the cause of the society especially in problem solving. To my mind, besides their contributions to knowledge, what Professors in NSUK have done thus far, presenting their inaugural lectures, is to really address societal problems using the insights and knowledge from their respective disciplines or professions.

The Nasarawa State University, Keffi Inaugural Lecture series Vol. 1 presents an opportunity to put together the first 10 inaugural lectures that were presented in the University. These are:

S/N	Presenter	Title of Lecture	Date
1	Prof. Olushola O. Agbede, Professor of Soil Science	Soil Husbandry: Lifeline for National Food Security and Economic Empowerment.	26th March, 2008
2	Prof. Nuhu G. Obaje, Professor of Geology	Geology and Mineral Resources of Nigeria: Development Option for Economic Growth and Social Transformation.	2nd February, 2009
3	Prof. Olayemi D. Akinwumi, Professor of Inter-Group Relations	Before we Set the House Ablaze, Let's Consult the Oracle (History)	11th December, 2013
4	Prof. Shehu Abdul Rahman, Professor of Agricultural Economics & Extension	Farm Production Efficiency: The Scale of Success in Agriculture.	26th June, 2013
5	Prof. Muhammad Akaro Mainoma, Professor of Accounting and Finance	Most Acceptable Index Needed Of Measuring Accounting (MAINOMA)	8th January, 2013
6	Prof. Sam O. Smah, Professor of Criminology Studies	Researching Criminal Justice and Security Administration in Nigeria: Issues, Challenges and Opportunities.	12th March, 2014

7	Prof. Emmanuel Hala Kwan-Ndung, Professor of Plant Genetics and Breeding	Unlocking Genetic in Search of Food Security	17th September, 2014
8	Prof. Zaynab Alkali, Professor of Literature and Literary Studies	The Relevance of Gender Studies in Nigeria's Higher Institutions of Learning: Why Gender Studies?	17th December, 2014
9	Prof. Haruna Kuje Ayuba, Professor of Biogeography and Environmental Science	Habitat and our Habits, Ecological Community and Common Unity	22nd April, 2015
10	Prof. Folorunso Abiodun Ajayi, Professor of Agricultural Entomology/Crop Protection	Insects, Plants and Humanity: The Organic Agriculture and Stored Products Protection Axis	18th November, 2015

This publication is intended to provide easy reference material to the academic community, policy makers and the general public. It is hoped that we shall continue with this tradition with subsequent editions.

While congratulating those that are part of this publication, I recommend this publication, to the professional colleagues of the inaugural lecturers, University community, policy makers and the general public.

Professor M. A. Mainoma
Vice-Chancellor

Table of Contents

7

UNLOCKING GENES IN SEARCH OF FOOD SECURITY

EMMANUEL HALA KWON-NDUNG
(B.Sc (ABU), M.Sc, Ph.D (JOS)
Professor of Plant Genetics and Breeding

Wednesday, 17th September 2014.

PROTOCOL
The Vice Chancellor, Sir,
Principal Officers of the University,
Deans and Directors,
Heads of Departments and Units,
My Lords Spiritual and Temporal,
Academic and Professional Colleagues,
Colleagues in NSUK Community,
Colleagues from FULafia,
Special Guests,
Ladies and Gentlemen of the Press,
Distinguished Ladies and Gentlemen,
Great NSUKITES!

1.0 PREAMBLE

Vice-Chancellor, Sir, I am here today to deliver this Inaugural Lecture by the mercies of God. Foremost, therefore, is my return of all praise, honour, adoration and thanksgiving to God Almighty, the father of the orphan, the husband of the widow, the everlasting redeemer and prince of peace, for His grace, which has made it possible for me to give this Inaugural Lecture. There are numerous individuals who have desired to give Inaugural Lectures, but could not qualify to give one. Others who qualified to present one never had the occasion to do so and this is common in the Nigerian University system where some Professors get to retirement without having an opportunity to share their experiences. There are possibly yet others who got the opportunity, prepared their lectures, decided on a date, but for one reason or the other, never got to deliver them. It is for all these reasons, Sir, that I declare that this privilege to deliver this lecture today is an endorsement of the mercies of God. May I use this

opportunity to wish all that are aspiring to achieve this prominence, success. Amen.

I specially thank the Ag. Vice-Chancellor, Prof. Muhammad Akaro Mainoma for making it possible for me to give this inaugural lecture. At the point that I had to relocate my services from the University, the intention to present my Inaugural Lecture was received with sundry moods and I thought I might have lost an opportunity to do so. I feel greatly honoured and humbled, to be given the opportunity to deliver the seventh Inaugural Lecture of this great University as the second from the Faculty of Natural and Applied Sciences and indeed the first from the Department of Biological Sciences. By tradition, an inaugural lecture is a Professor's academic report and an occasion to enlighten colleagues, the University community and the general public on the significance of their research work and their past contributions to knowledge in the wider academic community as well as to discuss their present research and their future plans. I am obliged by the rule of the game to present my stewardship in the academic realm spanning about 22 years for a period of just one hour.

My career in Science and more precisely a specialisation in Genetics and Breeding was an act of inspired destiny. In my Secondary School, I was a good student of the Arts subjects with English Literature being one of my favourite subjects. Mr Vice-Chancellor sir, the lessons from a story we read in our Literature classes in Form Three helped in shaping my destiny. Jonathan Swift, the Irish writer and clergyman in his novel "Gulliver's Travels" written in 1726 and amended in 1735 gave an account of Lemuel Gulliver's travels into several remote nations of the World. The book which is a satire on human nature and a sarcasm of the "travellers' tales" shows in part two of the book, how Gulliver is abandoned by his companions and found by a farmer who is 72 feet (22 m) tall in Brobdingnag. The farmer brings Gulliver home and his daughter cares for Gulliver. The farmer treats him as a curiosity and exhibits him for money. After a while the constant shows make Gulliver sick, and the farmer sells him to the queen of the kingdom. The farmer's daughter who accompanied her father while exhibiting Gulliver is taken into the queen's service to take care of the tiny man. Since Gulliver is too small to use their huge chairs, beds, knives and forks, the queen commissions a 'travelling box' (a small house) to be built for him so that he can be carried around in it. Between small adventures such as fighting giant wasps and being carried to the roof by a monkey, he discusses the state of Europe with the King. He makes a proposal he feels is of much advantage to the king, which the king rejects. The learning of that country is very imperfect and confined and the laws, and military affairs, and parties in the state highly undeveloped. Gulliver feels the king is highly ignorant in politics.

The King is not happy with Gulliver's accounts of Europe, especially upon learning of the use of guns and cannons. The King in response to Gulliver's account of Europe gives his opinion, "that whoever could make two ears of corn, or two blades of grass, to grow upon a spot of ground where only one grew before, would deserve better of mankind, and do more essential service to his country, than the whole race of politicians put together."

Mr Vice Chancellor sir, this book which compares the truly moral man to the representative man had a great impact in my young life. The response of this King swayed my choice of subjects into the Science Class on resumption in Form Four and I dropped English Literature in which I was a favourite of Mrs. Iliya, our Teacher and enrolled into the Science class. And very true to Karl Marx's school-leaving essay "Reflections of a young man on the choice of a profession", I looked forward to how I can work for perfection for the good of my fellow men, in line with the opinion of the King in Jonathan Swift's story.

Mr. Chairman, the nub of this discussion is titled 'Unlocking Genes in Search of Food Security' and I will try to convey to you how my research work in Plant Genetics and Breeding has contributed in the searching of national and global food security. Permit me to give a brief descriptions of some of the keywords that will be recurring in this lecture.

1.1.DEFINITIONS

1.1.1 Genes and Inheritance

Genes constitute the design of life and along with the environment, define the identity and the uniqueness of every organism through their phenotypic effects. In spite of this fundamental importance of genes in determining the physical, physiological and behavioural identities of organisms, their existence is only made known by mutations, the heritable changes in gene functions.

The knowledge of the natural resemblance between offspring and their parents has remained a conscious phenomenon in the life of man and consequently, man has constantly acknowledged that there is inheritance or heredity. The ignorance of man was nevertheless clouded in how this inheritance came about. In our local parlances, it is common to observe that when a man's children resembled him, he was viewed as a super-father. Similarly, the behaviour of children that please parents welcomes accolades such as 'you are the true son/daughter of your parents'. However if a child performs below the parent's expectation, it is common to hear disappointing retorting comments such as the Aten will exclaim 'ngyhe ngyhe hadele? meaning'who is the owner of this one?. Our knowledge of the role of genes in heredity came from the 19th century classical experiments of Gregor Mendel,

which was based on the inheritance of contrasting states of characters in the garden pea plant (Pisum sativum). He carried out series of monohybrid crosses (i.e. crosses involving only one character such as seed colour at a time) and established the classical second generation filial (F2) phenotypic ratio 3:1. He also carried out series of dihybrid crosses (i.e. crosses involving two characters such as seed colour and seed shape at a time) and established the classical second generation filial (F2) phenotypic ratio of 9:3:3:1.

Gregor Mendel was able to establish from his monohybrid experiments that genes which he referred to as particles or hereditary factors or determinants are responsible for the appearance of characters. Each hereditary factor was particulate in nature and formed the basic unit of heredity occurring in two alternative states known as dominant and recessive alleles, and were observed to be discrete and un-blending. Mendel also deduced that the members (alleles) of the gene pairs segregate (separate) equally into the gametes (eggs and sperms) prior to the random union of gametes from the different sexes to form new progeny. From his di-hybrid experiment, he established that the two members (alleles) of a gene pair separate and move into gametes independently of members of other gene pairs(i.e. that different gene pairs assort independently during gamete formation). Mendel's monohybrid and di-hybrid experimental results became his two laws of heredity, namely the Law of segregation and the Law of independent assortment respectively. The law of segregation of hereditary factors states that the two particulate members of a gene pair segregate from each other into the gametes, so that half the gametes carry one member of the pair and the other half of the gametes carry the other member of the pair. The law of independent assortment of genes, on the other hand, states that during gamete formation, the segregation of the alleles of one gene is independent of the segregation of the alleles of another gene. Although, these laws are fundamental to genetics and are true, they are more like the exceptions rather than the rules in nature. We now know that Mendel's hereditary factors were major genes of major discrete clear-cut phenotypic effects, but in reality, nature abounds with hereditary factors whose phenotypic effects are not so clear-cut. For example, incomplete dominance, co-dominance, additive gene action and linkages of genes are common in nature. In some of these cases, Mendel's classical ratios of 3:1 (monohybrid phenotypic ratio) and 9:3:3:1 (dihybrid phenotypic ratio) are modified and in others the ratios are completely obliterated. Mendel's second law is also only valid for genes that are on different chromosomes or distantly located on the same chromosome (i.e. not linked).

These observations, notwithstanding Mendel's experimental findings and laws of heredity, published in 1865, remain the basic principles of heredity and classical laws of genetics without which our understanding of genetics today would be incoherent. For this reason, Gregor Mendel is widely regarded as the father of modern genetics. His experiments carried out in his spare time in the Monastery did not only expose the existence and function of genes, but also exposed the rewards of his meticulous and dedicated experimentations in the garden in the Monastery.

1.1.2. Biotechnology and Genetic Engineering

Biotechnology is simply defined as the science of making useful products and services from any biological system. Food and Agricultural Organization (FAO) of the United Nations defines biotechnology as "any technique that uses living organisms or substances from these organisms to make or modify a product for a practical purpose" (FAO, 2004). Biotechnology exists in the traditional and modern forms.

Traditional Biotechnology is captured in the traditional processes of wine, bread and cheese making as well as traditional processing methods for foods and condiments such as akamu, akpu or fufu, daddawa and pito or burukutu. In addition, the domestication, breeding and selection of superior and desirable plants and animals by man are also regarded as traditional biotechnology. Modern biotechnology includes gene cloning with genetic engineering at its core.

Advances in modern breeding and selection methods have increased crop yields in the last three decades and the green revolution in developed countries is a significant basis of this progress. However, these advances are constrained by the natural diversity limitations of trait incompatibilities existing within crop species. This has led to a justification of the use of modern biotechnology techniques in crop breeding and selection.

Modern biotechnology has been defined as the application of in vitro nucleic acid techniques, including recombinant deoxyribonucleic acid (DNA), and direct injection of nucleic acid into cells or organelles; or fusion of cells beyond the taxonomic family that overcome natural physiological reproductive or recombination barriers, and that are not techniques used in traditional breeding and selection.

Modern biotechnology employs molecular techniques to identify, select and modify DNA sequences for a specific genetic trait (e.g. insect resistance) from a donor organism (microorganism, plant or animal), and transfer the sequence to a recipient organism so that it expresses this trait. A DNA molecule referred to as a vehicle or vector (which is usually plasmid or viral DNA) is

usually required to carry the DNA into the cell. A successful transfer, is referred to as a transformation of the receiving cell. Various transformation methods are used to transfer recombinant DNA into recipient species to produce a genetically modified organism (GMO). For plants, these include transformation mediated by Agrobacterium tumefaciens (a common soil bacterium that contains genetic elements for infection of plants), as well as biolistic, shooting recombinant DNA coated on microparticles such as gold, into recipient cells. Techniques used in transformation of some animal species include microinjection and electroporation. The insertion of foreign genes into organisms is part of the ongoing source of controversy for GMOs.

Genetic engineering which is the core of modern biotechnology is the manipulation of DNA to produce useful traits in living organisms. DNA is the blueprint of life and conveys genetic information that provides instructions for the development and survival of all organisms. DNA consists of a nitrogen base, a ribose sugar and a phosphate group. Two strands are wound together to form a double helix. The nitrogen bases, adenine (A), thymine (T), cytosine (C) and guanine (G), constitute the "alphabets" of DNA. After the discovery of the structure of DNA by Watson and Crick in 1953, there was a break in the life sciences, because no one knew how to cut or join the molecule. Science had to wait till the early 70s for the discovery of restriction enzymes which cut DNA at specific sequences, and DNA ligases that join it together again. Modern biotechnology is today driven by gene cloning and other DNA manipulations, made possible by the new molecular biology techniques.

1.1.3. Food Security The Rome Declaration on World Food Security and the World Food

Summit Plan of Action, convened by the United Nations Food and Agriculture Organization, resolved that "food security exists when all people, at all times, have physical and economic access to sufficient, safe and nutritious food to meet their dietary needs and food preferences for an active and healthy life." (FAO, 1996). Food security is, therefore, built on three pillars of food availability, food access and food use. The global challenges to achieving food security include: I).

Global water crisis especially in sub-Saharan Africa which has led to water deficits, which are in turn leading to large grain imports to many of these countries. It is estimated that by 2030, 75 million to 250 million people in Africa will be living in areas of high water stress, which will likely displace between 24 million and 700 million people as conditions become increasingly unliveable. Since majority of Africa depends on an agrarian lifestyle and about 90% of families in rural Africa depend on producing their own food, water scarcity will translate to a loss of food security.

i) Land degradation and desertification: Intensive farming has resulted into a vicious cycle of exhaustion of fertility of soils a subsequent decline of crop yields. About 40% of the world's agricultural land is seriously degraded and if current trends of soil degradation continue in Africa, the continent might be able to feed just 25% of its population by 2025.

ii) Climate change: Droughts and floods which affect crop productivity, are predictions to increased climate changes. It is predicted that by 2040, the entire Nile region, which once included large areas of irrigated agricultural land, is expected to become hot desert where cultivation is impossible due to water limitation. According to the Climate and Development Knowledge Network report, the impacts will include changing productivity and livelihood patterns, economic losses, and impacts on infrastructure, markets and food security. Food security in future will be linked to our ability to adapt agricultural systems to extreme events such as reviving and improving production of traditional crops, building up traditional methods of crop protection and soil conservation, conservation of wild plant species all with the aim to reduce the vulnerability to the threats of unstable weather patterns.

iii) Crop diseases: Diseases affecting crops can have adverse effects on food availability. The genetic diversity of the crop wild relatives (CWR) can be used to improve varieties which have resistance to such diseases. Crop wild relatives and modern varieties are crossed through means of modern plant breeding and resistance genes are transferred from the wild plants to the modern varieties.

1.1.4. Global Plant Genetic Resources and Food Security.

Plant genetic resources (PGR) are according to the international convention for biodiversity, living material that includes genes of present and potential value for humans. Plant genetic resources thus include all our agricultural crops and some of their wild relatives which too often have valuable traits. Plant genetic resources are the backbone of agriculture and play a positive and unique role in the development of new cultivars including the restructuring of existing ones (Malik and Singh, 2006). Genotypes which could withstand better under abiotic and biotic pressures are the keys for sustainable agriculture and genes for such traits are sometimes available in wild species and land races. Studies on genetic diversity of crop wild relatives (CWR) have been carried out and there are many CWRs existing for different crops.

PGR are, therefore, key to sustainable agriculture and food security. The Food and Agricultural Organisation of the UN (FAO) estimates that humans

have used some 10,000 species for food throughout history. However, only about 120 cultivated species provide around 90% of food requirements and ONLY 4 species (Maize, Wheat, Rice and Potatoes) provide about 60% of human dietary energy for the entire world's population. Of the countless varieties of these crops developed by farmers over millennia, which form an important part of agricultural biodiversity, more than 75%, have been lost in the past 100 years (Williams, 2009).

In terms of PGR for food and agriculture, all nations and regions of the world are highly dependent on genes and species generated and developed in some other place. There is no nation that is independent in terms of plant genetic resources for food and agriculture. For example, in developing a series of VEERY wheat lines in 1977 by CIMMYT (The Centro Internacional de Mejoramiento de Maíz y Trigo) in Mexico, about 3170 different crosses were made among 51 individual parents originating in 26 countries around the world. The pedigree chart, when printed out, runs to six metres. At one point VEERY's 62 sister lines were grown annually on some three million hectares, spreading across Asia from Chile to China.

This interdependence has bred an international commitment to cooperation in protection of and access to plant genetic resources. There is growing recognition of the importance of building strong national programmes and ensuring collaboration among them, as the best way to safeguard and use the tremendous wealth of biodiversity.

Since 1983, FAO has been developing a Global System for the Conservation and Utilization of Plant Genetic Resources for food and agriculture. The Global System gives FAO the instruments it needs to face its responsibility in promoting world food security. The aims of the FAO initiative are:

- Conservation of biological diversity;
- Sustainable use of its components;
- Fair and equitable sharing of the benefits arising from the utilization of genetic resources.

There are 11 core elements to the system in the Report on the State of the World's Plant Genetic Resources which includes certain international bodies and agreements, plant germplasm collections, scientific networks and an early warning system (FAO, 1996). There are now 171 countries participating actively in the development of the major components of the Global System.

Among the core elements agreed to by the FAO Conference, which governs the organization, are the intergovernmental Commission on Genetic Resources for Food and Agriculture and the International Undertaking on Plant Genetic

Resources. The Commission provides a global forum in which countries that are considered as donors and users of germplasm as well as funders and owners of technologies can meet, on an equal footing, to discuss and reach consensus on matters related to plant genetic resources for food and agriculture.

The Undertaking contains provisions for "exploration and collection of genetic resources; conservation in situ and ex situ; international cooperation in conservation, exchange and plant breeding; coordination of gene bank collections and information systems; it also includes Farmers' Rights and mechanisms for related funding. The principles embodied in the Undertaking - including national sovereignty, access to plant genetic resources for food and agriculture and recognition and reward for farmers and other informal innovators - form the basis for the equitable conservation and sustainable use of genetic resources. The revision of the Undertaking - to harmonize it with the UN Convention on Biodiversity is currently under negotiation between national governments through the FAO Commission on Genetic Resources for Food and Agriculture.

An International Code of Conduct regulates the collection and transfer of plant genetic resources. The objectives are to prevent the erosion of genetic resources, assist access to them and protect the rights of countries and local communities. A further code of conduct covering the application of agro-biotechnologies is being developed. The World Information and Early Warning System on Plant Genetic Resources, for example, collects and disseminates information on plant genetic resources for food and agriculture, and related technologies. It will also alert the world of threats to the security of gene banks and dangers posed by genetic erosion. A network of in situ conservation areas will be established to complement ex situ collections which includes the Consultative Groups on International Agricultural Research collections.

1.1.5. Dialectics of Genes and Food Security

Having considered these definitions, it is proper to relate the hub of this lecture to the three pillars of food security which are food availability, food abundance and food use and the major challenges of food security which are global water deficit, land degradation and desertification, climate change and crop diseases. It is significant to note here that the proper management of genes can play a significant role in achieving the 3 pillars as well as overcoming the challenges that confront global attainment of food security. My research work over the years has concentrated on unlocking genes to address the three pillars of food security as well as the major challenges confronting food security.

2.1. Breeding Methods in Crop Plants

2.1.1 Conventional or Orthodox Plant Breeding

Ever since the practice of agriculture began between eight to ten thousand years ago, farmers have been altering the genetic makeup of the crops they grow. Early farmers selected the best looking plants and seeds and saved them to plant for the next season. A better understanding of the science of genetics revolutionised the process of selection and plant breeders used what they knew about the genes of a plant to select for specific sought-after characters to develop improved varieties.

The selection for traits such as earliness or faster growth, higher yields, pest and disease resistance, or quality characteristics has significantly transformed domesticated plant species compared to their crop wild relatives. For example, when maize was first grown in North and South America, thousands of years ago, the maize cobs farmers harvested were smaller than one's little finger. Today, there are hundreds of varieties of maize, some of which produce cobs that are as lengthy as the human forearm.

Conventional plant breeding which has been in practice for several millennia is still commonly used today. While early farmers discovered that some crop plants could be artificially mated or cross-pollinated to increase yields, they also observed that desirable characteristics from different parent plants could also be combined in the offspring. When the science of plant breeding was further developed in the 20th century, plant breeders understood better how to select superior plants and breed them to create new and improved varieties of different crops. This dramatically increased the productivity and quality of the plants grown for food, feed and fiber.

The art of recognizing desirable traits and incorporating them into future generations is very important in plant breeding. Breeders carefully observe their field plots and they can travel several distances in search of individual plants that harbour or exhibit desirable traits. A few of these traits occasionally arise spontaneously through a process called mutation.

2.1.1. Breeding Self-Pollinated Crop Plants

1) Self-pollinated crops: Many cultivated plant species reproduce by self-pollination. Self-pollinated species are believed to have originated from cross-pollinated ancestors in response to the environmental conditions to which such species are typically subjected. Often in-breeders are found at the extremes of the species distribution in marginal habitats and particularly in stress environments. Plant species showing self- pollination, i.e. inbreeding, are generally annuals or in any case, short –lived. These species, as a rule, must

have hermaphrodite flowers. But in most of these species, self- pollination is not complete and cross-pollination may occur up to 5%. The degree of cross-pollination in self- pollinated species is affected by several factors, E.g. variety, environmental conditions like temperatures and humidity, and location.

i) **Mechanism Promoting Self Pollination:**
The various mechanisms that promote self- pollination are generally more efficient than those promoting cross pollination. These mechanisms are briefly summarised below.

a. Cleistogamy: In this case, flowers do not open at all. This ensures complete self-pollination since foreign pollen cannot reach the stigma of a closed flower. Cleistogamy occurs in some varieties of wheat (Triticum sp), oats (Avena sp), barley(Hordeum vulgare) and in a number of other grasses.

b. Chasmogamy: In some species, the flowers open, but only after pollination has taken place. This occurs in many cereals, such as wheat, barley, rice and oats. Since the flowers do open, some cross-pollination may occur.

c. In crops like tomato (Lycopersicon esculentum) and eggplant (Solanum melongena), the stigmas are closely surrounded by anthers. Pollination generally occurs after the flowers open. But the position of anthers in relation to stigmas ensures self-pollination.

d. In some species, flowers open but the stamens and the stigma are hidden by other floral organs. In several legumes, e.g. pea (Pisum sativum), Mung bean (Vigna radiata) , Urd (Vigna mungo), soybean (Glycine max) and gram (C. arientinum), the stamens and the stigma are enclosed by two petals forming a keel.

e In a few species, stigmas become receptive and elongate through the staminal columns. This ensures predominant self –pollination.

ii. Genetic Consequences of Self- Pollination: Self-pollination leads to a very rapid increase in homozygosity. Therefore, populations of self-pollinated species are highly homozygous. Self-pollinated species do not show inbreeding depression, but may exhibit considerable heterosis. Therefore, the aim of breeding method generally is to develop homozygous varieties.

iii. Examples of Self Pollinated Crop Species 16

a. Cereals and Millets: Wheat (Triticum aestivum), Rice (Oryza sativa), Barley (Hordeum vulgare), Oats Avena sativa), Foxtail millet (Setaria utalica), Finger millet (Eleusine coracana),

b. Legumes: Pea (Pisum sativum), Groundnut (Arachis hypogea) ,Common bean (Vigna radiata), Cowpea (Vigna anguiculata), Soybean (Glycine max), Lentil (Lens esculentus), Beans (Phaselous vulgaris), Sunhemp (Crotalaria juncea).

c. Vegetables: Tomato (Lycopersicon esculentum), Okra (Abelmoschus esculentus), Lettuce (Lactuca sativa), Eggplant (Solanum melongena), Pepper (Capsicum annum), Potato (Solanum tuberosum) Forage Crops: Burr clover (Medicago hispida) 2. Subterranean (Trifolium subterraneum) Velvet bean (Mucuna deeringiana) Slender wheatgrass (Agropyron pauciflorum), Several other grasses.
d. Oil seeds Beniseed (Sesamum indicum), Linseed (Limum ustitatissimum).

e. Fruit Trees: Apricot (Prunus armericana), Nectarine (Prunus persica), Citrus (Citrus sp), Peach (Prunus persica).

2) Methods of Breeding Self-Pollinated Crop Plants

i. Recurrent Selection

Recurrent selection refers to selecting for certain traits generation after generation. With the interbreeding of reselected plants, the breeder can access favorable recombinations as well as stabilize traits within the genepool. Select your ideotype in each inter breeding line (IBL), but don't be totally reliant on the phenotype because it's not always indicative of the actual genotype. Make yield and quality trials with test crosses and select the best ten lines. Intercross and repeat.

After recurrent selection is done, select new individuals to be the new parents of IBLs. These are then recurrently selected for four or five generations. After recurrent selection has been done in two separate programs, an F1 single cross of the two lines (A X B) is then produced. In reciprocal recurrent selection (RRS), pollen of multiple A males is used to pollinate ideal B females and pollen of B used to pollinate ideal plants of A. Thus A is used as a tester to select for the combining ability of B plants, and B is a tester for A. At the same time, inbred seed lots (A X A) and (B X B) are made, using mixed male pollen and the best females of each population. Store the resulting seed i.e. the seed lines with the best combining ability will be used as parents of the next RRS cycle.

The (A X B) hybrid progeny are simply used as visual indicators of the combining ability that lies in the saved seeds. These specific inbred parental lines are kept in reserve until the progeny testing of the different (A X B) hybrids has shown which has better SCA and will make the better hybrids. Since this is such a complicated strategy, good note taking and organization are definitely required.

ii. Mass Selection

In mass selection, seeds are collected from (usually a few dozen to a few hundred) desirable appearing individuals in a population, and the next generation is sown from the stock of mixed seed. This procedure, sometimes referred to as phenotypic selection, is based on how each individual looks. Mass selection has been used widely to improve old "land" varieties, varieties that have been passed down from one generation of farmers to the next over long periods.

An alternative approach that has no doubt been practiced for thousands of years is simply to eliminate undesirable types by destroying them in the field. The results are similar whether superior plants are saved or inferior plants are eliminated: seeds of the better plants become the planting stock for the next season.

A modern refinement of mass selection is to harvest the best plants separately and to grow and compare their progenies. The poorer progenies are destroyed and the seeds of the remainder are harvested. It should be noted that selection is now based not solely on the appearance of the parent plants but also on the appearance and performance of their progeny. Progeny selection is usually more effective than phenotypic selection when dealing with quantitative characters of low heritability. It should be noted, however, that progeny testing requires an extra generation; hence gain per cycle of selection must be double that of simple phenotypic selection to achieve the same rate of gain per unit time.

Mass selection, with or without progeny test, is perhaps the simplest and least expensive of plant-breeding procedures. It finds wide use in the breeding of certain forage species, which are not important enough economically to justify more detailed attention.

iii. Pure-Line Selection

Pure-line selection generally involves three more or less distinct steps:

a) numerous superior appearing plants are selected from a genetically variable population;

b) progenies of the individual plant selections are grown and evaluated by simple observation, frequently over a period of several years; and

c) when selection can no longer be made on the basis of observation alone, extensive trials are undertaken, involving careful measurements to determine whether the remaining selections are superior in yielding ability and other aspects of performance.

Any progeny superior to an existing variety is then released as a new "pure-line" variety. Much of the success of this method during the early 1900s depended on the existence of genetically variable land varieties that were waiting to be exploited. They provided a rich source of superior pure-line varieties, some of which are still represented among commercial varieties. In recent years the pure-line method as outlined above has decreased in importance in the breeding of major cultivated species; however, the method is still widely used with the less important species that have not yet been heavily selected.

A variation of the pure-line selection method that dates back centuries is the selection of single-chance variants, mutations or "sports" in the original variety. A very large number of varieties that differ from the original strain in characteristics such as colour, lack of thorns or barbs, dwarfness, and disease resistance have originated in this fashion.

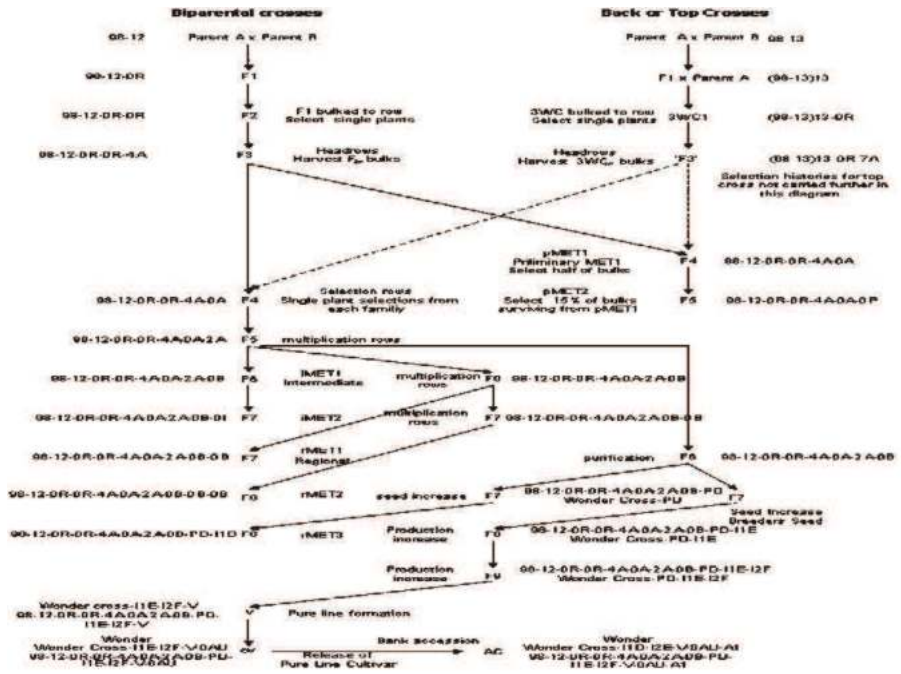


Fig. 1: Pureline selection procedure

iv. Hybridization

During the 20th century planned hybridization between carefully selected parents has become dominant in the breeding of self-pollinated species. The object of hybridization is to combine desirable genes found in two or more different varieties and to produce pure-breeding progeny superior in many respects to the parental types.

Genes, however, are always in the company of other genes in a collection called a genotype. The plant breeder's problem is largely one of efficiently managing the enormous numbers of genotypes that occur in the generations following hybridization. As an example of the power of hybridization in creating variability, a cross between hypothetical wheat varieties differing by only 21 genes is capable of producing more than 10,000,000,000 different genotypes in the second generation. At spacing normally used by farmers, more than 50,000,000 acres would be required to grow a population large enough to permit every genotype to occur in its expected frequency. While the great majority of these second generation genotypes are hybrid (heterozygous) for one or more traits, it is statistically possible that 2,097,152 different pure-breeding (homozygous) genotypes can occur, each potentially a new pure-line variety. These numbers illustrate the importance of efficient techniques in managing hybrid populations, for which purpose the pedigree procedure is most widely used.

v. Hybrid Varieties

The development of hybrid varieties differs from hybridization. The F1 hybrid of crosses between different genotypes is often much more vigorous than its parents. This hybrid vigour, orheterosis, can be manifested in many ways, including increased rate of growth, greater uniformity, earlier flowering, and increased yield, the last being of greatest importance in agriculture.

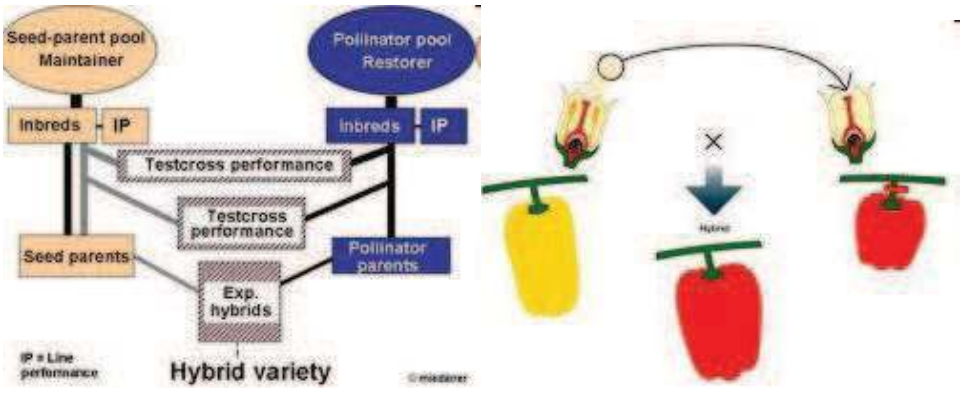


Fig. 2: Hybrid populations

vi. **Pedigree Breeding** starts with the crossing of two genotypes, each of which have one or more desirable characters lacked by the other. If the two original parents do not provide all of the desired characters, a third parent can be included by crossing it to one of the hybrid progeny of the first generation (F1). In the pedigree method superior types are selected in successive generations, and a record is maintained of parent–progeny relationships.

The F2 generation (progeny of the crossing of two F1 individuals) affords the first opportunity for selection in pedigree programs. In this generation the emphasis is on the elimination of individuals carrying undesirable major genes. In the succeeding generations the hybrid condition gives way to pure breeding as a result of natural self-pollination, and families derived from different F2 plants begin to display their unique character. Usually one or two superior plants are selected within each superior family in these generations. By the F5 generation the pure-breeding condition (homozygosity) is extensive, and emphasis shifts almost entirely to selection between families. The pedigree record is useful in making these eliminations. At this stage each selected family is usually harvested in mass to obtain the larger amounts of seed needed to evaluate families for quantitative characters. This evaluation is usually carried out in plots grown under conditions that simulate commercial planting practice as closely as possible. When the number of families has been reduced to manageable proportions by visual selection, usually by the F7 or F8 generation, precise evaluation for performance and quality begins. The final evaluation of promising strains involves:

(1) observation, usually in a number of years and locations, to detect weaknesses that may not have appeared previously;

(2) precise yield testing; and

(3) quality testing. Many plant breeders test for five years at five representative locations before releasing a new variety for commercial production.

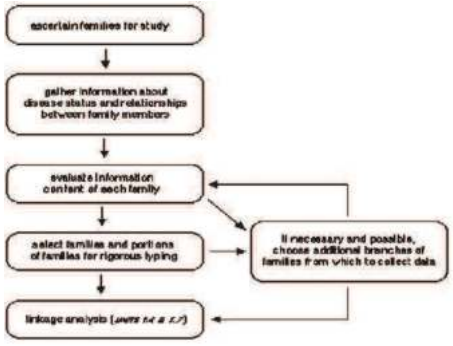


Fig. 3: Pedigree breeding

vii. The bulk-population method of breeding differs from the pedigree method primarily in the handling of generations following hybridization. The F2 generation is sown at normal commercial planting rates in a large plot. At maturity the crop is harvested in mass, and the seeds are used to establish the next generation in a similar plot. No record of ancestry is kept. During the period of bulk propagation natural selection tends to eliminate plants having poor survival value. Two types of artificial selection also are often applied:

a) destruction of plants that carry undesirable major genes and

b) mass techniques such as harvesting when only part of the seeds are mature to select for early maturing plants or the use of screens to select for increased seed size. Single plant selections are then made and evaluated in the same way as in the pedigree method of breeding. The chief advantage of the bulk population method is that it allows the breeder to handle very large numbers of individuals inexpensively.

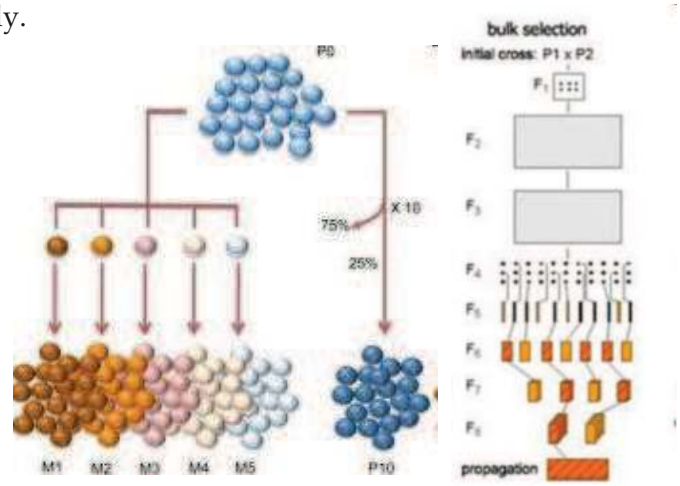


Fig. 4: Bulk method of breeding

viii. Backcrossing

Often an outstanding variety can be improved by transferring to it some specific desirable character that it lacks. This can be accomplished by first crossing a plant of the superior variety to a plant of the donor variety, which carries the trait in question, and then mating the progeny back to a plant having the genotype of the superior parent. This process is called backcrossing. After five or six backcrosses the progeny will be hybrid for the character being transferred but like the superior parent for all other genes. Selfing the last backcross generation, coupled with selection, will give some progeny pure breeding for the genes being transferred. The advantages of the backcross method are its rapidity, the small number of plants required, and the

predictability of the outcome. A serious disadvantage is that the procedure diminishes the occurrence of chance combinations of genes, which sometimes leads to striking improvements in performance.

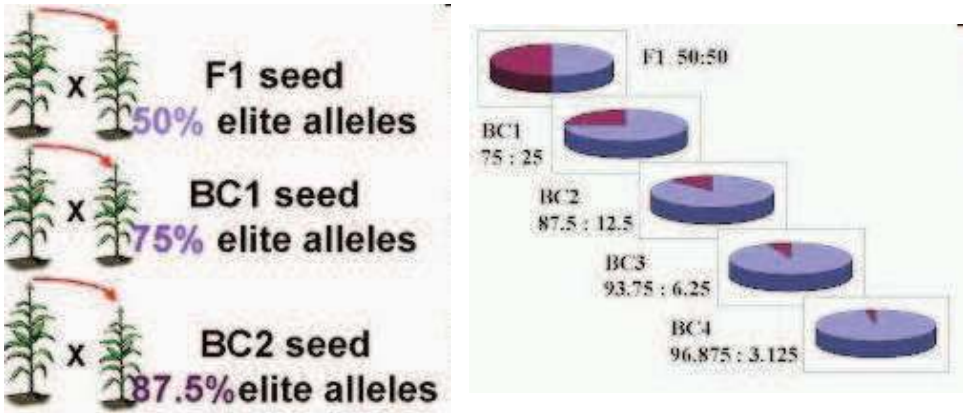


Fig. 5: Backcross breeding method

2.1.2. Breeding Cross Pollinated Species

1. Cross-pollinated species. In cross pollinating species, the transfer of pollen from a flower to the stigmas of the others may be brought about by wind (anemophily), water (hydrophily) or insects (entomophily). Many of the crop plants are naturally cross – pollinated. In many species, a small amount (upto 5-10 %) of selfing may also occur.

Mechanisms Promoting Cross Pollination:

There are several mechanisms that facilitate cross pollination, these mechanisms are descried briefly.

i. Dicliny, Dicliny, or Unisexuality is a condition, in which the flowers are either staminate (male) or pistilate (female). Dicliny is of two type's viz. 1) Monoecy and 2) Diaecy i. e. Monoecy: Staminate and pistilate flowers occur in the same plant, either in the same inflorescences. E.g. Castor, Mango, Banana, and coconut or in separate inflorescences. E. g, maize, other monoecious species are cucurbits (Cucurbits sp), walnut, chestnut,strawberry, rubber, grapes.

ii. Examples of Cross Pollinated Species.

Cereals: Include Maize (Zea mays), Rye (Secale cereale), Pearl millet (Pennisetum americanum), Finger millet (Eleusine corocana), Sugarcane (Saccharum oficinarum).

Legumes: Soybeans (Glycine max), Alfalfa (Medicago sativa), Red clover (Trifolium pratense), White clover (Trifoliumrepens), Crimson clover

(Trifolium incarnatum), Sweet clover (Melitotus officianalis), Birdsfoot trefoil (Lotus corniculatus) and Groundnut (Arachis hypogea).

Vegetables: Cabbage (Brassica oleracea), Carrot (Daucus carota), Cauliflower (Brassica oleracea), Cucumber (Cucumis sativus), Onion (Allium cepa), Watermelon (Citrullus vulgaris), Squash (Cucurbita elanosperma), Sweet potato (lpomoea batatas) Other cucurbits (Cucurbita sp), Beets (Beta vulgaris), Broccoli (Brassica oleracea), Brussels sprouts (Brassica oleracea), Spinach (Spinacea oleracea), Asparagus (Asparagus officinalis), Garlic (Allium sativum), Coriander (Coriandrum sativum).

Oil Seeds:Some strains of Brassica compestris, Sunflower (Helianthus annus), Castor (Ricinus communis).

Forage Crops: Ryegrass (Lolium perenne), Timothy grass (Phleum pratense), Smooth bromegrass, Bromus inermis), Johnson grass (Sorghum halepense).

Other crops: Some lines of potato (Solanum tuberosom), Hemp (Cannabis indica), Hops (Humulus lupulus).

Fruits:Apple (Pyrus malus), Avocado (Persea americana), Mango (Mangifera indica), Pear (Pyrus communis), Blackberries (Rubus fruticous), Raspberries (Rubus spp), Walnut (Juglans regia), Chestnut (Castanea sativa and C.vexa), Hazelnut (Corylus americana and cornuta), Banana (Musa spp), Date palm (Phenix dactifera), Fig (Ficus carica), Coconut (Cocos nucifera), Grapes (Vitis vinifera), Papaya (Carica papaya), Plum (Prunus divaricata), Loquat (Eriobotrya japonica), Strawberries (Fragaria sp), Almod (Prumus amygdalus), Pistachio nut (Pistacia vera).

ii) Methods of Breeding Cross-Pollinated Crop Plants

The most important methods of breeding cross-pollinated species are (1) mass selection; (2) development of hybrid varieties; and (3) development of synthetic varieties. Since cross-pollinated species are naturally hybrid (heterozygous) for many traits and they lose vigour as they become purebred (homozygous), the main goal of each of these breeding methods is to preserve retain or restore heterozygosity.

a) Mass Selection

Mass selection in cross-pollinated species takes the same form as in self-pollinated species; i.e., a large number of superior appearing plants are selected and harvested in bulk and the seed used to produce the next generation. Mass selection has proved to be very effective in improving qualitative characters, and, applied over many generations, it is also capable of improving quantitative characters, including yield, despite the low heritability of such characters. Mass

selection has long been a major method of breeding cross-pollinated species, especially in the economically less important species.

b) Hybrid Varieties or Hybrid Breeding

The outstanding example of the exploitation of hybrid vigour through the use of F1 hybrid varieties has been with corn (maize). The production of a hybrid corn variety involves three steps: (1) the selection of superior plants; (2) selfing for several generations to produce a series of inbred lines, which although different from each other are each pure-breeding and highly uniform; and (3) crossing selected inbred lines. During the inbreeding process the vigour of the lines decreases drastically, usually to less than half that of field-pollinated varieties. Vigour is restored, however, when any two unrelated inbred lines are crossed, and in some cases the F1 hybrids between inbred lines are much superior to open-pollinated varieties. An important consequence of the homozygosity of the inbred lines is that the hybrid between any two inbreds will always be the same. Once the inbreds that give the best hybrids have been identified, any desired amount of hybrid seed can be produced.

Pollination in corn (maize) is by wind, which blows pollen from the tassels to the styles (silks) that protrude from the tops of the ears. Thus controlled cross-pollination on a field scale can be accomplished economically by interplanting two or three rows of the seed parent inbred with one row of the pollinator inbred and detasselling the former before it sheds pollen. In practice most hybrid corn is produced from "double crosses," in which four inbred lines are first crossed in pairs (A × B and C × D) and then the two F1 hybrids are crossed again (A × B) × (C × D). The double-cross procedure has the advantage that the commercial F1 seed is produced on the highly productive single cross A × B rather than on a poor-yielding inbred, thus reducing seed costs. In recent years cytoplasmic male sterility, described earlier, has been used to eliminate detasselling of the seed parent, thus providing further economies in producing hybrid seed. Much of the hybrid vigour exhibited by F1 hybrid varieties is lost in the next generation. Consequently, seed from hybrid varieties is not used for planting stock but the farmer purchases new seed each year from seed companies.

Hybrid breeding takes advantage of the heterosis effect. This effect means that offspring of a crossing has higher yields than the respective parent lines. For hybrid breeding, inbred male and female lines are developed which are as different as possible. These true-breeding (homozygous) lines will then be crossed with each other.

In order to make sure that the inbred line used as mother parent will only be pollinated by the inbred father parent line, self-pollination must be

precluded. To ensure this, castrated or male sterile lines (lines not producing own pollen) are used as mother parent. Unisexual maize e.g. lends itself to manual castration of the mother plant by simply removing the tassels. In species with bisexual flowers (e.g. oilseed rape or rye), genetic sterility mechanisms are being applied.

The offspring of the crossing of the inbred lines are hybrids. Heterosis, i.e. superior performance, will only be strong in this first generation. As a consequence of Mendel's second Law of Segregation, it will already be lost in the next generation.

Hybrid breeding has been used mainly for open-pollinating species (maize, oilseed rape, sunflower and rye).

Perhaps no other development in the biological sciences has had greater impact on increasing the quantity of food supplies available to the world's population than has the development of hybrid corn (maize). Hybrid varieties in other crops, made possible through the use of male sterility, have also been dramatically successful and it seems likely that use of hybrid varieties will continue to expand in the future.

c) Synthetic Varieties

A synthetic variety is developed by intercrossing a number of genotypes of known superior combining ability—i.e., genotypes that are known to give superior hybrid performance when crossed in all combinations. (By contrast, a variety developed by mass selection is made up of genotypes bulked together without having undergone preliminary testing to determine their performance in hybrid combination.) Synthetic varieties are known for their hybrid vigour and for their ability to produce usable seed for succeeding seasons. Because of these advantages, synthetic varieties have become increasingly favoured in the growing of many species, such as the forage crops, in which expense prohibits the development or use of hybrid varieties.

d) Breeding of Open Pollinated or Hybrid Seed

The end result of plant breeding is either an open–pollinated (OP) variety or an F1(first filial) hybrid variety. OP varieties, when maintained and produced properly, retain the same characteristics when multiplied. The only technique used with OP varieties is the selection of the seed-bearing plants.

Hybrid seeds are an improvement over open pollinated seeds in terms of qualities such as yield, resistance to pests and diseases, and time to maturity.

Hybrid seeds are developed by the hybridization or crossing of parent lines that are 'pure lines' produced through inbreeding. Pure lines are plants that "breed true" or produce sexual offspring that closely resemble their

parents. By crossing pure lines, a uniform population of F1 hybrid seed can be produced with predictable characteristics.

The simplest way to explain how to develop an F1 hybrid is to take an example. Let us say a plant breeder observes a particularly good habit in a plant, but with poor flower colour, and in another plant of the same type he sees good colour but poor habit. The best plant of each type is then taken and self-pollinated (in isolation) each year and, each year, the seed is re-sown. Eventually, every time the seed is sown the same identical plants will appear. When they do, this is known as a 'pure line.'

If the breeder now takes the pure line of each of the two plants he originally selected and cross pollinates the two by hand the result is known as an "F1 hybrid." Plants are grown from the seed produced, and the result of this cross pollination should have the combined traits of the two parents.

This is the simplest form of hybridization, but there are complications, of course. A completely pure line can sometimes take seven or eight years to achieve. Sometimes, a pure line is made up of several previous crossings to build in desirable features. The resulting plant is then grown on until it is genetically pure before use in hybridization.

In addition to qualities like good vigour, trueness to type, heavy yields and high uniformity which hybrid plants enjoy, other characteristics such as earliness, disease and insect resistance and good water holding ability have been incorporated into most F1 hybrids.

Unfortunately, these advantages come with a price. Because creating F1 hybrids involves many years of preparation to create pure lines that have to be constantly maintained so that F1 seeds can be harvested each year, the seeds then become more expensive. The problem is compounded because to ensure that no self-pollination takes place, all the hybridization of the two pure lines, sometimes, has to be done by hand.

Another disadvantage is if the seeds of the F1 hybrids are used for growing the next crops, the resulting plants do not perform as well as the F1 material - resulting in inferior yields and vigour. As a consequence, the farmer has to purchase new F1 seeds from the plant breeder each year. The farmer is, however, compensated by higher yields and better quality of the crop.

Though more expensive, hybrid seeds have had a tremendous impact on agricultural productivity. Today, nearly all corn and 50% of all rice are hybrids (DANIDA).

In the US, the widespread use of corn hybrids, coupled with improved cultural practices by farmers, has more than tripled corn grain yields over the past 50 years from an average of 35 bushels per acre in the 1930s to 115 bushels

per acre in the 1990s. No other major crop anywhere in the world even comes close to equalling that sort of success story.

Hybrid rice technology helped China increase its rice production from 140 million tons in 1978 to 188 million tons in 1990. Research at the International Rice Research Institute (IRRI) and in other countries indicates that hybrid rice technology offers opportunities for increasing rice varietal yields by 15-20%. And this is achievable with the improved, semi-dwarf, and inbred varieties (IRRI).

Many cultivars of popular vegetables or ornamental plants are F1 hybrids. In terms of improved plant characteristics, breeders can point to some rather clear achievements over the last two decades: they include: 26

- Yield improvement. Hybrids often outyield traditional OP selections by 50-100% due to its improved vigor, improved genetic disease resistance, improved fruit setting under stress, and higher female/male flower ratios.
- Extended growing season. Hybrids often mature up to 15 days earlier than local OP varieties. For many crops, the hybrid's relative advantage over the OP is most pronounced under stress conditions.
- Quality improvement. Hybrids have helped stabilize product quality at a higher and more uniform level – this implies improved consumption quality (e.g. firm flesh of wax gourd, crispy taste of watermelon).

2.2. Mutation Breeding

In the late 1920s, researchers discovered that they could greatly increase the number of these variations or mutations by exposing plants to X-rays and chemicals. Mutation breeding was further developed after World War II, when the techniques of the nuclear age became widely available. Plants were exposed to gamma rays, protons, neutrons, alpha particles, and beta particles to see if these would induce useful mutations. Chemicals, too, such as sodium azide and ethyl methane sulphonate, have been used to create mutations.

Mutation breeding efforts continue around the world today. Of the 2,252 officially released mutation breeding varieties, 1,019 or almost half have been released during the last 15 years. Examples of plants that have been produced via mutation breeding include wheat, barley, rice, potatoes, soybeans, onions, sugarcane and maize.

2.2.1. Role of Mutation in creating Variation for Plant Breeding

Variation is the source from which plant breeders are able to produce new and important cultivars. Alleles of varying forms at given loci in a population can be selected and fixed within a new individual or line. We

depend on recombination and independent assortment of favourable alleles to produce new and unique individuals from which to select and produce the lines that will serve as our cultivars. With tens of thousands of genes within each crop species genome, the possibilities seem limitless. However, this is not so clearly the case.

Variation within a population can be exploited by selecting individuals with new combinations of desirable traits or alleles. Genetic diversity of crop plants of most crop species, which have been selectively bred for centuries, have large portions of their genome essentially fixed. This means then, that the portions of DNA, and therefore number of traits available for being engaged in crosses are reduced. This reduction, however unpromising it may seem, has still allowed us to make significant gains in crop yield and quality in recent decades.

So, while recombination of alleles provides offspring with presumably selectable variation for the spectrum of traits exhibited, it is only capable of creating new combinations of traits already existing. Recombination does not of itself produce novel traits. This ability is only attainable through the act of mutation, which can ultimately lead to new species. Harten gives his working definition of mutation in plants as "any heritable change in the idiotypic constitution of sporophytic or gametophytic plant tissue, not caused by normal genetic recombination or segregation" (Harten, 1998). These changes in our target plant can be passed on to progeny and used for human benefit through breeding. The occurrence of mutations within the genome of plants is rare, and in natural settings can be lethal. Through breeding and selection, beneficial mutants can be identified and used to improve target species. In this lecture, we will discuss the basic concepts surrounding mutation, as well as the application and exploitation of mutation in plant breeding programs.

2.2.2. Naturally occurring mutations

Mutations occur spontaneously in natural settings quite frequently. They can happen due to mistakes made during cell replication or exposure to mutagens such as radiation. It is estimated that a mutation occurs every 10-8 base pair per generation in eukaryotic genomes (Drake et al., 1998). In corn (Zea mays), mutations occur from 10-6 to 5 x 10-4 per base pair per generation (Stadler, 1930). Those that we can track easily in the offspring are mutations occurring in either the gametes or cells that give rise to the gametes. Mutations in somatic cells cannot be easily tracked, nor can they be passed on to future generations, and so are only important in vegetatively propagated species.

2.2.3. Mechanics of mutation

Before going any further in our discussion of mutation in plants, it is prudent to touch on the genetics behind mutations, the varying types of mutations, natural versus spontaneous, the mechanics of mutagenic agents, and the implications.

A mutation is any change within the genome of an organism that is not brought on by normal recombination and segregation. Causative agents are many, but include exposure to mutagenic agents such as radiation or certain chemicals, and mistakes made during normal cell division and replication. Most of these act upon the genome at random and are occurring all the time. These mutations are usually benign and go unnoticed in the organism due to the many cellular mechanisms that protect against these sorts of genetic mistakes. Mutations that are not caught by DNA repair mechanisms in the cell can go on to affect the organism and be present in future progeny.

Spontaneous mutations are those that occur without human intervention. These types of mutation happen randomly and the cause of them therefore not easily traceable. We do know, however, several things that cause mutations or increase their frequency. This includes the activity of mutagens found in nature such as solar radiation or reactive chemicals such as depurinators or free radicals. Mistakes during the replication of DNA during mitosis or unequal crossing-over events during meiosis can go un-repaired in a cell, leading to mutant progeny cells. It is hard to tell at what rate these occur, because the cellular machinery typically catches these mistakes. Occasionally, however, some mistakes make it permanently into the organism's genome.

2.2.4. Types of mutation

At the most basic level, there are only a handful of classifications of mutations regardless of causative event. Deletions and insertions involve the removal or addition of segments of DNA respectively. These segments can range from individual base-pairs to several thousand base-pairs long. Substitutions occur when a particular base is replaced with one of the other three nucleotide bases. Inversions are instances where a segment of chromosome is rotated and replaced in the opposite direction that the segment was facing. The last major classification is a reciprocal translocation. This involves the excision of segments from two non-homologous chromosomes. These excised portions are then inserted into the other chromosome. Chromosome A will gain the segment from Chromosome B and Chromosome B gains the segment from chromosome A.

2.2.5. Mutagens and implications of each

Several types of mutagenic agents exist and have been used extensively since their discovery to produce variation and answer genetic questions. HJ Muller first discovered and used the mutagenic properties of X-ray radiation to study the genetics of Drosophila flies and the mechanics of heredity (Muller, 1928). Following this discovery, the use of ionizing radiation and chemical mutagens has been used extensively in the study of genetics and contributed a great deal to our understanding of biology as a whole.

Ionizing radiation includes ultra-violet (UV) light, X-ray, Gamma rays, and neutrons. These high-energy forms of radiation cause double-strand breaks of the DNA double helix. Once pieces of the DNA are broken, cellular repair mechanisms stitch the pieces back together. These DNA repair systems can only handle low rates of radiation, however, and increases in the rate of exposure to ionizing radiation causes permanent mutations to occur and accumulate in an organism's genome. Radiation causes deletions of nucleotides from the DNA sequence. These deletions can cause reading-frame shifts, inactive protein products, or faulty transcripts. This typically results in null mutations, which are those in which a particular gene is inactivated.

Chemical mutagens affect the DNA molecule through chemical reactions within the genome. Base analogs are chemicals with similar properties to the DNA bases. They can be incorporated by the cell into the genome, replacing the proper base. Alkylating agents such as ethyl methanesulfonate (EMS), react with guanine or thymine by adding an ethyl group which causes the DNA replication machinery to recognize the modified base as an adenine or cytosine, respectively. This base substitution typically does not result in reading frame shifts, but instead causes altered forms of a triplet sequence. Changing a single base within a coding region causes either a nonsense codon which stops transcription or an altered codon which changes the amino acid transcribed, which can de-activate, reduce efficiency of, or produce a new protein. Nitrous acid, a deaminating agent, removes the amine group from adenine or cytosine. When the cell replicates this altered area, it matches adenine to the deaminated cytosine, and cytosine to the deaminated adenine, resulting in similar effects to that of alkylating agents. The last type of chemical mutagen, intercalating agents, causes deletions, reading frame shifts, or random base insertions. These compounds insert themselves into the DNA between adjacent base pairs, thus disrupting replication and transcription machinery.

Transposable elements are a special class of mutagen. They are self-replicating segments of DNA that excise and/or insert themselves within the genome. Also known as transposons, these strange sequences were first proposed by the pioneering Barbara McCLintock working on maize

(McClintock, 1948). Transposable elements, unlike other forms of mutagenesis, do not act upon the genome in a completely random fashion. Rather, they have certain "hot-spots" where they are more likely to insert or replicate themselves. By their insertion or deletion, they act upon the genes in which they are located or those adjacent to them. Transposable elements can cause gene disruptions, protein product alterations, or large-scale genome rearrangements. If inserted into the intron of a gene, they can cause transcriptional inefficiency (Hartwell et al., 2008).

2.2.6. Use of Mutation in Plant Breeding

Mutagenesis, the act of inducing mutations within an organism's genome, has been used in plant breeding since Muller's discovery of the mutagenic effects of X-rays on Drosophila flies (Muller, 1927). Table 1 shows a representative sample of the 3000 varieties that have been improved using mutagenesis (JointFAO/IAEA, 2011). The first crop species to be mutagenized was barley by LJ Stadler, who began using X-rays to induce mutations independently of Muller at around the same time (Stadler, 1928), although he published his first paper on the subject the following year. These early mutation experiments were designed mainly to discern genetic truths of inheritance and chromosomal theory. Recall that at this point Watson and Crick's double-helix DNA model had still not been arrived at.

Much of the early work done with ionizing radiation and chemical mutagens was an effort to determine efficient doses and exposures of the various agents to effect high percentages of mutations without causing lethality. The researchers noticed that the rates and doses varied tremendously for species, genotype, ploidy level, and the conditions in which treatment were conducted. Grays (Gy) are the measurement unit of radiation dose. For the sterilization of food products, processors typically use rates as high as 10 kGy. In the mutagenic treatment of plant material, doses can range from as low as 2 Gy for cell cultures or leaf tissues, to as high as 700 Gy for seed material (Ahloowalia and Maluszynski, 2001).

When determining the most efficient dose for one's crop species, it is important to first consult the literature for any information on the mutagenic agent to be used and the crop it will be used on. Chances are good that someone has already used the particular mutagenic agent on your crop. If not, it is important to consider several factors. (1) The first of course is safety issues regarding the mutagen. A researcher needs to know what sort of certifications, licenses, and precautions must be taken while carrying out the experiment and handling the plant material after the experiment is complete. (2) Next is the mutagen's type and mechanism. Knowing how the mutagen affects the

experimental tissue will not only allow for greater safety, but will also help in making better decisions on how to carry-out the experiment. For instance, if using X-rays, distance from the source of radiation reduces dose. It would be unwise to place a bucket of seed in front of an X-ray source and assume all the seeds in the bucket received equivalent doses of radiation. Similarly, the mutagenic chemical, EMS, requires very stringent experimental conditions to effect mutations. (3) Tissue specific reactions. Seeds react differently than stem cuttings, meristem tissues or callous tissue to the same level of radiation. (4) Species and ploidy level affect mutational response to the mutagen a great deal. Some crop species are equipped to handle a greater mutational load than others. They can more efficiently repair damage to their DNA. Ploidy level of the target species also influences mutation response and will be discussed in a later section.

Recall that most agents used to induce a mutagenic response act upon the target genome in a random fashion. There is no precise control of where mutations will occur within the genome, within particular cells, or to what degree or number of mutations will occur within the target genome. To limit or maximize the number of mutations occurring, it is possible to adjust the dosage of mutagen treatment to the desired effect. For instance, if the mutation response desired is a high level, the researcher will expose the experimental material to high doses, which will result in high lethality of plants, but a high mutational response. Lower doses will result in fewer mutations per genome, a higher survival rate, and possibly also a higher level of non-mutant recovery. The purposely ambiguous terms low and high are used here due to the variable nature of mutation experiments and the large number of factors involved. For example, Auld exposed germinating cotton seeds to 3 to 5 times the LD50 rate of EMS (3% v/v) to ensure recovery of mutants in his tetraploid Gossypium hirsutum subjects (Auld et al., 1998). In contrast, EMS treatment of germinating sugar beet seeds only required 0.5% v/v EMS to elicit a sufficiently mutagenic response (Hohmann et al., 2005).

Once the desired dose-response relationship has been established in the experimental materials, the next step is the implementation of the "screen." The first level of the screen is simple, the M1 generation (M notation denotes generations after mutagenic treatment, so the parent is the M0 and the first generation after mutagenesis is the M1 generation) must be grown out. Most mutant alleles are recessive, so successful mutants would not be seen until the M2, at which point lethality and infertility will often significantly affect the plants in the population. So the first level of the screen is identifying viable mutants.

Next, a cheap, fast, high throughput method of phenotyping and screening for the trait of interest must be in place. This is the most important factor in any mutagenesis experiment. Due to the chimeric nature of mutation, it is likely that some of the viable plants seen in the M2 population will be non-mutagenized parent types. Identification of the desired mutants requires looking at and accurately identifying the mutants. Accurate measurements must be fast and affordable to process the necessary number of individual plants or lines to achieve success. Like all plant breeding methods, mutation breeding plays with a lot of numbers.

In the sugar beet experiment noted above, of over 3200 M2 families derived from an early bolting line treated with EMS, only 9 families exhibited the desired non-bolting trait and eventually gave rise to 5 lines with the non-bolting phenotype (Hohmann et al., 2005). The success of this program was in its simple and efficient screen. The experimenter observed the M2 population for non-bolting visually. Many other traits are not so simply characterized, but can still be done fairly cheaply and quickly.

In an experiment with cotton from above, Auld et al., (1998) treated 2 kg of germinating cotton seeds with EMS and the fibre from nearly 2000 individual M3 plants characterized using the High Volume Instrument (HVI). This machine measures cotton fibre quality but is considered less accurate than other methods. HVI measurement, however, is cheap, fast, and highly correlated to yarn and textile performance. Although not perfectly accurate, it is good enough for processing large numbers. These 2000 M3 individuals gave rise to 2 M4:5 lines with fibre lengths that exceeded the parent value by 10%. One out of every thousand plants was a desirable mutant.

2.2.7. Mutation breeding in Self Fertilizing Species

Breeding mutant traits is fairly straightforward in crops that are capable of self-fertilization. Because many mutations are recessive, after mutagenic treatment, the material should be self-fertilized and advanced to at least the M2 before phenotypic screening. At this point plants will be segregating for the recessive mutant trait. Positive mutant identifications should be kept for future selection. Because mutagens act randomly upon the genome, it is important to collect as many positive mutants as possible. This allows the breeder to have a series of lines from which to select for performance in addition to the presence of the mutant trait.

2.2.8. Mutation breeding in Cross Fertilizing Species

Cross-fertilizing species raise some difficulties. Because species which are predominantly cross-fertilizing typically exhibit significant inbreeding

depression, the necessary self-fertilizations to identify mutants in the population result in reduced plant vigour due to the genetic background and not necessarily the mutations. This compounds the difficulty of successfully identifying mutations. Dominant mutations can be identified, but these occur very rarely. Crop species with self-infertility mechanisms are especially hard to use mutation breeding methods without elaborate crossing schemes. The numbers required to make this feasible, however, make this impractical if not essentially impossible.

2.2.9. Mutation breeding in vegetatively propagated species

When attempting to effect mutation in vegetatively propagated species such as sugarcane or banana, it is important to note the chimeric nature of mutagenic treatment. All cells exposed to the mutagen will not necessarily incur mutations, but those that do incur mutations, will give rise to cells exhibiting the mutation. For this reason it is important to treat parts of the plant that will give rise to either seed or vegetative propagules. Identification and propagation of the necessarily large numbers of plants to identify successful mutants is difficult for many vegetatively propagated plants, however, once one is identified, the mutation is fixed in the cloned progeny. Crop species where in vitro techniques exist and can be used to mutate plant material, allows for the regeneration of large numbers of plantlets. This system is highly amenable to both vegetatively and seed propagated species.

2.2.10. Mutation breeding in seed propagated species

Seeds treated with mutagenic agents give rise to chimeric plants. Chimeric plants produce both mutant and non-mutant seed. This can be problematic; however, one just needs to plant more seeds to find the desired mutants. As long as an efficient screening method is in place, this should produce no significant pitfalls. Mutagenic treatment of seed is by far the most popular method in mutation breeding programs.

2.2.11. Ploidy and how it affects mutation breeding

Mutagenesis of polyploid plant species is difficult. Because most mutations are recessive, plants must be homozygous to display the trait. Polyploid conditions can further complicate the process of reaching homozygosity for the mutation, so must it be selfed for additional generations to ensure presence of the mutation.

2.2.12. The future of mutation breeding

Recent advances in genomics technology have led to a radiation of genomic techniques into applied breeding in general and mutational breeding specifically. Technologies such as high throughput sequencing has allowed for the relatively cheap and fast genome sequencing of plants. Methods such as TILLING (Targeting Induced Local Lesions in Genomes), Zinc finger nuclease mediated mutagenesis, and the use of meganucleases, has allowed us to produce targeted mutations in crop plants to delineate gene function as well as improve cultivars. These new and more specific methods are very promising.

TILLING relies on high throughput sequencing to assemble an array of mutants for a particular target sequence. Plant materials are mutagenized, the DNA is extracted and the target sequence PCR amplified and sequenced to identify mutants and locate the polymorphisms (McCallum et al., 2000). Although the mutations are induced randomly across the plant genome, they are detected only in the gene of interest. This allows the researcher to keep only those plants with mutations in the desired region. A similar process, EcoTILLING, screens for the spontaneous mutations present due to natural variation within a population.

Zinc finger nucleases (ZFN) and Meganucleases (MN) present a more targeted approach to induced mutation. ZFNs can be tailored to bind to specific recognition sites associated with the desired sequence. Once dimerized, the target DNA is cleaved, and a donor sequence introduced (Bibikova et al., 2003). The donor sequence typically exhibits desired mutations or it can be used to introduce new transgenes altogether into the target genome. Meganucleases have a similarly specific mode of action, and a great deal of research is going into both of these promising techniques for targeted mutagenesis as well as plant transformation.

Mutation breeding has long been a beneficial tool in not only the plant breeder's tool box, but also basic geneticist's. In crops where diversity for a given trait is low or non-existent, induced mutagenesis provides an avenue of possibility. With a clear objective, efficient mutagenic protocol, and a high throughput and efficient phenotypic screening method, mutagenesis can be of great benefit for the improvement of crop plants.

2.3. Molecular Breeding

The conventional process of developing new crop varieties takes time. However, biotechnology has considerably shortened the time for new crop varieties to be brought to the market. One of the tools which can make it easier and faster for scientists to select plant traits is molecular breeding. Molecular breeding may be defined in a broad-sense as the use of genetic manipulation

performed at DNA molecular levels to improve characters of interest in plants and animals, including genetic engineering or gene manipulation, molecular marker-assisted selection, genomic selection, etc. However, molecular breeding most often implies molecular marker-assisted breeding (MAB) and is defined as the application of molecular biotechnologies, specifically molecular markers, in combination with linkage maps and genomics, to alter and improve plant or animal traits on the basis of genotypic assays (Korzun, 2003; FAO, 2006). This term is used to describe several modern breeding strategies, including marker-assisted selection (MAS), marker-assisted backcrossing (MABC), marker-assisted recurrent selection (MARS), and genome-wide selection (GWS) or genomic selection (GS) (Ribaut et al., 2010).

MAS is a process whereby a marker (morphological, biochemical or one based on DNA/RNA variation) is used for indirect selection of a genetic factor or a trait of interest for example yield, disease resistance, stress tolerance and quality. This process can be used in plant and animal breeding.The variances that differentiate one plant from another are encoded in the DNA. DNA is packaged in chromosome pairs (strands of genetic material), one coming from each parent. The genes, which control a plant's characteristics, are located on specific segments of each chromosome. The totality of a plant's genes make up its genome. Certain traits such as flower color, may be controlled by only a gene but some more complex traits such as crop yield or sugar content, might be influenced by many genes. Plant breeders are known to select plants based on their phenotypic traits and this process can be difficult, slow, influenced by the environment, expensive and farmers can suffer crop losses. Plant breeders now use MAS to circumvent these obstacles and hasten identification of specific genes which scientists refer to as molecular or genetic markers. The markers are a string or sequence of nucleic acid which makes up a segment of DNA located near the DNA sequence of the desired gene and are usually transmitted by the standard laws of inheritance from one generation to the next. Since the markers and the genes are close together on the same chromosome, they tend to stay together as each generation of plants is produced through genetic linkage. This linkage helps scientists to predict whether a plant will have a desired gene. If researchers can find the marker for the gene, it means the desired gene itself is present.

The location of markers on a chromosome, and how close they are to specific genes, enables scientists to create a genetic linkage map. Such maps show the location of markers and genes, and their distance from other known genes. Such detailed linkage maps can only be produced in only one generation of plant breeding and interpretation of such maps and better knowledge of the molecular structure of the DNA in a plant can unravel to researchers how to

analyze only a tiny bit of plant tissue, even from a newly germinated seedling. Once the tissue is analyzed, scientists know whether that seedling contains the appropriate gene. If it does not, they can quickly move on and concentrate on analysis of another seedling, eventually working only with the plants which contain a specific trait. Molecular breeding through MAS is slightly restricted in scope compared to genetic engineering or modification because: 1) it is applicable to only traits that are already present in a crop; 2) it cannot be used effectively to breed crops which have long generation times such as perennials and 3) its effective use is limited among crops which are clonally propagated because they are sterile or do not breed true (this includes many staples such as yams, bananas, plantain, sweet potato, and cassava).

2.3.1. Genetic markers in plant breeding

1) Origin

Genetic markers are the biological features that are determined by allelic forms of genes or genetic loci and can be transmitted from one generation to another. They can be used as experimental probes or tags to keep track of an individual, a tissue, a cell, a nucleus, a chromosome or a gene. Genetic markers are classified into two types: classical markers and DNA markers (Xu, 2010). Classical markers include morphological markers, cytological markers and biochemical markers. Collard et al., (2005), observed that DNA markers have developed into many systems based on different polymorphism-detecting techniques or methods (southern blotting – nuclear acid hybridization, PCR (polymerase chain reaction) and DNA sequencingsuch as RFLP, AFLP, RAPD, SSR and SNP.

2) Types

i) Classical markers

a. Morphological markers: Use of morphological markers as an assisting tool to select the plants with desired traits has been used since the early history of plant breeding. The markers used mainly involved visible traits, such as leaf shape, flower colour, pubescence colour, pod colour, seed colour, seed shape, hilum colour, awn type and length, fruit shape, rind (exocarp) colour and stripe, flesh colour and stem length. These morphological markers generally represent genetic polymorphisms which are easily identified and manipulated. Therefore, they are usually used in construction of linkage maps by classical two and or three-point tests. Some of these markers are linked with other agronomic traits and can be used as indirect selection criteria in practical breeding. The selection of semi-dwarfism in rice and wheat was one of the critical factors that contributed to the success of high-yielding cultivars during

the green revolution. This is a typical example of successful use of morphological markers to modern breeding. In wheat for example, the dwarfism controlled by gene Rht10 was introgressed into nuclear male-sterile wheat variety Taigu, by backcrossing, and a tight linkage was generated between Rht10 and the male-sterility gene Ta1. The dwarfism was used as the marker for identification and selection of the male-sterile plants in breeding populations (Liu, 1991). This is most useful inapplication of recurrent selection in wheat. However, morphological markers are generally limited, and many of these markers are not associated with important economic traits (e.g. yield and quality) and have been observed to have undesirable effects on the development and growth of plants.

b. Cytological markers: In cytology, the structural features of chromosomes can be shown by chromosome karyotype and bands. The banding patterns, displayed in color, width, order and position, divulge the difference in distributions of euchromatin and heterochromatin. For instance, Q bands are produced by quinacrine hydrochloride, G bands are produced by Giemsa stain, and R bands are the reversed G bands. These chromosome landmarks are used not only for characterization of normal chromosomes and detection of chromosome mutation, but also widely used in physical mapping and linkage group identification. The physical maps based on morphological and cytological markers lay a foundation for genetic linkage mapping with the aid of molecular techniques. However, direct use of cytological markers has been very limited in genetic mapping and plant breeding.

c. Biochemical/protein markers: Protein markers are sometimes categorized into molecular markers though the latter are more referred to as DNA markers. Isozymes are alternative forms or structural variants of an enzyme that have different molecular weights and electrophoretic mobility but have the same catalytic activity or function. Isozymes reflect the products of different alleles rather than different genes because the difference in electrophoretic mobility is caused by point mutation as a result of amino acid substitution (Xu, 2010). Hence, isozyme markers can be naturally mapped onto chromosomes and used as genetic markers to map other genes. They are also used in seed purity test and occasionally in plant breeding. Only a minor number of isozymes exist in many species of crops and some of them can be identified only with a specific strain. Their use is consequently restricted.

ii) DNA markers

DNA markers are a fragment of DNA revealing mutations or variations, which can be used to detect polymorphism between different genotypes or alleles of a gene for a particular sequence of DNA in a population or gene pool. Such fragments are associated with a certain location within the genome and may be detected by means of certain molecular technology. Simply speaking, DNA marker is a small region of DNA sequence showing a polymorphism (base deletion, insertion and substitution) between different individuals. There are two basic methods to detect the polymorphism: Southern blotting, a nuclear acid hybridization technique (Southern, 1975), and PCR (polymerase chain reaction) technique (Mullis, 1990). Using PCR and/or molecular hybridization followed by electrophoresis (e.g. PAGE – polyacrylamide gel electrophoresis, AGE – agarose gel electrophoresis, CE – capillary electrophoresis), the variation in DNA samples or polymorphism for a specific region of DNA sequence can be identified based on the product features, such as band size and mobility. In addition to Sothern blotting and PCR, more detection systems have been also developed. For instance, several new array chip techniques use DNA hybridization combined with labeled nucleotides, and new sequencing techniques detect polymorphism by sequencing. DNA markers are also called molecular markers and in many cases play a major role in molecular breeding. Ideal DNA markers for efficient use in marker-assisted breeding should meet the following criteria (although this may depend on the application and species involved:

1. High level of polymorphism
2. Even distribution across the entire genome (not clustered in certain regions)
3. Co-dominance in expression (so that heterozygotes can be distinguished from homozygotes)
4. Clear distinct allelic features (so that the different alleles can be easily identified)
5. Single copy and no pleiotropic effect
6. Low cost to use (or cost-efficient marker development and genotyping)
7. Easy assay/detection and automation
8. High availability (un-restricted use) and suitability to be duplicated/multiplexed (so that the data can be accumulated and shared between laboratories)
9. Genome-specific in nature (especially with polyploids)
10. No detrimental effect on phenotype

2.3.2. Commonly used DNA markers in plant breeding

The most extensively used and promising DNA markers for plant breeding include: the restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), random amplified polymorphic DNA (RAPD), microsatellites or simple sequence repeat (SSR), and single nucleotide polymorphism (SNP). (Farooq and Azam, 2002;Gupta et al., 2001; Semagn et al., 2006; Xu, 2010).

i. RFLP markers: RFLP markers are the first generation of DNA markers and one of the important tools for plant genome mapping. They are a type of Southern-Boltting-based markers. In living organisms, mutation events (deletion and insertion) may occur at restriction sites or between adjacent restriction sites in the genome. Gain or loss of restriction sites resulting from base pair changes and insertions or deletions at restriction sites within the restriction fragments may cause differences in size of restriction fragments. These variations may cause alternation or elimination of the recognition sites for restriction enzymes. As a consequence, when homologous chromosomes are subjected to restriction enzyme digestion, different restriction products are produced and can be detected by electrophoresis and DNA probing techniques. RFLP markers are powerful tools for comparative and synteny mapping. Most RFLP markers are co-dominant and locus-specific. RFLP genotyping is highly reproducible, and the methodology is simple and no special equipment is required. By using an improved RFLP technique, i.e., cleaved amplified polymorphism sequence (CAPS), also known as PCR-RFLP, high-throughput markers can be developed from RFLP probe sequences. Very few CAPS are developed from probe sequences, which are complex to interpret. Most CAPS are developed from SNPs found in other sequences followed by PCR and detection of restriction sites. CAPS technique consists of digesting a PCR-amplified fragment and detecting the polymorphism by the presence/absence of restriction sites (Konieczny and Ausubel, 1993). Another advantage of RFLP is that the sequence used as a probe need not be known. All that a researcher needs is a genomic clone that can be used to detect the polymorphism. Very few RFLPs have been sequenced to determine what sequence variation is responsible for the polymorphism. It can however be problematic to interpret complex RFLP allelic systems in the absence of sequence information. RFLP analysis requires large amounts of high-quality DNA, has low genotyping throughput, and is very difficult to automate. Radioactive autography involved in genotyping and physical maintenance of RFLP probes limits its use and share between laboratories. RFLP markers were predominantly used in 1980s and 1990s. Most plant breeders would think that RFLP is too laborious and demands too much pure DNA to be important for plant breeding. It however remains fundamental for several kinds of research.

ii. RAPD markers: RAPD is a PCR-based marker system. In this system, the total genomic DNA of an individual is amplified by PCR using a single, short (usually about ten nucleotides/bases) and random primer. The primer which binds to many different loci is used to amplify random sequences from a complex DNA template that is complementary to it (maybe including a limited number of mismatches). Amplification can take place during the PCR, if two hybridization sites are similar to one another (at least 3000 bp) and in opposite directions. The amplified fragments generated by PCR depend on the length and size of both the primer and the target genome. The PCR products (up to 3 kb) are separated by agarose gel electrophoresis and imaged by ethidium bromide (EB) staining. Polymorphisms resulted from mutations or rearrangements either at or between the primer-binding sites are visible in the electrophoresis as the presence or absence of a particular RAPD band.

RAPD predominantly provides dominant markers. This system yields high levels of polymorphism and is simple and easy to be conducted. First, neither DNA probes nor sequence information is required for the design of specific primers. Second, the procedure does not involve blotting or hybridization steps, and thus it is a quick, simple and efficient technique. Third, relatively small amounts of DNA (about 10 ng per reaction) are required and the procedure can be automated, and higher levels of polymorphism also can be detected compared with RFLP. Fourth, no marker development is required, and the primers are non-species specific and can be universal. Fifth, the RAPD products of interest can be cloned, sequenced and then converted into or used to develop other types of PCR-based markers, such as sequence characterized amplified region (SCAR), single nucleotide polymorphism (SNP), etc. However, RAPD also has some limitations/disadvantages, such as low reproducibility and incapability to detect allelic differences in heterozygotes.

iii. AFLP markers: AFLPs are PCR-based markers, simply RFLPs visualized by selective PCR amplification of DNA restriction fragments. Technically, AFLP is based on the selective PCR amplification of restriction fragments from a total double-digest of genomic DNA under high stringency conditions, i.e., the combination of polymorphism at restriction sites and hybridization of arbitrary primers. Because of this AFLP is also called selective restriction fragment amplification (SRFA). An AFLP primer (17-21 nucleotides in length) consists of a synthetic adaptor sequence, the restriction endonuclease recognition sequence and an arbitrary, non-degenerate 'selective' sequence (1-3 nucleotides). The primers used in this technique are capable of annealing perfectly to their target sequences (the adapter and restriction sites) as well as a small number of nucleotides adjacent to the restriction sites. The first step in AFLP involves restriction digestion of genomic DNA (about 500 ng) with two

restriction enzymes, a rare cutter (6-bp recognition site, EcoRI, PtsI or HindIII) and a frequent cutter (4-bp recognition site, MseI or TaqI). The adaptors are then ligated to both ends of the fragments to provide known sequences for PCR amplification. The double-stranded oligonucleotide adaptors are designed in such a way that the initial restriction site is not restored after ligation. Therefore, only the fragments which have been cut by the frequent cutter and rare cutter will be amplified. This property of AFLP makes it very reliable, robust and immune to small variations in PCR amplification parameters (e.g., thermal cycles, template concentration), and it also can produce a high marker density. The AFLP products can be separated in high-resolution electrophoresis systems. The fragments in gel-based or capillary DNA sequencers can be detected by dye-labeling primers radioactively or fluorescently. The number of bands produced can be manipulated by the number of selective nucleotides and the nucleotide motifs used.

A typical AFLP fingerprint (restriction fragment patterns generated by the technique) contains 50-100 amplified fragments, of which up to 80% may serve as genetic markers. In general, AFLP assays can be conducted using relatively small DNA samples (1-100 ng per individual). AFLP has a very high multiplex ratio and genotyping throughput, and is relatively reproducible across laboratories. Another advantage is that it does not require sequence information or probe collection prior to generating the fingerprints, and a set of primers can be used for different species. This is especially useful when DNA markers are rare. However, AFLP assays have some limitations also. For instance, polymorphic information content for bi-allelic markers is low (the maximum is 0.5). High quality DNA is required for complete restriction enzyme digestion. AFLP markers usually cluster densely in centromeric regions in some species with large genomes (e.g., barley and sunflower). In addition, marker development is complicated and not cost-efficient, especially for locus-specific markers. The applications of AFLP markers include biodiversity studies, analysis of germplasm collections, genotyping of individuals, identification of closely linked DNA markers, construction of genetic DNA marker maps, construction of physical maps, gene mapping, and transcript profiling.

iv. SSR markers: SSRs, also called microsatellites, short tandem repeats (STRs) or sequence-tagged microsatellite sites (STMS), are PCR-based markers. They are randomly tandem repeats of short nucleotide motifs (2-6 bp/nucleotides long). Di-, tri- and tetra-nucleotide repeats, e.g. (GT)n, (AAT)n and (GATA)n, are widely distributed throughout the genomes of plants and animals. The copy number of these repeats varies among individuals and is a source of polymorphism in plants. Because the DNA sequences flanking microsatellite regions are usually conserved, primers specific for these regions

are designed for use in the PCR reaction. One of the most important attributes of microsatellite loci is their high level of allelic variation, thus making them valuable genetic markers. The unique sequences bordering the SSR motifs provide templates for specific primers to amplify the SSR alleles via PCR. SSR loci are individually amplified by PCR using pairs of oligonucleotide primers specific to unique DNA sequences flanking the SSR sequence. The PCR-amplified products can be separated in high-resolution electrophoresis systems (e.g. AGE and PAGE) and the bands can be visually recorded by fluorescent labelling or silver-staining.

SSR markers are characterized by their hyper-variability, reproducibility, co-dominant nature, locus-specificity, and random genome-wide distribution in most cases. The advantages of SSR markers include that they can be readily analyzed by PCR and easily detected by PAGE or AGE. SSR markers can be multiplexed, have high throughput genotyping and can be automated. SSR assays require only very small DNA samples (~100 ng per individual) and low start-up costs for manual assay methods. However, SSR technique requires nucleotide information for primer design, labor-intensive marker development process and high start-up costs for automated detections. Since the 1990s SSR markers have been extensively used in constructing genetic linkage maps, QTL mapping, marker-assisted selection and germplasm analysis in plants. In many species, plenty of breeder-friendly SSR markers have been developed and are available for breeders. For instance, there are over 35,000 SSR markers developed and mapped onto all 20 linkage groups in soybean, and this information is available for the public (Song et al., 2010).

v. SNP markers: An SNP is a single nucleotide base difference between two DNA sequences or individuals. SNPs can be categorized according to nucleotide substitutions either as transitions (C/T or G/A) or transversions (C/G, A/T, C/A or T/G). In practice, single base variants in cDNA (mRNA) are considered to be SNPs as are single base insertions and deletions (indels) in the genome. SNPs provide the ultimate/simplest form of molecular markers as a single nucleotide base is the smallest unit of inheritance, and thus they can provide maximum markers. SNPs occur very commonly in animals and plants. Typically, SNP frequencies are in a range of one SNP every 100-300 bp in plants (Edwards et al., 2007; Xu, 2010). SNPs may present within coding sequences of genes, non-coding regions of genes or in the intergenic regions between genes at different frequencies in different chromosome regions. Based on various methods of allelic discrimination and detection platforms, many SNP genotyping methods have been developed. A convenient method for detecting SNPs is RFLP (SNP-RFLP) or by using the CAPS marker technique. If one allele contains a recognition site for a restriction enzyme while the other does not,

digestion of the two alleles will produce different fragments in length. A simple procedure is to analyze the sequence data stored in the major databases and identify SNPs. Four alleles can be identified when the complete base sequence of a segment of DNA is considered and these are represented by A, T, G and C at each SNP locus in that segment. There are several SNP genotyping assays, such as allele-specific hybridization, primer extension, oligonucleotide ligation and invasive cleavage based on the molecular mechanisms (Sobrino et al., 2005), and different detection methods to analyze the products of each type of allelic discrimination reaction, such as gel electrophoresis, mass spectrophotometry, chromatography, fluorescence polarization, arrays or chips, etc. At the present, SNPs are also widely detected by sequencing (Gupta et al. 2001 and Xu, 2010).

SNPs are co-dominant markers, often linked to genes and present in the simplest/ultimate form for polymorphism, and thus they have become very attractive and potential genetic markers in genetic study and breeding. Moreover, SNPs can be very easily automated and quickly detected, with a high efficiency for detection of polymorphism. Therefore, it can be expected that SNPs will be increasingly used for various purposes, particularly as whole DNA sequences become available for more and more species (e.g., rice, soybean, maize, etc.). However, high costs for start-up or marker development, high-quality DNA required and high technical/equipment demands limit, to some extent, the application of SNPs in some laboratories and practical breeding programs. The features of the widely used DNA markers discussed above are compared in Table 1.

The advantages or disadvantages of a marker system are relevant largely to the purposes of research, available genetic resources or databases, equipment and facilities, funding and personnel resources, etc. The choice and use of DNA markers in research and breeding is still a challenge for plant breeders. A number of factors need to be considered when a breeder chooses one or more molecular marker types (Semagn et al., 2006). A breeder should make an appropriate choice that best meets the requirements according to the conditions and resources available for the breeding program.

Table 1: Composition of most widely used DNA marker systems in plants

Feature and description	RELP	RAPD	AFLP	SSR	SNP
Genomic abundance	High	High	High	Moderate to high	Very high
Genomic coverage	Low copy coding region	Whole genome	Whole genome	Whole genome	Whole genome
Expression/inheritance	Co-dominant	Dominant	Dominant/co-dominant	Co-dominant	Co-dominant
Number of loci	Small(<1,000)	Small(<1,000)	Moderate(1000s)	High(1,000s 10,000s)	Very high
Level of polymorphism	Moderate	High	High	High	High
Type of polymorphism	Single base changes, indels	Single base changes, indels	Single base changes, indels	Changes in single length of repeats	Single base changes indels
Types of probes/primers	Low copy DNA cDNA clones or	10 random nucleotides	bp Specific sequence	Specific sequence	Allele specific PCR primers
Cloning and/or sequencing	Yes	No	No	Yes	Yes
PCR-based	Usually no	Yes	Yes	Yes	Yes
Radioactive detection	Usually yes	No	Yes or no	Usually no	No
Reproducibility/reliability	High	Low	High	High	High
Effective multiplex ratio	Low	Moderate	High	High	Moderate to high
Marker index	Low	Moderate	Moderate to high	High	Moderate
Genotyping throughput	Low	Low	High	High	High
Amount of DNA required	Large(5-50ug)	Small(0.01-0.1ug)	Moderate(0.5-1.0ug)	Small(0.05-0.12ug)	Small(≥0.05ug)
Quality of DNA required	High	Moderate	High	Moderate to high	High
Technically demanding	Moderate	Low	Moderate	Low	High
Time demanding	High	Low	Moderate	Low	Low
Ease of use	Note easy	Easy	Moderate	Easy	Easy
Ease of automation	Low	Moderate	Moderate to high	High	High
Development/start-up cost	Moderate to high	Low	Moderate	High	High
Cost per analysis	High	Low	Moderate	Low	Low
Number of polymorphic loci per analysis	1.0-3.0	1.5-5.0	20-100	1.0-3.0	1.0
Primary application	Genetics	Diversity	Diversity and genetics	All purposes	All purposes

Adapted from Collard et al. (2005), Semagn et al. (2006) and Xu (2010).

Several marker systems have been developed and are applied to a range of crop species. These are the Restriction Fragment Length Polymorphisms (RFLPs), Random Amplification of Polymorphic DNAs (RAPDs), Sequence Tagged Sites (STS), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) or microsatellites, and Single Nucleotide Polymorphism (SNPs). The benefits and shortcomings of these marker systems are shown in Table 2.

Table 2: Comparison of most commonly used marker systems (adopted from Korzun, 2003).

Feature	RFLPs	RAPDs	AFLPs	SSRs	SNPs
DNA required (g)	10	0.02	0.5-1.0	0.05	0.05
DNA quality	High	High	Moderate	Moderate	High
PCR-based	No	Yes	Yes	Yes	Yes
Number of polymorph loci analyzed	1.0-3.0	1.5-50	20-100	1.0-3.0	1.0
Ease of use	Not easy	Easy	Easy	Easy	Easy
Amenable to automation	Low	Moderate	Moderate	High	High
Reproducibility	High	Unreliable	High	High	High
Development cost	Low	Low	Moderate	High	High
Cost per analysis	High	Low	Moderate	Low	Low

These molecular techniques have been widely used to monitor differences in DNA sequence in and among species. They also allow the creation of new sources of genetic variation by introducing new and desirable traits from wild varieties into elite lines. While RFLP markers have been the basis for most genetic work in crop plants, AFLPs and SSRs are currently the most popular techniques used due to ease in detection and automation. The adoption of the new marker system, SNPs, is now highly preferred, with the increasing amount of sequence information, and the determination of gene function due to genomic research.

The main applications of these molecular markers in crop genetic studies include:

a. Assessment of genetic variability and characterization of germplasm
b. Identification and fingerprinting of genotypes
c. Estimation of genetic distances between population, inbreeds, and breeding materials
d. Detection of monogenic and quantitative trait loci (QTL)
e. Marker-assisted selection
f. Identification of sequences of useful candidate genes.

2.3.3. Requirements of effective marker-assisted breeding

Compared with conventional breeding approaches, molecular breeding mainly referred to as DNA marker-assisted breeding, needs more complicated equipment and facilities. In general, the pre-requisites listed below are essential for marker-assisted breeding (MAB) in plants.

a. Appropriate marker system and reliable markers: For a plant species or crop, a suitable marker system and reliable markers available are critically important to initiate a marker-assisted breeding program. As discussed above, suitable markers should have following attributes:

a. Ease and low-cost of use and analysis;
b. Small amount of DNA required;
c. Co-dominance;
d. Repeatability/reproducibility of results;
e. High levels of polymorphism; and
f. Occurrence and even distribution genome wide

In addition, another important desirable attribute for the markers to be used is close association with the target gene(s). If the markers are located in close proximity to the target gene or present within the gene, selection of the markers will ensure the success in selection of the gene. Although they can also be used in plant breeding programs, the number of classical markers possessing these features is very small. DNA markers for polymorphism are available throughout the genome, and their presence or absence is not affected by environments and usually do not directly affect the phenotype. DNA markers can be detected at any stage of plant growth, but the detection of classical markers is usually limited to certain growth stages. Therefore, DNA markers are the predominant types of genetic markers for MAB. Each type of markers has advantages and disadvantages for specific purposes. Relatively speaking, SSRs have most of the desirable features and thus are the current marker of choice for many crops. SNPs require more detailed knowledge of the specific, single nucleotide DNA changes responsible for genetic variation among individuals. However, more and more SNPs are present in many species, and are considered an important type for marker-assisted breeding.

2.3.4. Advantages of MAS

a. Quick DNA extraction and high throughput marker detection: For most plant breeding programs, hundreds to thousands of plants/individuals are usually screened for desired marker patterns. In addition, the breeders need the results instantly to make selections in a timely manner. Therefore, a quick DNA extraction technique and a high throughput marker detection system are essentially required to handle a large number of tissue samples and a large-scale

screening of multiple markers in breeding programs. Extracting DNA from small tissue samples in 96- or 384-well plates and streamlined operations are adopted in many labs and programs. High throughput PAGE and AGE systems are commonly used for marker detection. Some labs also provide marker detection services using automated detection systems, e.g. SNP chips based on thousands to ten thousands of markers.

b. Genetic maps: Linkage maps provide a framework for detecting marker-trait associations and for choosing markers to use in marker-assisted breeding. Therefore, a genetic linkage map, particularly high-density linkage map is very important for MAB. To use markers and select a desired trait present in a specific germplasm line, a proper population of segregation for the trait is required to construct a linkage map. Once a marker or a few markers are found to be associated with the trait in a given population, a dense molecular marker map in a standard reference population will help identify makers that are close to (or flank) the target gene. If a region is found associated with the desired traits of interest, fine mapping also can be done with additional markers to identify the marker(s) tightly linked to the gene controlling the trait. A favorable genetic map should have an adequate number of evenly-spaced polymorphic markers to accurately locate desired QTLs/genes (Babu et al., 2004).

c. Knowledge of marker-trait association: The most crucial factor for marker-assisted breeding is the knowledge of the associations between markers and the traits of interest. Only those markers that are closely associated with the target traits or tightly linked to the genes can provide sufficient guarantee for the success in practical breeding. The more closely the markers are associated with the traits, the higher the possibility of success and efficiency of use will be. This information can be obtained in various ways, such as gene mapping, QTL analysis, association mapping, classical mutant analysis, linkage or recombination analysis, bulked segregant analysis, etc. In addition, it is also critical to know the linkage situation, i.e. the markers are linked in cis/trans (coupling or repulsion) with the desired allele of the trait. Even if some markers have been reported to be tightly linked with a QTL, a plant breeder still needs to determine the association of alleles in his own breeding material. This makes QTL information difficult to directly transfer between different materials.

d. Quick and efficient data processing and management: In addition to above-mentioned pre-requisites, quick and efficient data process and management may provide timely and useful reports for breeders. In a marker-assisted breeding program, not only are large numbers of samples handled, but multiple

markers for each sample also need to be screened at the same time. This situation requires an efficient and quick system for labeling, storing, retrieving, processing and analyzing large data sets, and even integrating data sets available from other programs. The development of bioinformatics and statistical software packages provides a useful tool for this purpose.

2.3.5. Steps in marker-assisted breeding

Marker-assisted breeding involves the following activities provided the prerequisites are well equipped or available:

a. Planting the breeding populations with potential segregation for traits of interest or polymorphism for the markers used.
b. Sampling plant tissues, usually at early stages of growth, e.g. emergence to young seedling stage.
c. Extracting DNA from tissue sample of each individual or family in the populations, and preparing DNA samples for PCR and marker screening.
d. Running PCR or other amplifying operation for the molecular markers associated with or linked to the trait of interest.
e. Separating and scoring PCR/amplified products, by means of appropriate separation and detection techniques, e.g. PAGE, and AGE.
f. Identifying individuals/families carrying the desired marker alleles.
g. Selecting the best individuals/families with both desired marker alleles for target traits and desirable performance/phenotypes of other traits, by jointly using marker results and other selection criteria.
h. Repeating the above activities for several generations, depending upon the association between the markers and the traits as well as the status of marker alleles (homozygous or heterozygous), and advancing the individuals selected in breeding program until stable superior or elite lines that have improved traits are developed.

2.3.6. Marker-assisted selection (MAS)

Marker-assisted selection (MAS) refers to such a breeding procedure in which DNA marker detection and selection are integrated into a traditional breeding program. Taking a single cross as an example, the general procedure can be described as follow:

a. Select parents and make the cross, at least one (or both) possesses the DNA marker allele(s) for the desired trait of interest.
b. Plant F1 population and detect the presence of the marker alleles to eliminate false hybrids.

c. Plant segregating F2 population, screen individuals for the marker(s), and harvest the individuals carrying the desired marker allele(s).

d. Plant F2:3 plant rows, and screen individual plants with the marker(s). A bulk of F3 individuals within a plant row may be used for the marker screening for further confirmation in case needed if the preceding F2 plant is homozygous for the markers. Select and harvest the individuals with required marker alleles and other desirable traits.

e. In the subsequent generations (F4 and F5), conduct marker screening and make selection similarly as for F2:3s, but more attention is given to superior individuals within homozygous lines/rows of markers.

f. In F5:6 or F4:5 generations, bulk the best lines according to the phenotypic evaluation of target trait and the performance of other traits, in addition to marker data.

g. Plant yield trials and comprehensively evaluate the selected lines for yield, quality, resistance and other characters of interest.

In practical MAS, a breeder is also concerned about how the markers should be detected, how many generations of MAS have to be conducted, and how a large size of the population is needed. In general, detection of marker polymorphism is performed at early stages of plant growth. This is true especially for marker-assisted backcrossing and marker-assisted recurrent selection, because only the individuals that carry preferred marker alleles are expected to be used in backcrossing to the recurrent parent and/or inter-mating between selected individuals/progenies. The generations of MAS required vary with the number of markers used, the degree of association between the markers and the QTLs/genes of interest, and the status of marker alleles. In many cases, marker screening is performed for two to four consecutive generations in a segregating population. If fewer markers are used and the markers are in close proximity to the QTL or gene of interest, fewer generations are needed. If homozygous status of marker alleles of interest is detected in two consecutive generations, marker screening may not be performed in their progenies. Bonnett et al. (2005) discussed the strategies for efficient implementation of MAS involving several issues, e.g. breeding systems or schemes, population sizes, number of target loci, etc. Their strategies include F2 enrichment, backcrossing, and inbreeding.

In MAS, phenotypic evaluation and selection is still very helpful if conditions permit to do so, and even necessary in cases when the QTLs selected for MAS are not so stable across environments and the association between the selected markers and QTLs is not so close. Moreover, one should also take the impact of genetic background into consideration. The presence of a QTL or marker does not necessarily guarantee the expression of the desired trait. QTL

data derived from multiple environments and different populations help a better understanding of the interactions of QTL x environment and QTL x QTL or QTL x genetic background, and thus help a better use of MAS. In addition to genotypic (markers) and phenotypic data for the trait of interest, a breeder often pays considerable attention to other important traits, unless the trait of interest is the only objective of breeding.

There are several indications for adoption of molecular markers in the selection for the traits of interest in practical breeding. The situations favorable for MAS include:

i. The selected character is expressed late in plant development, like fruit and flower features or adult characters with a juvenile period (so that it is not necessary to wait for the plant to become fully developed before propagation occurs or can be arranged)

ii. The target gene is recessive (so that individuals which are heterozygous positive for the recessive allele can be selected and/or crossed to produce some homozygous offspring with the desired trait).

iii. Special conditions are required in order to invoke expression of the target gene(s), as in the case of breeding for disease and pest resistance (where inoculation with the disease or subjection to pests would otherwise be required), or the expression of target genes is highly variable with the environments.

iv. The phenotype of a trait is conditioned by two or more unlinked genes. For example, selection for multiple genes or gene pyramiding may be required to develop enhanced or durable resistance against diseases or insect pests.

2.3.7. Use of MAS in improvement of qualitative and quantitative traits

Many qualitative traits of economically important crop plants are controlled by major genes/QTLs. Such characteristics include resistance to diseases/pests, male sterility, self-incompatibility and others related to shape, color and architecture of whole plants and/or plant parts. These traits are often of mono- or oligogenic inheritance in nature. Even for some quality traits, one or a few major QTLs or genes can account for a very high proportion of the phenotypic variation of the trait (Bilyeu et al., 2006; Pham et al., 2012). Transfer of such a gene to a specific line can lead to tremendous improvement of the trait in the cultivar under development. The marker loci which are tightly linked to major genes can be used for selection and are sometimes more efficient than direct selection for the target genes.

Quantitative traits constitute most of the important agronomic traits and they are polygenic or controlled by multiple QTLs. MAS for the improvement of

such quantitative traits is a complex and difficult task because it is related to many genes or QTLs involved, QTL x E interaction and epistasis. Usually, each of these genes has a small effect on the phenotypic expression of the trait and expression is affected by environmental conditions. Phenotyping of quantitative traits becomes a complex venture consequently, and determining marker-phenotype association is a difficult task. Therefore, repeated field tests are required to accurately characterize the effects of the QTLs and to evaluate the stability across environments.

In order to improve the efficiency of MAS for quantitative traits, appropriate field experimental designs and approaches have to be employed. Attention should be given to replications both over time and space, consistency in experimental techniques, samplings and evaluations, robust data processing and statistical analysis.

2.3.8. Types of MAS

i. Marker-assisted or marker-based backcrossing (MABC). It is regarded as the simplest form of marker-assisted selection, and at the present it is the most widely and successfully used method in practical molecular breeding. MABC aims to transfer one or a few genes/QTLs of interest from one genetic source (serving as the donor parent and maybe inferior agronomically or not good enough in comprehensive performance in many cases) into a superior cultivar or elite breeding line (serving as the recurrent parent) to improve the targeted trait. Unlike traditional backcrossing, MABC is based on the alleles of markers associated with or linked to gene(s)/QTL(s) of interest instead of phenotypic performance of target trait. The efficiency of MABC depends upon several factors, such as the population size for each generation of backcrossing, marker-gene association or the distance of markers from the target locus, number of markers used for target trait and RP background, and undesirable linkage drag. Success in integrating MABC as a breeding approach lies in identifying situations in which markers offer noticeable advantages over conventional backcrossing or valuable complements to conventional breeding effort. MABC is essential and advantageous when:

1. Phenotyping is difficult and/or expensive or impossible;
2. Heritability of the target trait is low;
3. The trait is expressed in late stages of plant development and growth, such as flowers, fruits, seeds, etc.;
4. The traits are controlled by genes that require special conditions to express;
5. The traits are controlled by recessive genes; and
6. Gene pyramiding is needed for one or more traits.

MABC has been widely and effectively used in plant breeding. It has been useful in improving different types of traits (e.g. disease/pest resistance, drought tolerance and quality) in many species, e.g. rice, wheat, maize, barley, pear millet, soybean, tomato, etc. (Collard et al., 2005; Dwivedi et al., 2007; Xu, 2010).

ii. Marker-assisted gene pyramiding

Marker-assisted gene pyramiding (MAGP) is one of the most important applications of DNA markers to plant breeding. Gene pyramiding has been proposed and applied to enhance resistance to disease and insects by selecting for two or more than two genes at a time. For example in rice such pyramids have been developed against bacterial blight and blast (Huang et al., 1997; Singh et al., 2001; Luo et al., 2012).The advantage of using markers in this case allows selecting for QTL-allele-linked markers that have the same phenotypic effect. To enhance or improve a quantitatively inherited trait in plant breeding, pyramiding of multiple genes or QTLs is recommended as a potential strategy (Richardson et al., 2006. A suitable breeding scheme for MAGP depends on the number of genes/QTLs required for improvement of traits, the number of parents that contain the required genes/QTLs, the heritability of traits of interest, and other factors (e.g. marker-gene association, expected duration to complete the plan and relative cost).

iii. Marker-assisted recurrent selection (MARS)

For complex traits such as grain yield, biotic and abiotic resistance, MARS has been proposed for "forward breeding" of native genes and pyramiding multiple QTLs (Ragot et al., 2000; Ribaut et al., 2000, 2010; Eathington, 2005; Crosbie et al., 2006). As defined by Ribaut et al. (2010), MARS is a recurrent selection scheme using molecular markers for the identification and selection of multiple genomic regions involved in the expression of complex traits to assemble the best-performing genotype within a single or across related populations

iv. Genomic selection

Genomic selection (GS) or genome-wide selection (GWS) is a form of marker-based selection, which was defined by Meuwissen (2007) as the simultaneous selection for many (tens or hundreds of thousands of) markers, which cover the entire genome in a dense manner so that all genes are expected to be in linkage disequilibrium with at least some of the markers. In GS genotypic data (genetic markers) across the whole genome are used to predict complex traits with accuracy sufficient to allow selection on that prediction alone. Selection of desirable individuals is based on genomic estimated breeding value (GEBV) (Nakaya and Isobe, 2012), which is a predicted breeding value calculated using

an innovative method based on genome-wide dense DNA markers (Meuwissen et al., 2001). GS can be possible only when high-throughput marker technologies, high-performance computing and appropriate new statistical methods become available. This approach has become feasible due to the discovery and development of large number of single nucleotide polymorphisms (SNPs) by genome sequencing and new methods to efficiently genotype large number of SNP markers. GS has been highlighted as a new approach for MAS in recent years and is regarded as a powerful, attractive and valuable tool for plant breeding. However, GS has not become a popular methodology in plant breeding, and there might be a far way to go before the extensive use of GS in plant breeding programs. However, from a plant breeder's point of view, GS can be practicable for a few breeding populations with a specific purpose, but may be impractical for a whole breeding program dealing with hundreds and thousands of crosses/populations at the same time. Therefore, GS must shift from theory to practice, and its accuracy and cost effectiveness must be evaluated in practical breeding programs to provide convincing empirical evidence and warrant a practicable addition of GS to a plant breeder's toolbox (Heffner et al., 2009). Development of easily understandable formulae for GEBVs and user-friendly software packages for GS analysis is helpful in facilitating and enhancing the application of GS in plant breeding.

2.3.9. Challenges and perspectives of conventional breeding and marker based breeding

Marker-assisted breeding evolved in the family of plant breeding as several kinds of molecular markers in crop plants were developed during the late 1980s and 1990s. The wide application of molecular markers in various fields of plant science, e.g. germplasm evaluation, genetic mapping, map-based gene discovery, characterization of traits and crop improvement, has proven that molecular technology is a powerful and reliable tool in genetic manipulation of important agronomic traits in crop plants. Compared with conventional breeding methods, MAB has significant advantages:

i. MAB can allow selection for all kinds of traits to be carried out at seedling stage and thus reduce the time required before the phenotype of an individual plant is known. For the traits that are expressed at later developmental stages, undesirable genotypes can be quickly eliminated by MAS. This feature is particularly important and useful for some breeding schemes such as backcrossing and recurrent selection, in which crossing with or between selected individuals is required.

ii.. MAB can be not affected by environment, thus allowing the selection to be performed under any environmental conditions (e.g. greenhouse and off-season nurseries). This is very helpful for improvement of some traits (e.g. disease/pest resistance and stress tolerance) that are expressed only when favourable environmental conditions present. For low-heritability traits that are easily affected by environments, MAS based on reliable markers tightly linked to the QTLs for traits of interest can be more effective and produce greater progress than phenotypic selection.

iii. MAB using co-dominance markers (e.g. SSR and SNP) can allow effective selection of recessive alleles of desired traits in the heterozygous status. No selfing or test crossing is needed to detect the traits controlled by recessive alleles, thus saving time and accelerating breeding progress.

iv. For the traits controlled by multiple genes/QTLs, individual genes/QTLs can be identified and selected in MAB at the same time and in the same individuals, and thus MAB is particularly suitable for gene pyramiding. In traditional phenotypic selection, however, to distinguish individual genes/loci is problematic as one gene may mask the effect of additional genes.

v. Genotypic assays based on molecular markers may be faster, cheaper and more accurate than conventional phenotypic assays, depending on the traits and conditions, and thus MAB may result in higher effectiveness and higher efficiency in terms of time, resources and efforts saved.

The research and use of MAB in plants has continued to increase in the public and private sectors, particularly since 2000s. However, MAS and MABC were and are primarily constrained to simply-inherited traits, such as monogenic or oligogenic resistance to diseases/pests, although quantitative traits were also involved. The application of molecular markers in plant breeding has not achieved the results as expected previously in terms of extent and success (e.g. release of commercial cultivars). Improvement of most agronomic traits that are of complicated inheritance and economic importance like yield and quality is still a great challenge for MAB including the newly developed GS. From the viewpoint of a plant breeder, MAB is not universally or necessarily advantageous. The application of molecular technologies to plant breeding is still facing the following drawbacks and/or challenges:

a. Not all markers are breeder-friendly. This problem may be solved by converting of non-breeder-friendly markers to other types of breeder-friendly markers (e.g. RFLP to STS, sequence tagged site, and RAPD to SCAR, sequence characterized amplified region).

b. Not all markers can be applicable across populations due to lack of marker polymorphism or reliable marker-trait association. Multiple mapping populations are helpful in understanding marker allelic diversity and genetic background effects. In addition, QTL positions and effects also need to be validated and re-estimated by breeders in their specific germplasm.
c. Incorrect selection may occur due to recombination between the markers and the genes/QTLs of interest. Use of flanking markers or more markers for the target gene/QTL can help.
d. Inaccurate assessments of QTL locations and effects result in slower progress than expected. The efficiency of QTL detection is attributed to multiple factors, such as algorithms, mapping methods, number of polymorphic markers, and population type and size (Wang et al., 2012). High marker density fine mapping with large populations and well-designed phenotyping across multiple environments may provide more accurate estimates of QTL location and effects.
e. A large number of breeding programs have not been equipped with adequate facilities and conditions for a large-scale adoption of MAB in practice.
f. The methods and schemes of MAB must be easily understandable, acceptable and implementable for plant breeders, unless they are not designed for a large scale use in practical breeding programs.
g. Higher start-up expenses and labour costs.

2.4. Genetic Engineering and Transgenic Crops

Genetic engineering, also called genetic modification, is the direct manipulation of an organism's genome using biotechnology. New DNA may be inserted in the host genome by first isolating and copying the genetic material of interest using molecular cloning methods to generate a DNA sequence, or by synthesizing the DNA, and then inserting this construct into the host organism. Genes may be removed, or "knocked out", using a nuclease. Gene targeting is a different technique that uses homologous recombination to change an endogenous gene, and can be used to delete a gene, remove exons, add a gene, or introduce point mutations.

2.4.1. Benefits of transgenic crops

Crops generated through genetic engineering are specifically called transgenic crops or more generally genetically modified organisms (GMOs), when they include plants, animals or micro-organisms. Transgenic crops have been modified for insect protection, herbicide resistance, virus resistance, enhanced nutrition, tolerance to environmental pressures and the production of edible vaccines. Transgenic crops are the most commercialized GMOs among which we have the insect resistant and the herbicide tolerant crop plants. Genetic

modification of food raw materials offers several potential advantages and benefits compared to traditional selective breeding techniques. Some of the major advantages are:

a. It can provide more food, more economically. Yield is increased due to decreased loss to pests and disease, as in Bt corn, soybean, sugar beet and canola.

b. It is faster, cheaper and more multipurpose. A change that could take so many years to effect with conventional breeding, can be achieved within a shorter period and at a reduced budget, and between species between whom it was previously impossible to exchange genes.

c. It is more precise in selecting particular desirable characteristics. Conventional breeding blend entire genomes and the desired offspring is obtained in subsequent segregating generations. However, genetic modification cuts out or copies and transfers, only the desired gene, and the current technology of Zinc finger nucleases makes the insertion more precise.

d. More traits can be improved. Most GM crops in the market today are either herbicide tolerant, insect resistant or both. Abiotic-stress-resistant crops, including crops that are resistant to heat, cold, water, drought, and salt, and improved nutrients are being developed. A drought resistant maize under the Water Efficient Maize for Africa (WEMA) programme, is undergoing trials in Kenya, and will be released by this year (2014) to Kenyan farmers (Karumbe et al., 2009). Such crops have the potentials to change the fortunes of dry lands of Northern Nigeria which is threatened by desertification.

e. GM crops can reduce the number of food-deficient regions in the world. This is achievable through the development of stress-resistant varieties more amenable to growing on poor and marginal soils.

f. GM crops can improve the shelf life of fresh fruits and vegetables. A long-shelf-life tomato was produced in India in 2010 by using RNA-interference to "silence" two genes encoding N-glycoprotein modifying enzymes, α-mannosidase and β-D-N-acetylhexosaminidase, which make fruits to soften. This strategy can be applied to other vegetables and fruits such as tomatoes, onions, peppers, citrus, guavas, mango, cashew, avocado pears and so many others in Nigeria.

g. GM crops can reduce allergens and toxins in crops. Post-transcriptional gene silencing technology, has been used to eliminate allergens from some crops such as soybeans, tomato and apples. Similarly, RNA silencing, as well as the over-expression of a beneficial gene, have been used in transgenic cassava to reduce toxic cyanides.

h. GM crops can increase health promoting food constituents. Food is no longer eaten only for nutrition. The consumer now expects his food to help him cure and prevent disease. Genetic engineering makes possible, increases in levels of

beneficial disease-fighting and prevention components in food, as well as the introduction of such components in foods where they naturally do not occur, but which are more convenient for us to eat. Some of such foods are: High Omega 3 fatty acid foods which occur naturally in fish such as sardine and salmon and have been reported to aid individuals live longer and healthier lives. The engineering of life-saving fatty acids into other foods that people can choose from, gives the consumers options and those who may not like fish can still use this product in other foods.

i. GM technology can be used in producing edible vaccines. The idea of expressing recombinant vaccines against important human diseases such as AIDS, Hepatitis etc in crop plants is an old idea among scientists. This breakthrough will help in circumventing the difficulties associated with conventional vaccines.

j. GM crops can reduce pesticide and herbicide use. Bt crops which are insect resistant GM crops have drastically reduced agricultural use of insecticides, thereby saving money, labour, fuel, and creating wealth as well as improving health and cleaning up the environment. The use of GM herbicide-resistant crops such as Roundup Ready crops means the farmer can spray post emergence with less herbicide and costs as well as preserving the environment.

k. GM crops encourage zero tillage

Herbicide resistant crops encourage low or zero tillage agriculture and resulting in low run-off and high soil conservation. The erosion problems of many parts of Nigeria will enormously benefit from the use of herbicide-resistant crops.

2.4.2. Regulation of transgenic crops

The regulation of transgenic crops concerns the approaches taken by governments to assess and manage the risks associated with the development and release of genetically modified crops. Major differences exist in in the regulation of GM crops across countries, and these regulations vary in a given country subject on the intended use of the products of genetic engineering. Currently, the Nigerian national assembly has passed into law the Biosafety regulations bill and is still awaiting accent by the Presidency.

2.4.3. Controversies surrounding GMOs and Anti-GM Activists.

Opponents of GMOs have challenged use of genetic engineering for several reasons based on ethical, ecological and economic concerns. Opponents have driven their concerns on the fact that the techniques and GMOs are subject to intellectual property law. The key areas of controversy related to transgenic crops are: whether GM food should be labelled, the role of government regulators, the effect of GM crops on health and the environment, the effect on

pesticide resistance, the impact of GM crops for farmers, and the role of GM crops in feeding the world population.

A very strong anti GM movement, is in place in the developed world, where food insecurity is not a problem and they are trying hard to adversely influence the attitude of Africans to GM foods. One of the founders of the movement apologized to the world in 2010 for his anti GM activities. The "born-again" approach of the anti GM activist and environmental campaigner Mark Lynas should be emulated by the anti-GM crusaders, some of which we have in Nigeria. His speech to the Oxford Farming Conference in late 2010, is very instructive and I quote "I apologise for having spent several years ripping up GM crops, I am also sorry that I helped to start the anti-GM movement back in the mid-1990s, and that I thereby assisted in demonizing an important technological option which can be used to benefit the environment. As an environmentalist, and someone who believes that everyone in this world has a right to a healthy and nutritious diet of their choosing, I could not have chosen a more counter-productive path. I now regret it completely". Mark Lynas added that the anti GM activists Greenpeace and the

Soil Association, claim to be guided by consensus science, but that there was a "rock-solid" scientific consensus, backed by the American Association for the Advancement of Science, the Royal Society, UK, health institutes and national science academies around the world on the safety of GM foods (Lynas, 2010).

2.4.4. GM crops are safe

There is a wide-ranging scientific consensus that transgenic crops in the market or fields poses no greater risk than crops that are obtained from conventional breeding methods. Since the commercial release and consumption of GM foods in 1996, i.e. in the past eighteen years of its use, there has been no single report of any ill effect that has been documented in the human population from any genetically modified food in any part of the world. Thousands of field tests conducted so far on various genetically improved crops with more than one hundred new traits, or their commercial planting on 28 million hectares worldwide have failed to provide any serious evidence of food safety or environmental concern. Gene altered corn and soyabean products alone including baby food, are currently in nearly 4,000 food products in supermarkets in America and to date, there is yet, no single dispute of reported food safety. It is worth noting that the American food safety standards remain the highest in the world. The regulatory agency, the Food and Drug Administration, has one of the world's strictest standards and thus enjoys considerable public trust.

Many genes used in genetically improved crops, such including the Bt gene isolated from soil bacteria, have a long history of perfect safety and ecological record. Further, many genes introduced into crop plant (such as those used to develop slow ripening tomato) are derived essentially from the same crop but inserted in a reverse manner to silence the undesirable genes, so as to slow down the ripening in tomato or prevent cyanide production in cassava.
This is not to say that genetically improved crops will not have any unforeseen effects. But the possible negative effects of each crop should be scientifically evaluated on a case-by- case basis, and the regulatory system should evolve over time based on new knowledge. As Nigeria is a centre of the diversity of some crop plants with many wild relatives, we should be prudent to minimise any potential gene transfer to weedy relatives. Many of these concerns are technical issues that could be addressed through appropriate research, and not through emotive debates or militant activism.

The precautionary principle which most African countries including Nigeria are signatories to, states that if an action or policy has a suspected risk of causing harm to the public or to the environment, in the absence of scientific consensus that the action or policy is not harmful, the burden of proof that it is not harmful falls on those taking an action. The principle is used by policy makers to justify discretionary decisions in situations where there is the possibility of harm from taking a particular course or making a certain decision when extensive scientific knowledge on the matter is lacking. The principle implies that there is a social responsibility to protect the public from exposure to harm, when scientific investigation has found a plausible risk. These protections can be relaxed only if further scientific findings emerge that provide sound evidence that no harm will result.

2.4.5. GM technology and food security in Nigeria

The green revolution in the world took place about 50 years ago and the industrialized nations and developing nations in Asia and Latin America such as China, India, Brazil, Peru and Chile joined the revolution and are today food exporters. The continent of Africa, with the least per capita income remained spectators and are today major food importers. Now that the biotechnology revolution is cruising, we are also merely just paying lip service to the technology. The expertise in this technology as well as the infrastructure is anything but 'traditional' as far as the current progress in the global science of biotechnology is concerned. Nigeria is merely carrying out field tests on two GM crops i.e Cassava and Cowpea and there is even no biosafety regulation in place. Burkina Faso is the only West African country growing GM crops. Egypt, South Africa, and recently Sudan are the only other countries that have planted any

GM crops for commercial production (James, 2010). I cannot agree less to James (2011) who stated that "for a continent that is hungry, biotechnology, provides one of the best ways to substantially increase agricultural productivity, and thus ensure food security to the people". While the African Union heads of states and Governments did decide during their Extra Ordinary Summit held in Sierte, Libya in February 2004 and at the 5th Ordinary Session held in Sierte Libya 2005, to explore the potentials of GMOs in agriculture (NEPAD, 2005), it is increasingly clear that this failure to join in this revolution is mainly due to lack of political will among other sundry reasons. I also fully concur with Alhassan (2010), who expressed confidence that most of the negative socio-economic indicators for sub-Saharan Africa, can only be changed for the better if there is a conscious effort to apply biotechnology, to the production challenges of agriculture in an enabling policy environment.

The Agricultural Transformation Agenda (ATA) was officially launched in 2012 with a vision to achieve a hunger-free Nigeria through the agricultural sector that will drive income growth, accelerate achievement of food and nutritional security, generate employment and transform the country into a leading player in global food markets, to grow wealth for millions of farmers. The agenda states that one of the strategies for achieving this is to empower farmers on the adoption and application of research results, technologies, and techniques for agricultural production. Part of the action plan, is the provision and availability of improved inputs, such as seeds and fertilizer, and the action plan focuses on some priority agricultural commodities namely; rice, cassava, sorghum, cocoa, cotton, maize, oil palm, dairy, beef, leather, poultry and fisheries. Uzochukwu (2013), has argued that most of the commodities to be focused upon already have varieties genetically modified for superior performance, disease resistance or nutrition, and should form part of the improved inputs to drive this highly commendable agenda and recommends that the beginning of the strategy for production of improved seeds and planting materials should be a sustained and massive human and infrastructural capacity building in agricultural biotechnology research and development, and I add that the genetically improved or modified varieties already have yield levels that are below optimum standards and therefore should not be celebrated. It is only the availability of modern infrastructure and the correct integration and application of modern breeding approaches into the currently used conventional breeding that will multiply current yields and set the nation in a pedestal that will reverse the current trend of food imports as a result of low outputs. This is only when the transformation agenda will be different from previous interventions.

3.1. My contributions to Scientific Knowledge:

3.1.1 Investigation of cyanide content in leaves of two cassava varieties in Zaria.

The study was initiated to compare the levels of cyanogenic glycosides present in two types of cassava commonly grown and used by local farmers in the Zaria area. The picric acid and sodium cyanide method of colorimetric procedure analysis was used to determine the concentration of weak acid dissociable (WAD) cyanide in the cassava leaves. In the presence of free cyanide, picric acid was reduced to the coloured isopurpuric acid, with the colour intensity directly proportional to the concentration of free cyanide originally present in the sample. The procedure ensures that cyanide that is weakly complexed with metals such as cadmium, copper, nickel and zinc is first dissociated by the addition of a chemical ligand, and the resulting free cyanide is then able to react with picric acid. A spectronic 20 was used to determine the absorbance of samples. The results of this study which was my B.Sc project so much excited me and actually propelled my interest in research.

3.1.2 Potato Breeding and Varietal development.

The potato - Irish potato (Solanum tuberosum) remains an important cultivated root crop in Nigeria and about 95% of total production comes from Jos, Plateau. Jos Plateau is located on about 1,230 meters above sea level and the low prevailing temperatures is a major factor favouring its production. Being a temperate crop, potato requires a minimum temperature of 15-20oC for three consecutive months for successful growth and tuberisation. This condition eliminates many parts of Nigeria considered too hot for potato production. Apart from the Jos Plateau, potato can also be grown on the Obudu highlands in Cross River state, Mambilla Plateau in Taraba state and Biu Plateau in Borno state. Similarly, the cold harmattan months of between November and February in some Northern states of Borno, Yobe, Zamfara, Bauchi, Katsina, Kano, Gombe, Jigawa, Sokoto, Kaduna and Kebbi are suitable for potato growth and tuberisation under irrigation.In 1991 about 400,000 tonnes was produced in Nigeria (Ifenkwe and Suchomel, 1993). Current production estimate is about 800,000 tonnes (NRCRI, 2012).

i**) Development of improved Potato Varieties**

Seed potato is the most limiting factor in potato production in Nigeria. Most of the commercially grown potato varieties grown in Nigeria are imported elite varieties and they include Nicola, Bertita, Diamant, Kondor, Famosa and BR63-18 which are popular among farmers. In an attempt to develop improved local varieties, two sets of studies were initiated at the NRCRI Vom Sub-station

between 1991 and 1992 by initiating reciprocal crosses among the elite clones and collecting berries from the F1 parents and growing the true potato seeds (TPS) to select promising seedlings and secondly to evaluate some advanced potato genotypes received from CIP (International Potato Centre) which are promising selections from their breeding programme and are at advanced stages of evaluation preparatory to release. These two studies are significant because one of the selections from the local crosses turned out to be a promising selection and some of the advanced potato genotypes from CIP are among the locally adapted selections being considered for release as a variety by the NRCRI. The TPS has proven to have several advantages over the normal seed potatoes because of reduced production costs of over 40%, use of only 150 grammes for planting one hectare as against 2.0 tonnes of seed tubers for same area, reduced storage cost of seed tuber by about 30% as seed tubers only store outside refrigeration for maximum of five months whereas TPS can be viable after five years of storage, TPS use eliminates most tuber-borne diseases of potato such as bacterial wilt and finally transportation costs of seed tubers are reduced as a result of use of the TPS technology.

ii) Studies on field resistance to late blight disease of potatoes,Phytophthora infestans(Mont. de Bary) among tuber families and clones in Vom area of Jos Plateau, Nigeria.

Twenty tuber families (or true potato seed progenies from a cross) of potato Solanum tuberosum L.and twenty clones (uniform or identical seeds from asexual reproduction) were obtained from the International Potato centre (CIP) in Lima Peru and screened in the field for their resistance to late blight during the rainy season of 1990. The problem of late blight in potato is universal and apart from occurring everywhere potato is grown, it is the most important fungal disease and severity depends on the weather. It was first reported in the Jos Plateau in 1962 (Ifenkwe, 1981). Results of this study revealed by the infection rate which was determined by the log regression transformations of the disease progress curves from the late blight evaluation scores confirmed that clones tested for blight were generally less susceptible than the tuber families (Table 3).

Table 3: Late blight evaluation scores and yield data for some clones

CIP Accession No.	Late blight scores* (Means of replicates) at days after planting (DAP)					Infection rate	Tuber weight (t/ha)
	54 DAP	61 DAP	68 DAP	75 DAP	82 DAP		
380013-12	3	4	5	6	9	0.0159	17.33
720073	1	2	2	4	4	0.0680	17.13
380025-5	2	2	3	5	8	0.1275	20.67
381378-33	2	3	3	3	6	0.0880	15.33
381396-16	1	1	2	3	6	0.0810	18.00
381379-15	1	2	4	7	8	0.1510	20.67
381403	2	3	5	7	9	0.1680	15.33
382119-2	1	1	3	4	7	0.1187	11.67
382122-15	1	1	1	2	4	0.0440	20.33
382151-2	1	2	3	4	8	0.1200	12.00

*1=No infection and 9 =All leaves dead

(Source: Kwon-Ndung, 1991; Kwon-Ndung and Ifenkwe, 1993).

The implication of these results was that the infection rate which is an indirect measure of field resistance was generally higher among the tuber families than the clones. Consequently, the clones in this study exhibit a better field resistance than the tuber families. This is supported by the fact that clones had earlier been screened for late blight resistance as tuber family lines.

Table 4: Late blight scores and yield data for some tuber families

CIP Accession No.	Late blight scores* (Means of replicates) at days after planting (DAP)					Infection rate	Tuber weight(t/ha)
	54 DAP	61 DAP	68 DAP	75 DAP	82 DAP		
3879092	3	4	5	6	9	0.0159	10.8
387094	1	2	2	4	4	0.0680	3.3
387098	2	2	3	5	8	0.1275	1.0
387100	2	3	3	3	6	0.0880	2.8
387197	1	1	2	3	6	0.0810	2.1
387201	1	2	4	7	8	0.1510	7.1
387207	2	3	5	7	9	0.1680	1.3
388716	1	1	3	4	7	0.1187	12.6
388717	1	1	1	2	4	0.0440	13.5
388721	1	2	3	4	8	0.1200	12.8

*1=No infection and 9 =All leaves dead

(Source: Kwon-Ndung, 1991; Kwon-Ndung and Ifenkwe, 1993).

The process of screening also resulted in the selection of tuber family and clonal lines that combined sufficient field resistance with yield. The following lines which appeared promising during the evaluations were recommended for future late blight resistance breeding: CIP 387092, 397097, 388705, 388723, 374080.5, 380025.5, 381396.16, 381379.15 and 382122.15.

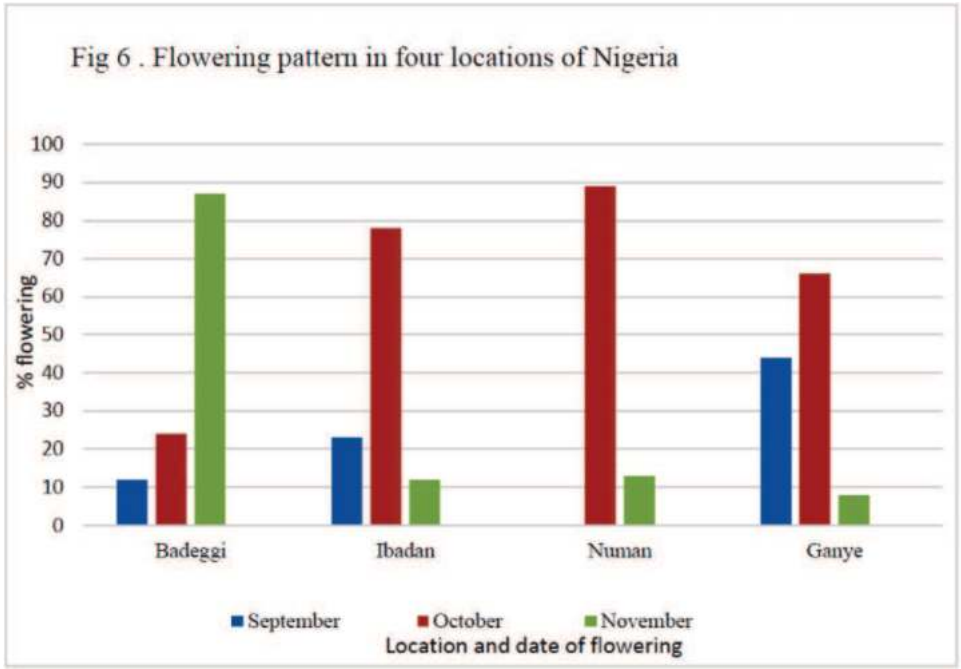
3.1.3 Sugarcane Breeding and Varietal Development

The main purpose of any sugarcane breeding is to produce new hybrid varieties that will be immune, or resistant, to diseases and insect pests and will increase the production of sugar per unit area, yielding canes of higher sugar content and better fabrication qualities.

The main challenge in any sugarcane breeding programme is the inability of the seeds to set well, the crop is a complex polyploid with a fairly long reproductive cycle and it flowers very poorly. Sugarcane has been described as a quantitative intermediate day plant and successive developmental stages have shorter less critical day length requirements (Midmore, 1980). Its flowering behaviour is therefore very important. Flowering is such an interesting characteristic in sugarcane in a manner that while this trait is essential for breeding purposes, it is a trait that is not desirable in commercial cane cultivation as flowering varieties are considered to be poor in sucrose accumulation due to competition of the use of assimilates for reproductive growth and sucrose accumulation. Ethirajan (1987) described flowering as a seasonal phenomenon under the control of environmental and genetic factors. Biparental matings involving two known flowering parents are the most popular kind of controlled crosses in sugarcane. The first responsibility of any cane breeding is to obtain new cane seeds by crossing selected parent varieties, and then selecting seedlings from the new seeds. The traditional crosses have been effected by enclosing in a cloth lantern two tassels from two different cane varieties selected as a male and a female parent. Sugarcane which is monoecious in nature generally produces non-viable florets in an inflorescence. It is an established and well known fact that the imported and exotic commercially superior bred varieties in Nigeria are not necessarily ideal parents in local breeding programmes. This is mainly because many of the available best varieties were bred from parents unsuitable for commercial use in Barbados, Java, Coimbatore and Brazil. The process of planting and testing of seedlings from nurseries to field can take up to ten years before being released as a new commercial variety. The following specific research studies were aimed at overcoming the constraint of breeding sugarcane and disengage these limitations in breeding for improved varieties.

i) Flowering and pollen fertility of sugarcane

In an effort to realize this goal, we initiated the determination of the flowering pattern and pollen fertility of 65 sugarcane clones in Badeggi, Southern Guinea Savannah ecological zone of Nigeria and Ibadan, in the Rain Forest ecology of Nigeria as well as Numan, Northern Guinea Savannah and Ganye, Northern Guinea Savannah ecologies of Nigeria. Midmore (1980) very much described the effect of photoperiodism on fertility and flowering in sugarcane flowering. Our study on the flowering pattern at Badeggi, Ibadan,Numan and Ganye locations revealed considerable variation of flowering pattern among 65 evaluated clones (Fig 6). The flowering initiation commenced earlier in Ibadan than in Ganye, but the propensity was higher in Ganye than in Ibadan in the month of September (Fig. 6). Flowering was more prevalent in Numan in the month of October than all other locations while Badeggi recorded the highest propensity of flowering in the month of November (Kwon-Ndung et al., 1994).



Source: Kwon-Ndung (1994).

ii) Area crosses at Badeggi and Ganye

The establishment of a pioneer area cross (modified bi-parental cross) of sugarcane at Badeggi was initiated to circumvent the problem of facilities for specific crosses. An area cross is a modified biparental cross in which one strong elite male is grown around identified and selected male sterile (female) lines in isolation to prevent chances of foreign pollen contamination. The first area cross in our local breeding programme was successfully carried out in Badeggi in 1993 and this cross produced a total of 405 seedlings from fuzz collected from three female (male sterile) parents (Kwon-Ndung et al., 1993). Another area cross was repeated in Ganye, North eastern Nigeria in 1994/95 cropping season and a total of 1,733 seedlings were raised from the crossing block. The strong elite male Co285 was grown in isolation around four male sterile females namely CO997, Co1148, CP63-588 and F141. Fuzz or matured sugarcane seeds collected from the females was used in raising seedlings as shown in the Table 5 below.

Table 5: Fuzz or sugarcane seeds evaluated in area crosses

Male parent	Female parent	Weight of	Number of	Number of seedlings transplanted	Number of	Number of	Number of
		harvested fuzz (gm)	seedlings raised		seedlings selected	seedlings in PYT*	seedlings in AYT*
Co285	CP 63-588	65.7	398	218	91	18	6
Co285	Co 997	76.2	423	201	56	12	4
Co285	Co 1148	67.5	402	202	34	09	4
Co285	F141	79.1	510	203	67	15	5
TOTAL		288.5	1,733	824	248	54	**19**

*PYT = Preliminary yield trials
*AYT= Advanced yield trials

This study was a breakthrough in the local breeding programme as selected seedlings advanced into advanced yield trials formed some of the candidate varieties that were recommended for release as local candidate varieties.

iii) Assessment of the ploidy level and chromosome of germplasm clones

The national sugarcane germplasm at Ibadan and Badeggi (Kwon-Ndunget al., 1994; Iwo et al., 1996; Kwon-Ndung and Misari, 1996) were assessed to understudy the ploidy levels and chromosome composition of germplasm materials.The cyto-morphology and ploidy levels studied among clones are

variable. The ploidy level studies for the two locations confirmed the existence of a wide array of ploidy levels ranging from tetraploids to octaploids. (Kwon-Ndung and Iwo, 1992; Kwon-Ndung, Agboire and Ishaq, 1993; Iwo and Kwon-Ndung, 1996, Iwo et al., 1996).

Table 6 : Pollen viability and sex characterization of sugarcane germplasm accessions

Pollen source accession	% Germination	Pollen size (µm)	Sex
BD 06	0.1	45	Female
B6481	0.5	55	Female
Co349	18	40	Female
Co421	0	50	Female
Co453	0.3	40	Female
CO473	0.5	50	Female
Co496	0.4	40	Female
LS 08	0.5	60	Female
MEX 25/29	0.8	40	Female
OG 06	1.5	40	Female
OG 10	0.8	60	Female
OY 21	10	50	Female
OY 22	15	55	Female
USRI 124	03	60	Female
USRI 125	01	50	Female
B4362	30	50	Hermaphrodite
B59162	37	62	Hermaphrodite
B63340	50	56	Hermaphrodite
B69162	25	50	Hermaphrodite
BJ6252	50	50	Hermaphrodite
Co396	54	62	Hermaphrodite
CO6304	36	54	Hermaphrodite
KD 10	20	54	Hermaphrodite
KN 10	46	48	Hermaphrodite
OY 12	38	50	Hermaphrodite
BD 07	75	65	Male
B47258	50	61	Male
B70607	92	50	Male
Co285	75	60	Male
Co301	80	60	Male
Co331	20	61	Male
Co740	68	58	Male
Co1158	56	60	Male
Co1001	35	60	Male
F141	70	59	Male

Source (Iwo *et al.*, 1996)

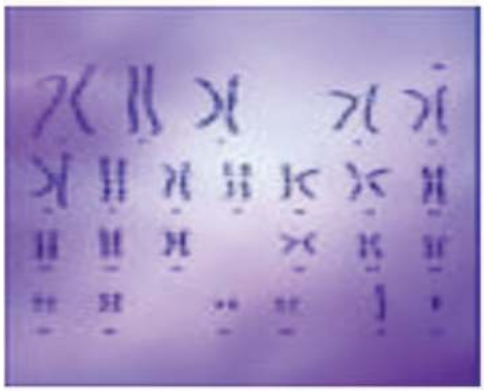


Fig. 7: Sugarcane cnromosome
Source: Iwo and Kwon-Ndung, (1996).

iv) Identification of the dose sensitivity range for inducing sugarcane clones with gamma rays. The dose levels of 4 to 8 kilograys (kgy) of gamma rays were confirmed as
the safe and adequate dose limit for the germination of sugarcane buds. The dose levels of 30
to 40 kgy led to a lethality dose of 50% (LD50) and levels of 50 kgy led to complete lethality
in some clones and others attained the complete lethality (LD100) at 60kgy (Kwon-Ndung et
al., 1995).

v) Gamma mutagenesis in sugarcane (mutation breeding).

Additional variability created in sugarcane through Cobalt 60 gamma cell resulted in a wide array of mutants which were selected for different traits and most especially for smut disease resistance (Kwon-Ndung, 1999; Kwon-Ndung and Ifenkwe, 2000). Screenhouse and field trials of mutants which commenced in 1995 and involved the inoculation of clones with smut spores resulted in the selection of resistant clones to smut disease Ustilago scitaminiea Syd. The M1V3

sub-clones of B47419 were completely free from smut under severe inoculation pressure. These selections constituted clones that were engaged in the Preliminary Yield Trials and multilocational Advanced Yield Trials. Their nomination as candidate varieties to the National Variety Release committee was confirmed by their release as commercial sugarcane varieties in December 1999, June 2000 and July 2001 after confirmatory on-farm trials. (NACGRAB, 2005).

vi) Sugarcane germplasm collection in eighteen states of Northern Nigeria.

A total species diversity of one hundred and seventy accessions were collected from 18 states of Northern Nigeria. The diversity in colour of stems, internodes length and shape, stem girth, tillering ability, stool habit, thrashing ability and some more common morphological traits observed in the field during the collections as well as sucrose % using hand refractometer confirmed a preponderance of the soft, purple, high water and less sucrose canes over the green, hardier, less water and high sucrose canes (Kwon-Ndung et al., 2000).

3.1.4 Research on some Neglected and Underutilized Species 4

i) Acha or Fonio Digitaria exilis Kippis Stapf and Digitaria iburua

Neglected and underutilised species are sometimes described as 'orphan crops' or 'minor crops' due to their lesser importance in terms of global production and consumption patterns. In view of their significance in their local areas of production, researchers have realized their great potential in food security, sustainable agriculture and the upliftment of the socio-economic status of the rural poor who are the major curators of such species. Acha (Digitaria exilis (Kippist) Stapf) is a glumaceous monocot of the genus Digitaria of the family Gramineae (or Poaceae). It is one of the most important NUS with the potential to provide food security. There are over 300 Digitaria species, which are sometimes grown as fodder crops. Acha genetic resources are cultivated accessions and their wild relatives which have valuable traits and they constitute the backbone of any Acha Research and Development programme. In addition to playing a positive and unique role in the development of new Acha cultivars or varieties, they also help in restructuring existing cultivars. I have undertaken the following significant research projects in an effort to unlock this genetic resource so as to promote and safeguard its food security potential.

a. Evaluation of thirteen local accessions in Badeggi

Pioneer research work on Acha at the National Cereals Research Institute was initiated in June 1995 when thirteen local accessions from Jos Plateau area were planted in non-replicated strips of 1m by 3m. Prior to this, there was no recorded information on evidence of growing of this crop in this location. The yield responses of this trial in November 1995 confirmed that Acha can do well in this location when adequately managed (Table 7).

Table 7: Evaluation responses of thirteen Acha accessions

Acession Name	No.of spikes/plant	Spike length/plant	No. of days to maturity	Grain yield(kg/ha)
Ashui	3.24	12.65	118	968
Gyong'ekwot	3.08	13.21	112	548
Gong'erandong	2.91	12.53	119	841
Gwandara	2.97	13.25	112	758
Nkpwos	3.84	12.82	114	698
Gyong'eseng	3.45	12.32	111	880
But'esi	3.65	11.96	117	952
Nchonshong	3.29	12.11	116	687
Waku	3.05	13.24	113	935
Tsala	2.96	13.61	110	1060
Mburu	3.12	13.35	116	598
Vakahal	2.87	12.65	98	1231
Sunchip	3.24	12.84	113	854
Means	3.21	12.82	113	846.9
S.E of Means	0.07	0.01	1.16	52.5

Source: Kwon-Ndung et al., 2003)

Acha germplasm collection survey and conservation in Nigeria.

The genetic conservation of Acha is very essential to avoid genetic erosion and loss of food security. Survey missions were therefore embarked upon to six states of Nigeria between 1st November to 31st November 1995. The germplasm collecting expedition resulted in an interaction and interviews of 263 farmers in 27 LGAs of 5states and FCT Abuja. A total of 138 accessions were collectedfrom131 farmers (Kwon-Ndung et al., 1998). These collections in addition to the results of Acha adaptability studies in Badeggi became the foundation from which Acha Research and Development took off at the National Cereals Research Institute in 1995. In addition, the survey was also able to unravel the production practices of Acha among the farmers in all the Acha growing communities. Oral interviews through structured questionnaires revealed that land preparation was predominantly manual by hoe across all the states. Only a few farmers (15%) from Plateau State reported the use of tractors. Planting by broadcasting seeds on ridges was practiced in 3 states while planting on flat lands was common in two. A high number of diversity of Digitaria species was observed in Plateau and Kaduna states and production land area in these locations for individual farmers was observed to exceed3 hectares. Fertliser use was very unpopular except for a few respondents in Tafawa Balewa area of Bauchi and Niger states confirming the low nutrient requirement of this crop (Kwon-Ndung and Misari, 1999). Weeding was

observed to constitute the greatest production constraint across all states. Intercropping with other crops was reported in some states and harvesting was carried out by majority respondents using hand held sickles or by hand pulling of sheaves by a few. Processing commences with threshing of harvested sheaves which also varied among respondents. While some used sticks, others trampled the harvested and neatly tied sheaves. Dehulling was popularly by manual except for a few respondents from Plateau state that used a mechanical dehuller. The grain use varied across respondents ranging from use as hard paste 'tuwo', light or hard porridge and couscous and was specific to customs and traditions in the different localities (Kwon-Ndung and Misari, 1999; Kwon-Ndung et al., 2001). The study confirmed that Acha production in Nigeria is limited by high costs associated with several operations in its husbandry. Also, the popularity of the crop is increasing because of its low glycemic content which ranks it as a preferred diet for diabetic patients. Study concluded and recommended the national and international scientific communities to embrace strategies that will involve innovative strategies to improve farmers' present practices and boost local production.

Table 8: Survey of Acha husbandry activities of farmers in different growing areas of Nigeria

Activity or Item	Farmers (%)				
	Bauchi	Kaduna	Kebbi	Plateau	Niger
Diversity of varieties under cultivation					
.....Growing different varieties	39.1	80.0	0.0	85.3	4.8
.....Only one or two major varieties	60.9	20	100	14.7	95.
Average land area for Acha					
.....Below 1 ha	100.0	90.8	100	70.6	100.0
.....2-3 ha	0.0	9.2	0.0	25.7	0.0
.....above 3 ha	0.0	0.0	0.0	3.7	0.0.
Problem with pests and diseases	30.4	32.3	55.6	38.2	29.4
Grain yield/ha					
.....Harvest below 800 kg/ha	43.5	73.8	55.6	76.4	28.6
.....800-1000kg/ha	3.5	15.4	38.8	11.8	71.4
.....Above 1000kg/ha	13.0	10.8	5.6	11.8	0.0
Application of fertilizers	43.2	0	0	0	48
Chemical weed control	0	0	0	0	0
Manual weed control	100	100	100	100	100

Source: Kwon-Ndung and Misari (1999).

c. Acha DNA fingerprinting

Under the project, Promotion of Fonio in West and Central Africa sponsored by International Plant Genetic Resources Institute (IPGRI), this project was initiated to unravel the extent of genetic diversity, the origin and phylogeny of Acha (fonio) in West Africa. This is due to the fact that despite the importance of this crop in national and global food security, the extent of genetic diversity, origin and phylogeny was not well understood. Ten accessions were used to optimise protocols in the DNA isolation and RAPD analysis of these acha germplasm accessions. A total of 100 RAPD OPERON primers were screened using four accessions and out of the 100, only 15 of the primers showed polymorphisms and were chosen to amplify the whole ten accessions (Table 9). A typical sample of PCR amplification and the dendrogram constructed using neighbour joining method of cluster analysis separated all the ten accession into two clusters at 0.55 similarity coefficient. This study clearly showed that there was no duplication among the accessions and that the protocols used yielded quality DNA and generated RAPD polymorphic bands.

Table 9: List and sequences of the 10-base nucleotide primers used for genetic characterisation

Primer Code	Nucleotide sequence 5' to 3'	No. of polymorphic bands in each primer
OPERON – AE 10	CTCAAGCGCA	3
OPERON – AG 20	TGCGCTCCTC	3
OPERON – AF 20	CTCCGCACAG	6
OPERON – AC 20	ACGGAAGTGG	2
OPERON – AE 01	TGAGGGCCGT	2
OPERON – AE 03	CATAGAGCGG	2
OPERON – AF 02	CAGCCGAGAA	4
OPERON – AC 15	TGCCGTGAGA	4
OPERON – AC 02	CTCTCGGCGA	3
OPERON – AE 15	CACGAACCTC	3
OPERON – AE 02	TCGTTCACCC	3
OPERON – AC 07	GTGCCCGATC	3
OPERON – AC 13	GACGCGATTG	2
OPERON – AD 20	TCTTCGGAGG	4
OPERON – AE 07	TGTCAGTGGC	2
OPERON – AC 10	AGTCCGCCTG	3

Acha agro-morphological characterisation.

Under the project, Promotion of Fonio in West and Central Africa sponsored by IPGRI, 62 accessions of Acha from four West African countries were characterised morphologically. The traits used in characterising the accessions are: grain clour, seed colour, leaf tip shape, internodes, percentage of leaf pigment, percentage culm pigment, leaf pubescence and culm type. The

data obtained was used to calculate the genetic similarity among the accession. Pairwise distance similarity matrices were computed using sequential, hieracrchial and nested (SAHN) clustering option of the NTSYS-pc version 2.02 software package. While some accessions were difficult to be differentiated at the 1.00 similarity (Table 10).

Table 10: Linkage of 62 accessions at 1.00 similarity level

Accession numbers difficult to differentiate at 1.00 similarity level	Local names of the accession
1, 2, 7	Aburu, Binchieh
5, 6	Babudama
26, 27	Guzuksar
15, 16	Ebut
40, 41, 41	Nibang
43, 44, 45, 46	Nipiya
35, 36	Kumbe
3, 4, 29, 30, 31, 32, 62	Arasbang, Gong'eseng, Harat'eseng, Waku
9, 10, 11, 12, 17, 37, 39	Chenesara, Exsum-1, Nchorong, Nelchun
19, 20, 21, 22, 23, 24, 25	Gong'erandong
58, 59, 60, 61	Tsala
14, 38	Chunrire, Ndatbutt
47, 48, 49, 50, 51, 52, 53, 54, 55	Nkpwos

Source: IPGRI (2004).

e. Evaluation of morphological diversity of Acha (fonio) (Digitaria exilis and Digitaria iburua) germplasm in Nigeria

Thirty five Acha accessions from Riyom Sub-station of the National Cereals Research Institute, was evaluated in the Research and Experimental Plot of the Plant Science & Biotechnology Programme in Nasarawa State University, Keffi. Morpho-agronomic variations and growth performance of the accessions were observed to have an influence on grain yield. Jakah variety produced the highest yield of 176.24kg/plot which differed significantly ($p<0.05$) with other accessions while morphological features of peduncle length, internodes length, spikelet per panicle number and plant height.

f. Genetic variations in Acha (Digitaria exilis and Digitaria iburua) using RAPD-PCR techniques in Nigeria

In view of the dearth of information in the area of morphological characteristics of Acha and the genetic diversity within Nigeria, this study evaluated some Acha accessions for their morphological and genetic characterization in order to unlock the genetic potential of each variety for breeding purposes. The PCR analysis diagnostic tools was used. A total of thirty

five accessions of Acha were also grown in the screen house in polythene bags containing rich topsoil. Young leaves were harvested from 3 weeks old seedlings, put in a sealable plastic bag, labeled properly and were used immediately for DNA extraction following the methods of Dellaporta et al., (1983). The extracted pure Acha DNA was quantified using a spectrophotometer before PCR analysis to obtain required concentration. PCR amplification was performed according to Arunyawat (1997), using primers synthesized by Operon Technologies (USA). The analysis of the molecular clusters obtained revealed a wide array of genetic diversity existing in Acha classification in Nigeria and similarly confirmed the use of RAPD-PCR in unravelling the phylo-genetic diversity of the Acha accessions.

Variations in the physical characteristics of Digitaria spp accessions seed in this study showed that the thirty five accessions have three main colours; White, Brown and Light Brown. Ampios, Napas, Kin, Gong-a-randong, Chun-hoss 1, Jakah, Munsung, Suhn, Napiya, Sha'alak, Dinat, Jipel, Gotip, Shalak, Tsala, Gopantor and Gwabi seed were of white colour. Gindiri 1, Kureep, Sheng, Tishi, Lalaku, Gindiri 2, Nkpwos, Ndat, Namuruk, Nashileng and Badama had light brown coloured seed while Chun-hoss 2, Chisu, Nding, Gong-halla, Chunpyeng, Npyeng and Maan seed were brown in colour while seed weights for all the accessions ranged between 0.013g and 0.093g. The morphology of the growing sections (Table 11) showed that there are variations in the tiller number, plant height, peduncle length, Internodes length, spikelet number per panicle, and leaf area among all the accessions.

Table 11: Morphological Variations among Digitaria spp accessions.

NO	ACCESSION	Tiller no/plant	Peduncle length (cm)	Internode length (cm)	Spiklet no/panicle	Leaf area (cm)
1	Ampiyos	19.00^{cde}	33.15^{m}	5.00^{mno}	4.00^{efg}	13.18^{c}
2	Chun-hoss 2	10.00^{klm}	32.72^{m}	5.00^{mno}	8.00^{ab}	11.66^{c}
3	Gindiri 1	21.00^{c}	38.66^{i}	5.66^{klm}	4.00^{efg}	11.15^{c}
4	Chisu	21.00^{c}	29.43^{pq}	5.66^{klm}	4.00^{efg}	13.18^{c}
5	Nding	4.00^{o}	31.32^{mn}	3.70^{opq}	4.00^{efg}	12.65^{c}
6	Kureep	18.00^{de}	29.23^{q}	4.33^{nop}	4.00^{efg}	12.67^{c}
7	Sheng	13.00^{hijk}	38.71^{i}	3.50^{pq}	3.00^{g}	10.64^{c}
8	Napas	19.00^{cde}	42.43^{g}	3.07^{q}	5.00^{cdef}	10.64^{c}
9	Gong-halla	14.00^{ghi}	32.40^{no}	5.52^{lmn}	6.00^{bcde}	9.12^{c}
10	Tishi	11.00^{jkl}	35.77^{l}	4.53^{mno}	4.00^{efg}	12.16^{c}
11	Kin	14.00^{ghi}	31.70^{no}	3.50^{opq}	4.00^{efg}	9.12^{c}
12	Chunpyeng	20.00^{cd}	30.99^{o}	4.50^{mno}	5.00^{cdef}	12.16^{c}
13	Npyeng	13.00^{ghij}	29.18^{p}	4.50^{mno}	4.00^{efg}	12.16^{c}
14	Maan	15.00^{fgh}	29.44^{q}	5.00^{mno}	4.00^{efg}	12.16^{c}
15	Gong-a-randong	11.00^{jkl}	27.72^{r}	5.33^{mno}	4.00^{efg}	9.12^{c}
16	Lalaku	13.00^{ghij}	39.46^{hi}	4.66^{mnop}	5.00^{defg}	12.16^{c}
17	Gindiri 2	18.00^{de}	50.03^{a}	4.50^{mno}	5.00^{fg}	13.68^{bc}

18	Nkpwos	15.00^{fghi}	35.46^{l}	4.33^{nop}	6.00^{bcde}	11.66^{c}
19	Ndat	17.00^{ef}	36.54^{k}	4.66^{mnop}	4.00^{efg}	12.67^{c}
20	Namuruk	20.00^{cd}	40.10^{h}	5.51^{jklm}	4.00^{efg}	13.69^{bc}
21	Chun-hoss 1	14.00^{ghi}	39.80^{h}	5.52^{jklm}	5.00^{cdef}	13.18^{c}
22	Jakah	20.00^{cd}	38.00^{j}	6.66^{hijk}	7.00^{ab}	3.04^{d}
23	Munsung	21.00^{c}	47.96^{d}	6.66^{hijk}	7.00^{ab}	2.03^{d}
24	Suhn	9.00^{klm}	47.44^{e}	6.33^{ijkl}	7.00^{ab}	1.52^{d}
25	Napiya	8.00^{mn}	37.86^{ik}	7.66^{efgh}	5.00^{cdef}	3.02^{d}
26	Sha'alak	7.00^{n}	27.43^{r}	6.70^{ghij}	5.00^{cdef}	1.52^{d}
27	Nashileng	18.00^{de}	35.45^{l}	11.06^{b}	8.00^{a}	10.39^{c}
28	Dinat	12.00^{ijk}	37.43^{k}	8.33^{def}	7.00^{ab}	3.04^{d}
29	Jipel	10.00^{klm}	43.66^{f}	13.00^{a}	8.00^{a}	10.14^{c}
30	Gotip	29.00^{a}	51.15^{a}	9.63^{bc}	7.00^{ab}	23.83^{a}
31	Shalak	13.00^{ghij}	48.62^{cd}	8.66^{de}	7.00^{ab}	23.83^{a}
32	Tsala	15.00^{fghi}	51.34^{ab}	7.52^{efg}	7.00^{ab}	19.77^{a}
33	Gopantor	15.00^{fg}	48.89^{cd}	9.33^{cd}	6.00^{bcde}	19.27^{ab}
34	Badama	27.00^{a}	30.84^{o}	7.33^{fghi}	5.00^{cdef}	10.65^{c}
35	Gwabi	24.00^{b}	49.00^{c}	12.26^{a}	7.00^{ab}	19.77^{a}
	Overall Mean	15.83	37.92	6.1	5.31	6.91
	SE of x	5.47	7.41	2.68	1.79	3.74

Source: Odeyemi and Kwon-Ndung (2012; Kwon-Ndung and Odeyemi, 2013).

Growth and yield performance of Digitaria spp shown in Table 12 shows that the highest yield of 176.24 kg of yield was recorded in Jakah accession and this is significant.

Table 12: Growth Performance and Yield of Various Digitaria spp.

Based on the morphological data obtained in the studies of thirty five accession of Acha, the phylogeny relationship grouped the accessions into twelve distinct races as shown in Fig. 5.

NO	ACCESSION	Germ% 14 Days After Planting	Days to 50% flowering	Days to maturity	Plant height (cm)	Grain Yield (kg)
1	Ampiyos	80.62^{cd}	77.42^{cd}	115.00^{f}	67.66^{i}	5.33^{opq}
2	Chun-hoss 2	40.40^{ij}	83.92^{b}	123.00^{cde}	67.33^{i}	5.87^{o}
3	Gindiri 1	59.60^{f}	77.42^{cd}	115.00^{f}	72.33^{g}	13.96^{m}
4	Chisu	59.85^{f}	84.15^{b}	123.00^{cde}	56.66^{klm}	15.92^{m}
5	Nding	70.52^{c}	84.25^{b}	121.00^{e}	67.00^{i}	15.14^{m}
6	Kureep	70.28^{c}	91.17^{a}	127.00^{ab}	58.33^{kl}	6.06^{o}
7	Sheng	50.85^{g}	84.25^{b}	121.00^{e}	75.00^{gh}	4.42^{opqr}
8	Napas	40.60^{ij}	84.11^{b}	124.00^{bcde}	100.40^{d}	9.56^{n}
9	Gong-halla	51.16^{g}	84.59^{b}	126.00^{abcd}	54.00^{lm}	2.90^{qrs}
10	Tishi	60.94^{f}	84.56^{b}	124.00^{bcde}	57.00^{klm}	1.51^{rs}
11	Kin	71.63^{e}	77.18^{cd}	115.00^{f}	57.00^{klm}	2.10^{rs}
12	Chunpyeng	50.36^{g}	91.26^{a}	127.00^{ab}	57.00^{klm}	4.85^{opqr}
13	Npycng	31.01^{k}	91.53^{a}	128.00^{ab}	55.66^{klm}	1.85^{rs}
14	Maan	30.05^{k}	91.19^{a}	128.00^{a}	58.66^{kl}	0.93^{s}
15	Gong-e-randong	50.75^{g}	91.19^{a}	127.00^{ab}	54.33^{lm}	2.50^{qrs}
16	Lalaku	33.14^{k}	91.46^{a}	128.00^{a}	57.00^{klm}	2.42^{rs}
17	Gindiri 2	41.31^{h}	77.42^{cd}	115.00^{f}	95.66^{e}	35.17^{l}
18	Nkpwos	40.79^{hi}	83.95^{b}	123.00^{cde}	75.33^{gh}	0.96^{s}
19	Ndat	30.93^{k}	91.61^{cd}	126.00^{abc}	75.66^{gh}	1.34^{s}
20	Namuruk	40.45^{hi}	84.34^{b}	121.00^{e}	77.66^{g}	30.83^{l}
21	Chun-hoss 1	30.22^{k}	90.01^{a}	127.00^{ab}	74.66^{gh}	5.43^{op}
22	Jakah	70.79^{e}	84.42^{b}	122.00^{de}	76.00^{gh}	176.24^{a}
23	Munsung	50.63^{g}	84.24^{b}	122.00^{cde}	112.66^{c}	122.41^{b}
24	Suhn	31.10^{k}	84.63^{b}	124.00^{bcde}	100.66^{d}	84.87^{e}
25	Napiya	30.84^{k}	84.01^{b}	121.00^{e}	76.00^{gh}	80.26^{d}
26	Sha'alak	21.03^{l}	77.65^{cd}	115.00^{f}	56.66^{klm}	49.40^{f}
27	Nashileng	30.64^{k}	77.65^{cd}	115.00^{f}	84.66^{f}	33.49^{lj}
28	Dinat	20.44^{l}	77.15^{cd}	115.00^{f}	77.00^{g}	33.85^{l}
29	Jipel	31.89^{k}	76.84^{d}	113.00^{f}	85.00^{f}	19.79^{jl}
30	Gotip	81.32^{c}	78.05^{cd}	115.00^{f}	120.66^{b}	33.26^{lj}
31	Shalak	89.87^{b}	76.37^{d}	114.00^{f}	112.66^{c}	10.51^{h}
32	Tsala	87.75^{b}	78.72^{c}	114.00^{f}	131.66^{a}	72.22^{e}
33	Gopantor	81.76^{c}	77.55^{cd}	114.00^{f}	113.33^{c}	42.41^{g}
34	Badama	78.61^{d}	77.83^{cd}	115.00^{f}	62.66^{j}	5.06^{opq}
35	Gwabi	94.62^{a}	78.64^{c}	115.00^{f}	112.00^{c}	25.15^{k}
	Overall Mean	50.57	82.8	119.80	77.07	28.23
	SE of x	20.13	5.50	5.50	21.85	38.10

Npyeng and Maan accessions formed distinct race of Acha plant based on their growth and yield parameters. The other 32 accessions have related phylogeny trait and can be traced to be of the same descent. The RAPD analysis showed that a total of 10 RAPD OPERON primers were screened using thirty five (35) of the Acha lines. Out of these, only eight of the primers showed polymorphisms with all the thirty five line. The dendogram of the DNA cluster variations of all the thirty-five accessions are shown in Fig. 5 below.

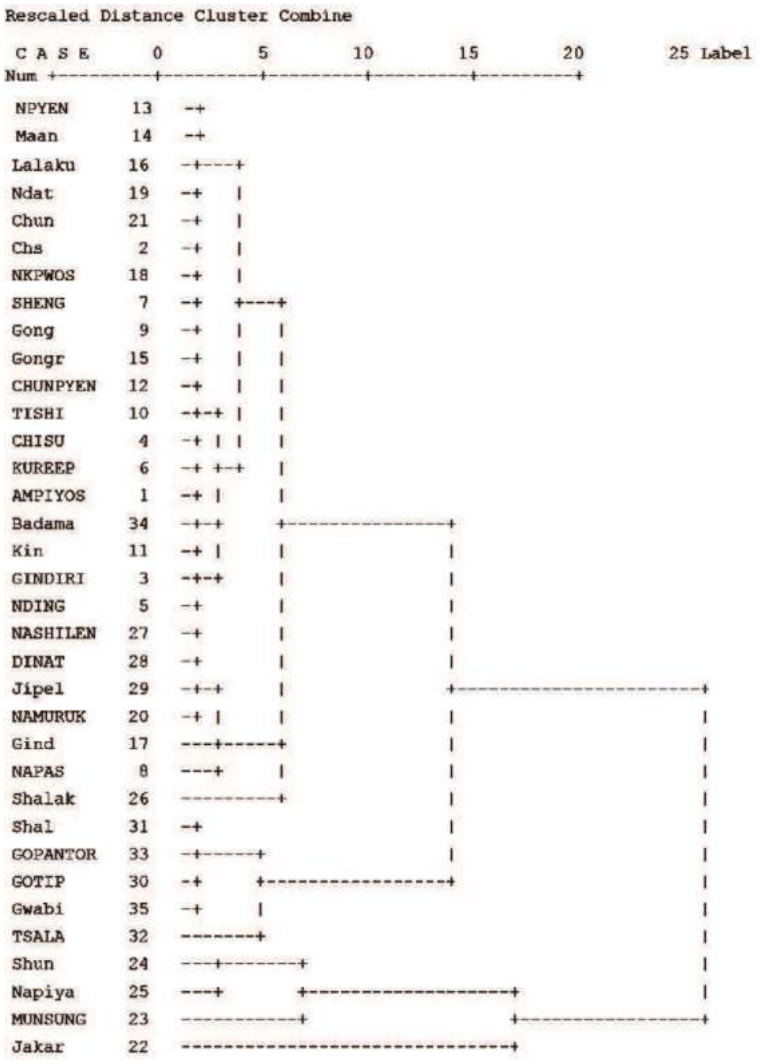


Fig. 8: Hierarchical Clusters Dendrogram of Digitaria Species Morphological Variations in Nigeria
Source: Odeyemi and Kwon-Ndung (2012); Kwon-Ndung and Odeyemi, 2013.).

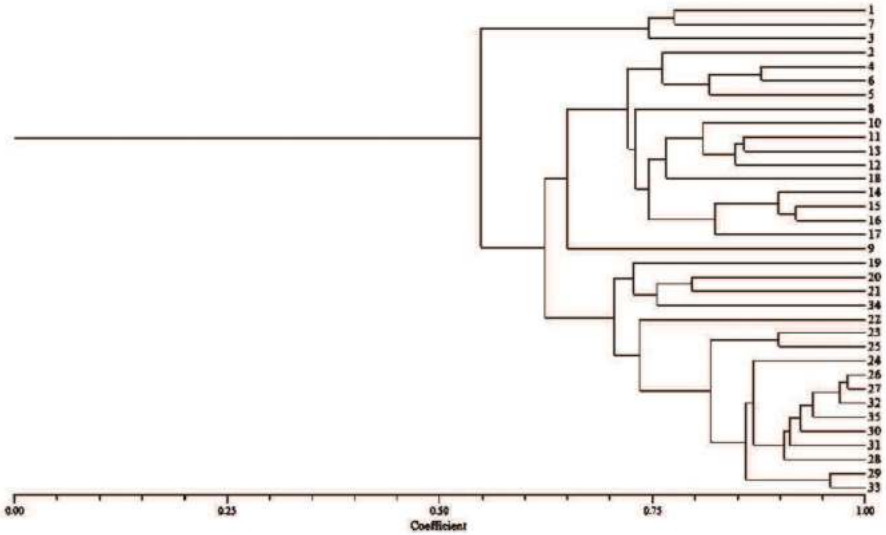


Fig. 9: Dendrogram of DNA Cluster Variations of Digitaria Species in Nigeria
KEY: 1.AMPIYOS, 2. CHUN-HOSS 2, 3.GINDIRI 1, 4. CHISU, 5. NDING, 6. KUREEP, 7. SHENG, 8. NAPAS, 9. GONG-HALLA, 10. TISHI, 11. KIN, 12. CHUNPYENG, 13. NPYENG, 14. MAAN, 15. GONG-A-RANDONG, 16. LALAKU, 17. GINDIRI 2, 18. NKPWOS, 19. NDAT, 20. NAMURUK, 21. CHUN-HOSS, 22. JAKAH, 23. MUNSUNG, 24. SUHN, 25. NAPIYA, 26. SHA'ALAK, 27. NASHILENG, 28. DINAT, 29. JIPEL, 30. GOTIP, 31. SHALAK, 32. TSALA, 33. GOPANTOR, 34. BADAMA, 35. GWABI
Source: Odeyemi and Kwon-Ndung (2012; Kwon-Ndung and Odeyemi, 2013).

The resultant eight morphoclusters obtained from the cluster analysis of the thirty five accessions confirm that the polymorphism of Acha was shown with the banding of eight primers with the extracted DNA. Contradiction that occurred in the morphology and molecular dendrogram plots with Chun-Hoss I forming a distinct morphocluster in the morphology cluster analysis might be attributed to the influence of environmental conditions on phenotypes of crops. The dendrogram plot of molecular classification gave multilinked single group, thus, showing that all accessions were of the same descent. This study confirmed that the use of only morphologic features in classifying Acha does not give the same result with the engagement of molecular techniques. However the study has confirmed the diversity in morphological traits of the Acha accessions. The study has also confirmed the use of RAPD-PCR in unraveling the phylo-genetic diversity of Acha accessions. The study identified the accessions that have the potential to be adopted in Acha selection and improvement programmes. Study identifies Jakah accession as a candidate variety for selection and on-station and on-farm trials.

ii) Research on Finger millet (Eleucine corocana) Gaerth

a. Assessment of phenotypic variations in finger millet (Eleusine coracana(L) Gaertn) landraces from Northern Nigeria.

The phenotypic variation and diversity of 10 germplasm accessions of Finger millet (Eleusine coracana (L) Gaertn) from diverse locations in the geographic region of Northern Nigeria during the 2008, 2009 and 2010 cropping seasons revealed a significant diversity for plant height, 1000 seed weight, leaf length and number of tillers. Cluster analyses revealed six distinct groups, with one landrace forming an independent colony confirming the presence of high phenotypic variability among the selected morphological traits. This is crucial in developing a local breeding and selection programme for this crop in Nigeria (Table 13 and Fig. 7) (Umar and Kwon-Ndung, 2014).

Table 13: Pooled Means of Morphological traits of finger millet Accessions grown in Northern Nigeria in the three cropping seasons.

Accession	Plant Height (cm)	Plant width (cm)	Leaf Length (cm)	Leaf width (cm)	Number of Fingers	Finger length (cm)	Finger width (cm)	Number of Ears	Seed Weight (1000)g
Ex-Dantse	54.66	10.68	49.02	1.43	73.50	61.30	2.60	20.00	175.70
Ex-Riyom	60.33	12.00	58.20	1.45	79.50	79.35	2.70	19.50	185.75
Ex-Bum	56.33	11.06	55.36	1.38	81.50	60.95	2.20	21.50	190.75
Ex-Gura	59.16	11.52	50.96	1.67	132.00	64.65	2.10	19.00	183.40
Ex-Kwakwi	58.28	10.42	55	1.57	115.50	61.15	2.30	20.00	210.95
ExT/Balewa	59.05	12.30	54.29	1.30	102.50	51.65	2.20	21.00	200.80
Ex-Biliri	64.96	11.78	54.32	1.38	77.50	54.00	2.40	19.00	180.90
Ex-Glada	60.47	10.15	53.16	1.50	85.00	44.90	2.60	16.50	150.90
Ex-Andaha	58.26	9.77	50.24	1.57	132.50	99.25	2.30	22.50	275.85
Ex-Kwi	62.50	11.39	54.15	1.94	171.50	70.90	2.50	25.50	245.75
TOTAL	567.9	110.74	535.3	15.50	1051.00	648.10	23.90	201.50	2000.0
MEAN	59.79	11.07	53.53	1.51	105.10	64.80	2.39	20.15	200.09
S.E.	3.38	0.32	3.37	0.106	3.97	5.26	0.07	1.88	3.38
LSD(0.05)	6.48	0.48	7.61	0.184	13.61	7.77	0.09	2.69	32.54
CV (%)	11.54	6.85	6.05	3.064	4.63	0.77	0.08	1.69	16.55

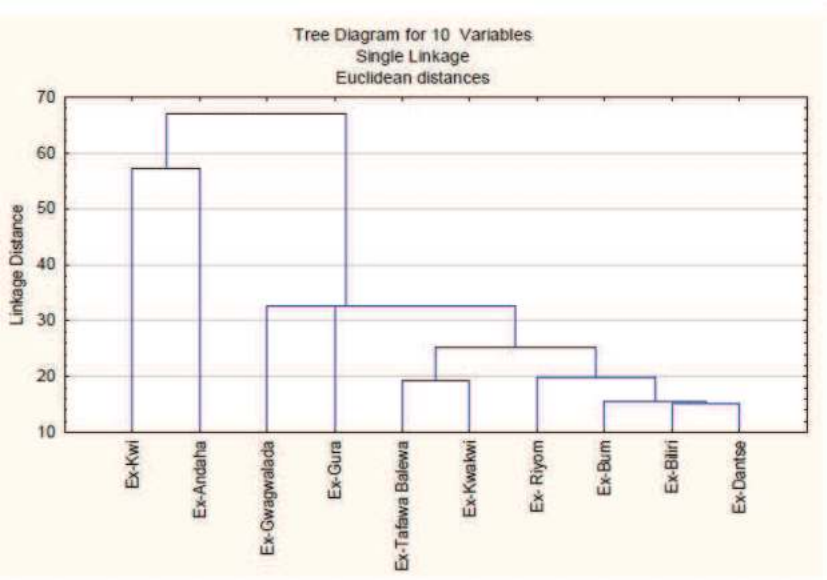


Fig 10: Dendrogram of morphological characters showing the linkages among ten accessions of finger millet grown in Northern Nigeria for the three cropping seasons.

b. **Molecular characterisation of finger millet (Eleusine coracana (L.) Gaertn) using RFLP**

Genetic characterization of 10 germplasm accessions of Finger millet (Eleusine coracana (L) Gaertn) using the molecular marker RFLP (Restriction Fragment Length Polymorphism confirmed existence of polymorphism among the accessions (Fig. 8). These results demonstrate high variability existing among the genetic traits for these germplasm accessions. This information is very useful in unravelling the pedigree genetic relationships, as well as, in designing breeding and selection experiments for this crop.

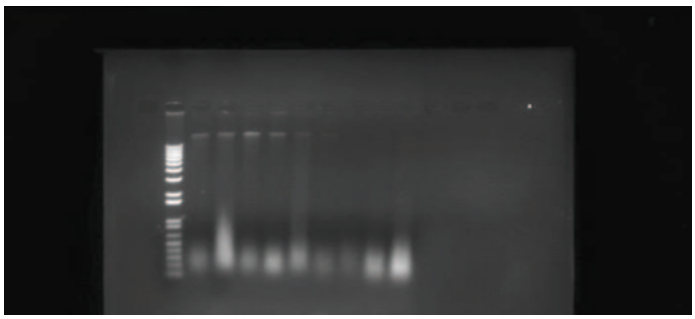


Fig 11. Restricted Fragment Length Polymorphs (RFLPs) from finger millet plant genomic DNA
Source: Umar and Kwon-Ndung (2014)

iii. Research on African locust bean (Parkia biglobossa)

The African locust bean Parkia biglobossa is a very important tree crop in the African savannas where the natives use it as a food, medicine, glaze for ceramic pots, fodder, firewood and charcoal production. However, its wide range of wild species which is quite restricted is seriously under threat of genetic erosion, although the need to develop improved seedlings or varieties of this tree with lesser growth cycles and other socioeconomic characteristics is under consideration. Specifc projects undertaken to unlock diversity in this species are:

a. Baseline study on the populations of Parkia biglobossa in selected locations in North Central Nigeria. A study to determine the genetic diversity of this crop in selected locations in north central Nigeria confirmed the predominance of this wild species in the Southern and Northern Guinea Savannah. However, overexploitation of this species for food and for timber is a great challenge for the sustainability of this important genetic resource (Kwon-Ndung et al., 2009).

b. Prospects of host resistance in improved and domesticated species of Parkia Biglobosa to African Mistletoes (Tapinanthus Spp.) in Central Nigeria. Studies on the outcome of parasitic mistletoes (Tapinanthus spp) on the fruit yields of Parkia biglobossa in Central Nigeria confirmed three Tapinanthus species as main parasites of this genetic resource across all locations and the serious threat of genetic erosion that this species is exposed to. A consistent relationship of fruit loss and girth size of host trees was established. This study identified the significance of host resistance in sustainable Parkia biglobossa tree management and the need for a deliberate breeding programme to select resistant progenies in Central Nigeria (Kwon-Ndung and Ismaila, 2009).

c. Study on the ecological implications of climate change on the genetic diversity of Parkia biglobossa in North Central Nigeria. So many factors are responsible for threat to loss of diversity in this species but the consequence of climate has been suspected as one of the most important causes. This study was therefore carried out to determine the ecological implication of possible response of climate change on the genetic distribution and diversity of this valuable source of biodiversity in selected locations in North Central Nigeria. Different agro climatic factors such as rainfall distribution, temperatures and relative humidity in ten locations in the north central region were undertaken. The effect of these climatic factors showed a decline in the fruit yield over the two cropping seasons using correlation coefficients. Rainfall distribution, temperature and relative humidity also significantly varied with crop prevalence across locations and these results suggested the probable effect of shifts in the main agro climatic

factors on the yield productivity and genetic diversity of this important germplasm in sub-Saharan Africa (Kwon-Ndung et al., 2009)

d. Embryogenesis and callus induction in Parkia biglobossa species in Nigeria. The difficulty associated with the generation of seedlings for the propagation of this crop led to this study. Explants of Parkia biglobossa were generated in vitro using culture protocols and the results clearly show the regenerative potential of explants under culture. (Kwon-Ndung and Nwaokoro, 2011; Nwaokoro, N. (2012).

Other studies with the aim of unlocking the genetic diversity on crops such as Rice, Soybeans, Beniseed, Phaseolus beans, Fluted pumpkin (Telfeiria occidentalis) Moringa oleifera, Peppers (Capsicum spp), Curcurbita pepo, have been concluded and some have also been reported (NCRI, 1997; 1998;1999; Kwon-Ndung and Igbenedion, 2012 Liamngee and Kwon-Ndung, 2013; Kwon-Ndung and Wachukwu, 2013; Kwon-Ndung et al., 2013).

3.2. Current and Future Research Focus:

a) Acha genetic transformation and release of Acha variety
b) Biotechnology of sugarcane / Marker assisted selection of sugarcane for sugar and energy (biofuels)
c) Provenance variations in Jathropha curcas and genetic characterisation of this energy crop
d) Marker Assisted Breeding of Parkia biglobossa for production of improved clones to replace the fast diminishing wild trees
e) Evaluation and conservation of plant species diversity in Nasarawa state, Nigeria
f) Assessment and reclamation of degraded mining soils using plant remediation
g) Plant breeding for Sustainable land use management of degraded mining soils using GIS and remote sensing.

4.1. Recommendations

1. Conventional breeding of crop plants must be complimentary to molecular breeding.
2. Without further delay, I humbly appeal to the Nigerian President and Commander-in-Chief, to sign into law the Biosafety law to promote and boost research activities on GM crops in our country. This will also open up opportunities for researchers to break new grounds in grants access and collaboration in this area. The current situation is hindering access to

collaborative researches on GM crops.
3. The media reports on GM crops and technology in Nigeria is sometimes carried out by non-science journalists who do not have a basic understanding on biotechnology and this can be misleading. The OFAB (Open Forum on Biotechnology) being promoted by NABDA is helping in creating awareness but the media must rise to the occasion to engage experts to properly educate the mass illiterate populace on this technology.
4. More scientists are encouraged to study the unknown plant genetic resources in our localities.
5. An Institute dedicated to research on use of Neglected and Underutilised Species (NUS) to be established in Nigeria to promote research on NUS. Proposed name of Institute to be NINUS with headquarters in Abuja.
6. Appeal to the management of the University to fund basic and applied research in biotechnology and upgrade the existing facilities with the scarce and competing resources so that the critical mass required to drive this revolution in the country can arise from this great University.

4.1.1 Reminiscences

Reflecting back on my academic stewardship at the Nasarawa State University, I am compelled to recall how we all worked very hard to build a University system that will be a centre of excellence that will meet the socio-economic aspirations of not only people of Nasarawa State but the nation as a whole. Mr. Vice-Chancellor, Sir, with all due respect and modesty, I plead with you to pull all available resources together to sustain that initial tempo so as to move this institution to the next level. Even though some of us have pulled out to develop other places, our hearts and our prayers are with you.

5.1. Conclusion

Plant breeding has a long history of development, especially since the fundamental principles of inheritance were established in the late 19th and early 20th centuries and it has become an important component of cultivated science, which has features of both science and arts. Conventional breeding methodologies have extensively demonstrated its use in successful development of varieties. However, subjective appraisal and experimental selection still play a considerable role in conventional breeding. Scientific breeding needs less practice and more science.

The marker assisted breeding using modern biotechnology has introduced great challenges and prospects for conventional breeding but it cannot replace conventional breeding but it remains a supplementary addition to conventional breeding. The high costs and technical or equipment demands

of MAB is a major obstacle for its large-scale use in the near future, especially in a developing country like Nigeria. Its integration into conventional breeding programmes is a hopeful approach for local crop improvement in the future in Nigeria and therefore we cannot afford to lag behind in embracing and investing in this technology. It is expected that any shortcomings of this technology will be gradually overcome, as its theory, technology and application are further developed and improved. This should lead to a wide adoption and use of MAB in practical breeding programs in Nigeria for more crop species and more technical experts.

It has been proven that spending on agricultural research and innovation is one of the most effective types of investments for sustained poverty reduction and food security. Agriculture-led growth addresses rural poverty directly because it uses rural people, including poor subsistence farmers, as the key agents of change, linking them with other parts of the economy through networks of suppliers, buyers, and markets. Up to 80% of Nigerians are rural people. Such investments has spill over effects and can be an offshoot of wider economic growth in other sectors.

This is the concept that has been adopted and is being pursued by the Federal Government's Agricultural Transformation Agenda (ATA). An honest and sustained commitment to the ideals of this agenda has the potential to propel Nigeria into unimaginable economic heights. Genetic engineering has been recognized as a necessary input for the success of any agricultural programme and food security in the world today. A compelling body of scientific evidence, generated in 29 countries around the world in the past 18 years, undoubtedly indicates that genetically engineered crops which are sometimes called biotech crops, should be an essential element in any strategy designed to achieve food security, sustainability and a more just society (James, 2011).

The safety of GM crops is not in any doubt. Most scientists and policy-makers in Nigeria know that biotechnology is not an answer for all the food production problems, but it is a tool that Nigeria can use to overcome this problem. Like any technology, there is risk, but over time, we have learnt as humans to evaluate the perceived and real risks against the benefits of any emerging technologies, and these have been responsibly assimilated to foster development. For example, use of electricity, automobiles, aviation transport and even vaccinations all involve some risks, but this has not prohibited the human race from promoting their use.

The public acceptance of biotechnology is motivated by the opinion of the risk rather than on the physical reality. We need a sensible and responsible approach to integrating agricultural biotechnology in the Nigerian research

system while ensuring that any risk posed by this technology is kept to a minimum and thorough rigorous scientific approach.

While GM crops are subjected to intensive testing for safety, conventional varieties have never been subjected to any such regulation for food safety or environmental impact. Traditional methods of developing crops involve wild crosses with weedy relatives of crop plants. Hundreds of unknown genes, whose traits are not known, are introduced into these food crops through conventional plant breeding methods and so many traits such as disease and pest resistance have been routinely introduced into crop plants from their wild and distant relatives over hundreds of years. These have posed no serious threat to the environment in terms of crop invasiveness, gene flows or the biodiversity. Yet, some of these fears are invoked for genetically- improved crops which possess similar traits, but just developed through a rapid genetic modification processes.

Agricultural production in Nigeria has relied on exotic introductions for a very long time and there is no question of the invaluable impact these imported species have made on our crop production, food culture and our economy. A wide range of such crops include rice, sugarcane, peppers, wheat, potato, tomato, cabbage, groundnut, cowpea, several other horticultural and ornamental crops, mango, citrus, grapes and numerous others. Genetically improved crops, on the other hand, do not involve any such blanket introduction of several new genes through new plants but only the modification of few genes with already identified traits into local varieties. It is so clear that non-acceptance of biotechnology when compared to the infinitesimal threats presented by genetically improved crops therefore, poses a far greater risk to the Nigerian people. The huge potential benefits from these crops, far outweigh any hypothetical risks posed by their use.

Nigeria is endowed with a wide diversity of plant genetic resources ranging from food crops, medicinal plants, ornamentals and forage species. There is however paucity of knowledge in many of these crops and their wild relatives in the diverse forests ecologies to the drier savannahs and the Sahel regions of Nigeria. In the words of my mentor, Prof. Olorode "There are so many things that remain unknown in our environment, things we must know before they will disappear, things whose knowledge will contribute immensely to global and national intellectual heritage in biology and genetics"(Olorode, 2013). The scientific research community must wake up to this reality and be engaged in not just knowing these heritage but be also engaged in preserving this heritage to ensure food security for the common good of this generation and the unborn generations.

This is the take home message from this lecture: Genes are the basis of heredity and managing the knowledge of genes is very critical in the production of improved seeds or planting materials that are very fundamental in any crop production programme. The quality of seeds that are used by farmers have been confirmed to be the basis of the efficiency of production of all other farm inputs. There is no single crop production practice that can increase crop yields outside the limits of the seed quality that is used, hence use of better-quality seeds guarantees superior harvests and more profits for the farmers under the same management schemes. Improved seeds deliver a reliable guarantee for the three pillars of food security namely, food availability, food abundance and food use. This is the message.

6.1. Acknowledgements

Now that the lecture is over, it is my duty to thank all those that have played significant roles in my upbringing and especially towards the attainment of this professorial chair that has brought me forward to this podium today. Permit me to start with the faithful departed, for the Bible has taught me that when Christ shall return, the dead in Christ shall rise first. Foremost are my late parents Late Mr/Mrs. Kwon Ndung Ganawuri, who brought me into this world. I so much appreciate our mother's strong will and faith in God after the untimely death of her husband and our father about six months after I was born. Her resilience and struggles that was bravely supported by her own mother, my grandmother, the great Late Ade Jaram Hala who did not only turn out to be a foster mother, but worked hard on me that her mentorship, discipline, perseverance, sacrifice and above all prayers produced this Professor of today. I appreciate the role played by my late Uncle Nuhu Ndung Grampolo towards my educational development. I thank my late father in-law, HRH Uhwe of Nyibgye, William Taimako Garba, a great man of wisdom who was always a great source of inspiration to me and my family until his demise last year. I enjoyed the warm and amiable relationship with my late in-law Habakkuk Davut until May this year. He was always inquisitive and demanded to know what an inaugural lecture was when he saw me with some manuscripts in December and I told him I was preparing my inaugural lecture. I am sure he would have loved to be here, but God decided otherwise. My late teachers are highly appreciated and they include Mrs. Bilhatu Nyam, Mr. Chakura Non, Mr. Net Dakere (Karl Marx), Mr D.P. Dung, Dr. S.E. Ebele, Dr. S. Sangowawa and Professor A.T.F. Rahman.

I am grateful to the Ag. Vice Chancellor Professor Muhammad Akaro Mainoma, and his Management Team, for making it possible for me to give this

lecture and I want to also congratulate you on the great efforts you are making in repositioning this University. I pay a special tribute to Professor Adamu D. Baikie, under whose tenure I was employed and he gave me opportunities to serve this University in various capacities. The experience of working with him is simply healthy and wholesome. His leadership style of impartiality, equity and responsibility cannot easily be compared to any and I personally learnt a lot from him. These are the legacies that emerging generations need to embrace at all cost. May God continue to keep you in good health Baba.

I thank the Dean of the Faculty of Natural and Applied Sciences, Professor Y.B. Ngwai, and the entire members of the Faculty as well as Dr. J.C. Onovo, HOD, Department of Biological Sciences and entire members of the Department for all their support. In line with this, I appreciate the goodwill and relationships developed with both my senior and junior colleagues in NSUK among whom include all the Professors that have presented inaugural lectures here before me. I learnt a lot from all of you and I doff my cap and bow before all of you. I am grateful. I also appreciate other colleagues: Late Prof. Dogara Gwamna Jediaye, Prof. P.C Onyenekwe (SHETSCO), Prof. Abah, Prof. F.A. Ajayi, Prof Shuaibu Ibrahim, Prof. Dalhatu Sangari, Prof. Smart Obiekezie, Prof. Fatokun (FU Dutsinma), Prof. Leke Aremu (FU Wukari), Dr. G.A. Amuga, Dr. D.M. Ogah, Dr. Mojeed Yakubu, Dr (Mrs) B.Atolaiye, Dr. Sam Tende, Mrs. Ruth Anda, Dr. Suleiman Aruwa, Dr. S D. Gyar (Rector, Nas. State Poly Lafia), Dr. GRI Pennap, Dr. M.D. Makut, Dr. Modibbo (SIEC, Lafia), Dr. J.P. Mairiga, Mr. Akpa Oyanika and the list can be endless if I didn't have limitation of space. Thank you all!

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A/Prof. Andrew Gana, Dr. S.N. Dachi, Mrs. Wadi Mamza, Eng/Mrs. Solomon Dauda, Mr/Mrs Anthony Monday, my drivers Abdullahi Garba Kabawa and Mallam Kudu Bida amongst many others.

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I am grateful to all my collaborators and benefactors for investigative facilities. I am grateful to Dr. Lazarus Dengwat (Rtd) of the BICOT project Vom, who assisted in the Irradiation of sugarcane setts with gamma cells at no fee and cheerfully volunteered handling the Irradiator so as to eliminate my exposure to the machine and avoid any risk of sterility on my part. In his words, "I don't want you to breed sugarcane and be unable to breed after you have married". Thank you so much, sir, for helping me to breed sugarcane and safeguarding my ability to also breed humans.

Today, I also testify that I have enjoyed the comfort and support given by my very own, endlessly affectionate, caring, pretty and charming wife, Mrs. Linda Kwon-Ndung. A very dutiful, trustworthy and reliable friend and mummy to our children, Jaram (Emmanuella), Jesse, Weng and Emmanuel Jnr. Jaram is habitually so lavish and caring and I certainly consider her as second to her mother in actuality of being selfless towards me. Jesse can be so defensive of me that he can rise up to shield me against any attack. Weng, who is ever so gentle and unassertive has tall ambitions he feels I must help him achieve. To Emma Jnr, the entirety of life appears alright and he does not seem to appreciate why of recent, daddy is not always at home. A combination of these delightful folks at the home front has always challenged me to strive to achieve the unusual.

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I have paid my due respect at the beginning of this lecture, to my creator, who knows the beginning from the end and the end from the beginning, whose great faithfulness has kept me thus far. I have come face to face with human designed life threatening experiences but his mercies have certainly remained new on each encounter. Indeed I raise my voice and proclaim:

> Great is thy faithfulness, O God my Father; there is no shadow of turning with thee; thou changes not, thy compassions, they fail not; as thou hast been thou forever will be. Refrain: Great is thy faithfulness! Great is thy faithfulness! Morning by morning new mercies I see; all I have needed thy hand hath provided; great is thy faithfulness, Lord, unto me!

I thank you all for leaving all that you had to do today, to honour the invitation of the Vice Chancellor to come here to listen to one of his Professors. I took time to prepare this lecture just because I would not want to disappoint you and I was very certain you would make it my day. I have had a wonderful day and I hope I have been able to make it worth your while too. I appreciate your patience. Thanks for listening. God bless you all!

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Plate1: Sugarcane Seedlings obtained from true seed (fuzz) in field ready for transplanting

Plate 2: Sugarcane Seedlings transplanted in single rows

Plate 3: Sugarcane seedlings in field at 1

Plate 4: NCS 003 at 5 MAP in the field 1

Plate 5:NCS 007 at 5 MAP in a commercial field at Bacita (2001)

Plate 6: NCS 005 at 11 MAP at advanced yield trial experiment

Plate 7: Control plot of M_1V_3 seedling in screenhouse trial

Plate 8: Heavy tillering of M_1V_3 of irradiated clone (4kgy)in screenhouse trial

CITATION OF PROFESSOR EMMANUEL HALA KWON-NDUNG.

The history of most men are written and read out in their absence. But for a man who has written his name in the sands of time, and is still writing, occasions abound for their history to be cited to serve as an encouragement to many upcoming men and women and to tell the world that the best of such people is even yet to see the light of day.

Professor Emmanuel Hala Kwon-Ndung was born with a silver spoon to Mr. & Mrs. Kwon-Ndung Ganawuri (both of blessed memory) on the 17th day of December 1964. Kwon-Ndung Ganawuri, a Government College Keffi Old Boy and a College of Administration, ABU Zaria trained Accountant was at the time of his demise, a Sales Representative of Northern Nigeria with the U.A.C, a world conglomerate and worked with the likes of His Excellency Ernest Shonekan. The young lad was not privileged to grow knowing his father or even eat with that silver spoon as death snatched him away when Emmanuel was barely six months old in 1965. This sad event would consequently cause the young Emmanuel to grow with his maternal grandmother in the village.

The absence of a father notwithstanding, God's purpose for Emmanuel was not cut short and very true to his name, God was with him. The destiny of being a botanist was thus shaped from the rural and eventful upbringing on the farm by his grandmother with whom he lived since the age of about three years. As early as age six, Emmanuel started going to the farm to help his grandmother. The desire to go to school was nurtured at the tender age and even when there was no one to take him to the EKAN Transferred School, a Sudan United Mission School, the young Emmanuel would usually go to the School and listen to the teachings through the window from outside. This drew the attention of the class teacher who discovered the potentials and the "professor" in him, being able to answer questions from just listening through the window. The teacher, Miss Bilhatu Chai (as she then was) admitted him, breaking all protocol of school enrolment.

Professor E H Kwon-Ndung thus began his academic journey in Ganawuri, in Riyom L.G.A. of Plateau state. He proceeded to the famous Boys Secondary School Gindiri, in 1978 and by 1984, he was at the School of Basic Studies, Ahmadu Bello University, Zaria. Thereafter, he was admitted to study for a B. Sc. Degree in Botany in the same University. After the compulsory National Youth Service in Akwa Ibom State in 1989, he proceeded to the University of Jos and by January 1991, he bagged a Master of Science degree in Cytogenetics and Plant breeding and a Ph.D from the same University in 1999.

Given his humble disposition to life, he took up a teaching appointment after his M.Sc programme with the Teachers Service Commission, Plateau State, where he taught Biology and Agricultural Science in a village school, Amo-

Katako in Bassa L.G.A of Plateau State. He served for barely seven months when he resigned to take up an appointment with the National Root Crops Research Institute, Umudike as a Plant Geneticist/Breeder and was posted to the Vom Outstation in Plateau state, with a clear mandate to be engaged in the genetic improvement of potato Solanum tuberosum (Irish potato). However, within a year, he moved his service to the National Cereals Research Institute (NCRI). The dream of becoming an accomplished academic was nurtured at the NCRI with the influence of researchers like late Dr. B.B. Wudiri, Prof. S.M. Misari and Professor O.P. Ifenkwe who were very instrumental in that direction. As early as 1995, E.H. Kwon-Ndung enrolled for the Ph.D programme at the University, Jos, and typical of him, he completed the programme on record time in 1999. While on the Ph. D programme, and as a research officer at the NCRI out station in Numan, Adamawa State, he was engaged as a part time Lecturer in the Department of Crop Production, School of Agriculture at Federal University of Technology, Yola.

Subsequently, Professor Kwon-Ndung swung into research programmes which turned out to be breakthroughs in the development of our nation's agricultural base. His novel research on using mutation breeding to select resistant variants to the dreaded disease of smut in sugarcane was a breakthrough and consequently led to commercial release of three indigenous smut resistant industrial sugarcane varieties for commercial cultivation in Nigeria. These varieties are NCS 003, NCS 006 and NCS 007 released by NCRI Badeggi by the National Variety Release Committee, Moor plantation, Ibadan, Nigeria between 1998 and 2000.

Visit http://www.nsdc.gov.ng/docs/pdf/nsdcsvl.pdf for details. Apart from Sugarcane, he has also worked on Acha (Fonio), Beniseed, Cassava, Potatoes, Rice, Finger Millet, African locust bean, Moringa, Phaseolus beans, Peppers and some others. Professor Kwon-Ndung's rural upbringing helped him to appreciate the role of neglected and underutilized species ((NUS) in food security and prompted his research interest on these NUS, especially Acha (Digitaria exilis and Digitaria iburua), Finger millet (Eleusine coracana) and African locust bean (Parkia biglobossa). While at NCRI, he prompted the memo that was raised to the National Council on Agriculture which eventually included Acha as one of the mandate crops of the Institute. He pioneered the international research linkages on Acha and with his colleagues assisted in bringing this small but mighty crop into international research limelight.

He has enjoyed both national and international research collaborations and accessed research grants from the Federal Government, AFCOTT, National Agricultural Research Projects (NARP), Third World Academy of Science (TWAS), International Centre for Genetic Engineering and Biotechnology

(ICGEB), International Institute of Tropical Agriculture (IITA), CTA, IPGRI (now Bioversity International), UNESCO, FAO, UNDP, NABDA, SHETSCO, USAID, Chinese Academy of Science (CAS), FARA (Forum for Agricultural Research in Africa), American Society for Plant Biologists, National Programme on Food Security, National Centre for Genetic Resources and Biotechnology (NACGRAB), International Potato Center (CIP), Global Facility for Underutilised Species (GFU), National Sugar Development Council (NSDC) and Federal Ministry of Environment.

His academic responsibilities can be dated back as far as 1994 when he was appointed the pioneer Resident Scientist of NCRI at the Savanah Sugar Company. Subsequently, as the Programme leader for sugarcane research activities on the station, he organized the Research Centre into a full Outstation of the Institute. He was subsequently appointed the Head of NCRI out station in Bacita, Team leader, REFILS(Research Extension Farmer Input Linkage) for Taraba State. He was the National Coordinator for the NCRI-IPGRI project and has also headed the Department of Biological Sciences, Nasarawa State University, which he joined in 2005 as associate Professor subject to favorable external assessment. He was promoted to full Professor on the 1st of October 2008. He has also served as Administrator/Caretaker, Geography Department of the same university. His appointment was to restore stability, decorum and orderliness to the Department. This particular appointment clearly revealed the trust and confidence reposed on the Professor by the then university management. He has headed many committees and been a member of so many others in the University system. He is currently the pioneer Head of Botany Department at the Federal University Lafia and has acted for the Vice Chancellor in a number of occasions. He is also currently serving as a member of the Board of Trustees of Bingham University Karu. It is therefore not surprising that these responsibilities placed on him are clear evidence of administrative capability developed over the years.

As a Professor of Plant Genetics and Breeding, he has been external examiner to the undergraduate programmes in the Department of Biological Sciences in the University of Abuja from 2007 -2012 and Bingham University from 2011 to 2013. At the post graduate level, he has been external examiner to the M.Sc and Ph.D programmes at the University of Calabar, University of Agriculture, Abeokuta, Ahmadu Bello University, Zaria, Federal University of Technology Minna and Owerri and Abubakar Tafawa Balewa University Bauchi. He was external assessor for professorial appointments in the University of Maiduguri (2011), Bingham University Karu (2013) and Benue state University, Makurdi (2013). He has supervised over 60 B Sc projects, 19 M.Sc

theses and five Ph.Ds,three of which are on-going. In addition to these very many responsibilities, Professor Kwon-Ndung at various times has been a Visiting Professor at the Department of Biological Science University of Agriculture Makurdi and the Department of Plant Science and Technology, University of Jos.

In promoting professionalism, Professor Kwon-Ndung has been part of the Organizing Committees of several Conferences and has served as Chairman for the LOC of Genetics Society of Nigeria, Nigerian Society of Microbiology, Zoological Society of Nigeria held at Nasarawa State University and Federal University Lafia. Between 1995 and 1997, he was the Vice-President of the Genetics Society of Nigeria. He is on the editorial Boards of many International and National journals some of which include: The International Journal of Agriculture Food Science & Technology (IJAFST), Global Journal of Applied Agricultural Research (GJAAR), Scientific Research and Essays, Cell and Animal Biology (Academic Publishers). He has been member, NCRI Publications and Editorial Committee (2000 to 2003, North Central Zonal Editor, Genetics Society of Nigeria Newsletter (2003-2004), Reviewer, Technology and Development (1998-Date), Reviewer, Nigerian Journal of Genetics (2001- Date), Reviewer, Nigerian Journal of Biotechnology (2003-Date), Reviewer, Nigerian Journal of Botany (2004-Date), Reviewer, The Dyke, (Academic Journal of Midlands State University, Zimbabwe), Managing Editor, Nasara Scientique (July 2006 - Date). He was recently inaugurated as the Editor of the TETFUND sponsored Journal for the Sciences for Federal University Lafia.

He is a member of the following Professional Societies: Genetics Society of Nigeria (GSN), Vice President (1995-1997), Biotechnology Society of Nigeria, Agricultural Society of Nigeria, Botanical Society of Nigeria, African Crop Science Congress, Foundation for African Development through International Biotechnology, WAPGRINET (West Africa Plant Genetic Resources Network, American Society of Plant Biologists and Global Facility Network for Underutilised Species.

He has also contributed immensely to the development of the University curricular by being in the NUC undergraduate accreditation teams and resource verification visits (and has served as Member and Chairman) in six different Universities. In the same vein, he has been a consultant and resource person to the World Bank, African Development Bank, NNPC, Jigawa State Government, Renewable Energy Division of the Federal Ministry of Environment, Federal Ministry of Agriculture, Fadama III, National programme on Food security, International Food Policy Research Institute,

Benue, Gombe and Plateau, states. Professor Kwon-Ndung has also been privileged to act as technical member to a number of ad-hoc committees in agricultural research and environmental programmes in the country. He has served as a reviewer for several EIA proposals on Ecology for the Federal Ministry of Environment. He was one of the few experts in biofuels engaged by the Federal Ministry of Environment to work on the Renewable Energy Strategy and Action Plan (RESAP) in 2010. The Hon. Minister of Science and Technology also engaged him as the Chairman of the Biotechnology Sub-Committee of the current National Science Technology and Innovation (STI) Policy in 2011.

Professor Kwon-Ndung is widely published and has authored over 70 academic publications in both national and international journals. In addition he has over 30 Conference Proceedings and 22 technical reports. He has attended over 40 Conferences between 1992 to date within and outside Nigeria, with some recognitions of best paper presentation in two of such conferences. Professor Kwon-Ndung is a beneficiary of several awards, both academic and social, including the U N based Youth Federation for Universal Peace Award as Ambassador for Peace. He is also a winner of the Third World Academy of Sciences postdoctoral fellowship and is a Fellow of the Academy of Science for the Developing World.

Professor Kwon-Ndung is a committed father, husband, brother and relation. He upholds dearly family values that are fast eroding in our society. He married Linda Kwon-Ndung (nee:Garba) on the 13th day of March 1999. Linda his wife is also in the academia, a Lecturer of Political Science at the Nasarawa State Univerity awaiting the Defense of her Ph.D thesis at the University of Abuja. Professor and Mrs. Kwon-Ndung are parents to four blessed children namely Jaram (Emmanuella), Jesse, Weng and Emmanuel Junior.

Professor Kwon-Ndung has traversed the length and breadth of Nigeria in his academic and research pursuits, as well as leisure. He has visited the 36 states at one time or the other, by road and by air. He has also visited many countries abroad for academic purposes. He speaks his mother tongue Aten very fluently in addition to the Hausa language.

Professor Kwon-Ndung loves reading and research and is up to date with scientific and political happenings around the world. He is very much up to date with ICT and would hardly need a secretary to type his work except a very competent one at that.

Professor Kwon-Ndung is a firm and principled personality and some people tend to see him as difficult especially his students. However, many have come back to thank him for showing them the path of honesty, integrity, sincerity and transparency. He is fearless and yet respects constituted authority. He is committed to any good course he undertakes whether it be academic,

political, social or religious. He is an active Rotarian and his penchant for Rotary has seen him as chartered member of three Rotary Clubs including the Rotary Club of Keffi. He is an Elder in the ECWA Goodnews Church Keffi.

Mr. Vice-Chancellor, Sir, Principal Officers of the University, Special Guests, Invited Guests, Staff and students, most respected ladies and gentlemen, May I humbly present to you a scientist, a researcher of pronounced character, an achiever, a community development advocate, a man who loves fair play and justice, a man who is continually writing his name in gold and stamping his footsteps in the sands of time for generations, to come forward to deliver the 7th Inaugural lecture of the Nasarawa State University. We present Professor Emmanuel Hala Kwon-Ndung.