FROM GENERATION TO GENERATION: PLANT GENETIC DIVERSITY, CONTINUITY AND DISCONTINUITY

By

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FUNAAB INAUGURAL LECTURE
Series No. 70

Wednesday, December 22, 2021

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The 70th Inaugural Lecture was delivered under the Chairmanship

of

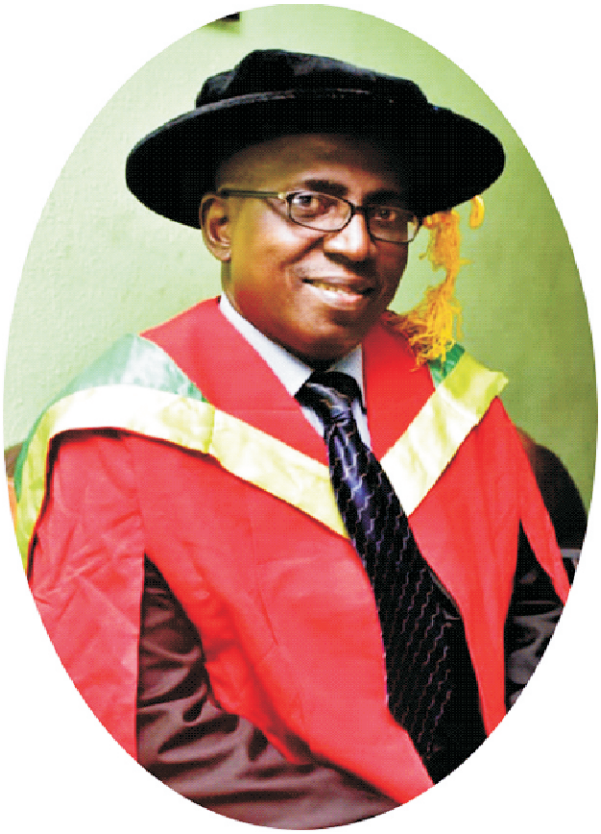
The Vice-Chancellor

Professor Felix Kolawole Salako
B. Agric (Soil Science), M.Sc (Soil Physics/Soil Conservation) (Nsukka), Ph. D. (Ibadan)

Published December, 2021

ISBN:978-978-992-967-8

FUNAAB INAUGURAL LECTURE SERIES



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1.0 Preamble

Many plans are in a man's mind, but it is the Lord's purpose for him that will stand. (Prov. 19:21 Amp).

It is with utmost sense of humility, honour and gladness of heart coupled with immense gratitude to the Lord Almighty that I stand before you today to present the 70th Inaugural Lecture of the Federal University of Agriculture, Abeokuta. This is the 2nd Inaugural Lecture from the Department of Plant Breeding and

Seed Technology and the 12th from the College of Plant Science and Crop Production (COLPLANT), one of the foundation Colleges of this University.

In this lecture entitled From Generation to Generation: Plant Genetic Diversity, Continuity and Discontinuity, I will endeavour to showcase some of my research efforts and contributions to knowledge in the field of Plant Breeding and Genetics as well as give suggestions on how to improve Nigerian agricultural sector as a nation.

2.0 Introduction

2.1 Historical Background

The earliest evidence of plant domestication found by man has been dated to 11,000 years ago. Initially, selection might have happened unintentionally but it is very likely that about 5,000 years ago farmers had a basic understanding of heredity and inheritance which are the foundations of genetics (Allard, 1999).

The field of plant genetics began with the work of Gregor Johann Mendel, who is often called the Father of Genetics (Plate 1). He was an Augustinian priest and scientist born on July 20, 1822 in Austria Hungary. His organism of choice for studying inheritance and traits was the pea plant (*Pisum sativum*). Mendel showed that the inheritance of these traits follows particular laws, which were later named after him. The laws include:

i. *Law of dominance:* When two alternative forms of a trait or character are present in an organism, only one factor (allele) expresses itself in F_1 progeny and is said to be dominant while the other allele that remains masked is called recessive.

ii. *Law of segregation*: The factors or alleles of a pair

segregate from each other such that a gamete receives only one of the two factors.

iii. *Law of independent assortment:* The two factors (alleles) of each contrasting character (trait) assort or separate independently of the factors of other characters at the meosis or time of gamete formation and get randomly rearranged in the offspring.

The "Mendelian Experiments on Plant Hybrids" was published in 1866 but went almost entirely unnoticed until the turn of the 20th century when his works were rediscovered and this prompted the foundation of modern genetics. His discoveries, deduction of segregation ratios and subsequent laws have not only been used in research to gain a better understanding of plant genetics, but also play a major role in plant breeding experiments.

Source:https://www.famousscientists.org/gregor-mendel

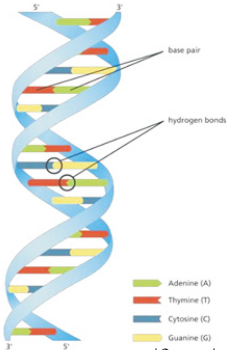
Plate 1: Gregor Johann Mendel (1822 – 1884)

In the early 1900s, genetic and plant breeding experiments in maize began and a phenomenon called inbreeding depression was discovered. Researchers like Nils Heribert Nilsson observed that by crossing plants and forming hybrids, they were not only able to combine traits from two desirable parents, but the crop also

experienced heterosis or hybrid vigour. This was the beginning of identifying gene interactions or epistasis.

While breeding experiments were taking place, other scientists often would travel to regions of high plant diversity and seek out wild species that had given rise to domesticated species after selection. Determining how crops changed from generation to generation was initially based on morphological features. It developed over time to chromosomal analysis, then genetic marker analysis and eventually genomic analysis. Identifying traits and their underlying genetics allowed for transferring useful genes and the traits they controlled from either wild or mutant plants to crop plants. In addition, the molecule of heredity, Deoxyribonucleic Acid (DNA), was also discovered, which allowed scientists to actually examine and manipulate genetic information directly.

DNA is a nucleic acid that contains the genetic instructions used in the development and functioning of all known living organisms and some viruses. The main role of DNA molecules is the long–term storage of information needed to construct other components of the cells such as proteins and RNA molecules. The DNA segments that carry this genetic information are called genes and their locations within the genome are referred to as genetic loci (Figure 1).



Source:https://www.yourgenome.org/facts/what-is-dna
Figure 1: DNA Structure

Plant geneticists use the sequence of DNA to the advantage to better find and understand the role of different genes within a given genome. Through research and plant breeding, manipulation of different plant genes and loci encoded by the DNA sequence of the plant chromosomes by various methods can be done to produce different or desired genotypes that result in different or desired phenotypes (Dudley, 1993)

2.2 Plant Genetics

Plant genetics is the study of genes, genetic variation and heredity, specifically in plants. Mendel studied trait inheritance‖, which means patterns in the way traits are handed down from parents to offsprings (i.e. from generation to generation). He observed that organisms (most famously pea plants, *Pisum sativum*) inherit traits by way of discrete units of inheritance. This term, still used today, is a somewhat ambiguous definition of what is referred to as a GENE. Plants, like all known organisms, use Deoxyribonucleic Acid (DNA) to pass on their traits.

Determining how crops changed over time with selection was initially based on morphological features. It developed over time to chromosomal analysis, thengenetic marker analysis and eventual genomic analysis. Identifying traits and their underlying genetics allowed for transferring useful genes and the traits that they controlled from either wild or mutant plants to cultivated crop plants.

Advance in plant genetics and genomics, when used in breeding, help support higher production and cultivation of crops resistant to pests, pathogens and drought. Indeed plant breeding the science of maximizing plants' positive genetic traits to produce desirable effects continues to open new frontiers in agricultural production.

Animal genetics often focuses on parentage and lineage, but this can sometimes be difficult in plant genetics because plants can, unlike most animals, be self– fertile. Speciation can be easier in many plants due to unique genetic abilities, such as being well adapted to polyploidy. In addition, plants can produce energy–dense carbohydrates via photosynthesis, a process which is achieved by the use of chloroplasts. Chloroplasts, like the superficially similar mitochondria, possess their own DNA. Hence, they provide an additional reservoir for genes and genetic diversity and an extra layer of genetic complexity not found in animals.

Self–fertilization in plants, which is a rare occurrence in animals, must be prevented by scientists who want to create hybrids between plant species for economic and aesthetic purposes. For example, the yield of maize has increased nearly five–fold in the past century, largely due in part to the discovery and proliferation of hybrid maize varieties. Plant genetics can be used to predict which combination of plants may produce a plant with hybrid vigour.

2.3 Genetically Modified Crops

Genetically Modified (GM) foods are produced from organisms that have had changes introduced into their DNA using the methods of genetic engineering. This technique allows for the introduction of new genetic material through the use of microorganisms into the genome of a plant. It involves the direct manipulation of one or more genes and the steps taken are:

1. The isolation of DNA fragments from a donor organism
2. The insertion of an isolated donor DNA fragment into a vector genome, and
3. The growth of a recombinant vector in an appropriate host.

Benefits of genetic engineering in agriculture include: increase

crop yields; reduce costs for food or drug production; reduce need for pesticides; enhance nutrient composition and food quality; resistance to pests and diseases; and greater food security. However, the potential harm to human health include: new allergens in food supply; antibiotic resistance; production of new toxins; enhancement of environment for toxic fungi; unexpected negative side effects and possibility of abuse. Consequently, there must be controls place to manage the negative effects if and when it occurs.

Genetically modifying plants is an important economic activity. In 2017, 89% of maize; 94% of soybeans and 91% of cotton produced in the USA were from genetically modified strains. Since the introduction of GM crops, yields have increased by 22% and profits to farmers have increased by 68% especially in the developing countries. An important side effect of GM crops has been decreased land requirements (Alliance for Science, 2018). Commercial scale of genetically modified foods began in 1994, when Calgene first marketed its unsuccessful Flavr Savr delayed–ripening tomato. Most food modifications have primarily focused on crops in high demand by farmers such as soybean, maize, and cotton. Genetically modified crops have been engineered for resistance to pathogens and herbicides as well as for better nutrient profiles. Other such crops include the economically important GM papaya which is resistant to the highly destructive papaya ringspot virus and the nutritionally improved golden rice (which is still being developed).

Of course, there is a scientific consensus that the currently available foods derived from GM crops pose no greater risk to human health than conventional foods but that each GM food needs to be tested on a case–by– case basis before introduction. However, members of the public are much less likely than scientists to perceive GM foods as safe. The legal and regulatory statuses of GM foods vary by country, with some nations banning

or restricting them, and others permitting them with widely differing degrees of regulation.

2.4 The Concept of Genetic Diversity

Diversity is the essence of the biological world. No two living things (even maternal twins) are exactly the same. As recognized by Convention on Biological Diversity, there are three levels of diversity (Figure 2). At the highest hierarchy lies the ecosystem diversity which represents variability among different communities of species. In the next level of hierarchy lies the species diversity representing different species within a community. The third level is the genetic diversity whichrefers to the diversity present within different genotypes of same species.

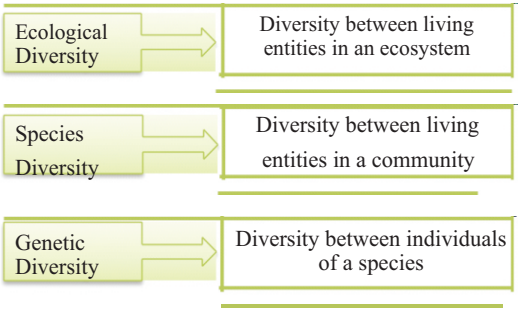


Figure 2: Hierarchy of Diversity

Genetic diversity is of fundamental importance in the continuity of a species as it provides the necessary adaptation to the prevailing biotic and abiotic environmental conditions and enables change in the genetic composition to cope with environmental changes. It is the foundation for survival of plants innature and also for crop improvement. Swingland (2001) defined genetic diversity as the variation of heritable characteristics present in a population of the same species. It can be described as the degree of differentiation within species. It includes genomic diversity which is the diversity at several gene–loci within the genome of an individual. The

variation in heritable characters may express itself in the form of altered morphology, anatomy, physiological behaviour or biochemical features.

Diversity in plant genetic resources provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, especially yield and quality aspects of major food crops to provide balanced diet to the ever–increasing human population. For the rapidly–changing breeding goals, different genes need to be preserved in cultivated and wild crop species in the form of germplasm resources. These can then be used by plant breeders to select superior genotypes either to be used directly as new variety or as parents in hybridization programmes. Genetic diversity between two parents is essential to realize heterosis and to obtain transgressive segregants. Diversity also helps with respect to adaptability of crop plants to varied environments with reference to changing climatic conditions.

Genetic diversity is primarily a function of sexual recombination. During meiosis, homologous chromosomes undergo crossing over which results in appearance of several new recombinations. Other forces like selection, mutation, linkage, migration and genetic drift act continuously and result in continuous changes in allelic frequency in a population and affect genetic diversity. Domestication or artificial selection favours few alleles at the cost of others resulting in increased frequency of selected alleles. Qualitative mutation expresses itself in the form of abrupt changes in morphological, anatomical, or biochemical features. On the other hand, quantitative or micro–mutations have smaller and gradual effects which accumulate over time and bring about changes. Mutation may also bring about several chromosomal aberrations in the form of alteredphenotype which may be lethal or non–lethal. Mating systems of crop plants affect genetic diversity. Inbreeding reduces while out–breeding increases genetic diversity.

2.5 Measurement and Analysis of Genetic Diversity

Diversity analysis can be carried out using morphological, cytological, biochemical and molecular characterization. A genetic marker is a gene or DNA sequence with a known location on a chromosome that can be used to identify individuals or species.

Analysis by morphological markers involves morphological characterization of different entries grown in the field. Morphological characteristics are the strongest determinants of the agronomic value and taxonomic classification of plants. This form of evaluation is inexpensive in terms of cost and technology but it suffers from the constraints of environmental– sensitivity and subjective characterization when compared to other methods.

Cytological analysis involves the study of chromosome number, chromosome size, secondary constriction in chromosomes, position of centromere, arm ratio, banding characteristics, DNA content, chromosome volume, etc. However, low resolution limits its application.

In using biochemical markers, proteins or their variants (isozymes) are separated into specific banding patterns. The isozymes reflect products of different alleles and can be mapped onto chromosomes and used as genetic markers for mapping other genes. They are affected by environmental fluctuations and cannot be used to construct a reliable genetic map.

Molecular markers involve the study of variation among genotypes at DNA/RNA level, and are classified as hybridization–based and PCR–based. Use of molecular markers is the method of choice for genetic diversity assessment because of their hyper variability, better genomic coverage, high

reproducibility, amenability to automation, being neutral and free from environmental fluctuations. They include; Random Amplified Polymorphic DNA(RAPD); Amplified Fragment Length Polymorphism(AFLP); Simple Sequence Repeat(SSR); Inter Simple Sequence Repeat(ISSR) and Sequence Related Amplified Polymorphism(SRAP).

Many studies on genetic diversity have been reported to use both morphological and molecular markers simultaneously.

Multivariate statistical techniques are used to assess genetic diversity among different strains/varieties/entries of a species. They provide reliable information regarding the real genetic distances between genotypes and can be used in the assessment of genetic divergence, classification of germplasm into groups and in the selection of diverse parents to develop transgressive segregants.

Some of the techniques are:

1. Metroglyph analysis
2. D2 statistics
3. Cluster analysis
4. Principal component analysis (PCA)
5. Canonical analysis
6. Factor analysis

3.0 My Research Thrust and Contributions to Knowledge

Mr. Vice-Chancellor sir, I started my research works in 1987as a student under the erudite scholar, Prof. Iyiola Fawole, at the then Department of Agricultural Biology, (now Department of Crop Protection and Environmental Biology), University of Ibadan. Upon completion of my Ph.D. degree in 1994, I got appointment into the University of Agriculture, Abeokuta (UNAAB).

In the past 30 years of my research activities, I have worked on Cowpea, Melon, Okra, African yam Bean, Tea, at varying degrees of involvement. My studies have been focused mainly on: inheritance studies and genetic analysis of qualitative and quantitative traits; assessing Genetic Diversity in crop species using morphological and molecular characterization; inter–character associations.

3.1 Inheritance Studies and Genetic Analysis of Qualitative and Quantitative Traits Cowpea, *Vigna unguiculata* (L.) Walp, is a widely cultivated crop in the tropical and sub–tropical regions of
the world. The inheritance of 3 traits — inverted V– shaped mark on leaves, pod dehiscence and dry pod colour — was studied in crosses between wild, weedy and cultivated varieties of cowpea. Both the wild and weedy parents belong to the subspecies *dekindtiana.* In this study, successful hybridizations were obtained on wild cowpea as female parents in contrast to previously reported failed attempts. Data collected on the parents, F_1, F_2 and backcross progenies indicated that each of the 3 traits is controlled by a single dominant gene (Tables 1– 3). The wild and weedy lines carry the dominant genes while the recessive alleles reside in the cultivated varieties. The symbols V_{sm}, D_{hp} and Bk–2 were assigned to the dominant genes that govern the traits (Aliboh *et al.*, 1996).

A study was initiated to investigate the linkage relations of 12 loci conditioning morphological characteristics in cowpea (Kehinde *et al.*, 1997), to facilitate selection procedures and also to initiate the construction of a genetic map for cowpea.

Table 1: Inheritance of V–shaped mark on leaves in crosses between wild and cultivated cowpea

Cross and Generation	№ of Plants with V–shaped Mark		Total Plants	Proposed Ratio	X^2	P
	Present	Absent				
'Ife BPC' x Wc Ibadan-10						
_Ife BPC'	-	16	16			
WC Ibadan-10	16	-	16			
F_1	16	-	16			
_Ife BPC' x F_1	10	14	24	1:1	0.666	0.25 – 0.50
Wc Ibadan-10 x F_1	24	-	24			
F_2	112	32	144	3:1	0.593	0.25 – 0.50
TVu 1 x Wc Ibadan-1						
TVu 1	-	16	16			
Wc Ibadan-1	16	-	16			
F_1	16	-	16			
TVu 1 x F_1	10	14	24	1:1	0.666	0.25 – 0.50
Wc Ibadan-1 x F_1	24	-	24			
F_2	100	44	144	3:1	2.370	0.05 – 0.10
'Ife BPC' x Wc Ibadan-8						
_Ife BPC'	-	16				
Wc Ibadan-8	16	-	16			
F_1	16	-	16			
_Ife BPC' x F_1	10	14	24	1:1	0.666	0.25 – 0.50
Wc Ibadan-8 x F1	24	-	24			
F_2	112	32	144	3:1	0.592	0.25 – 0.50
'Ife Brown' x Wc Ibadan-1						
_Ife Brown'	-	36	36			
Wc Ibadan-1	27	-	27			
F_1	29	-	29			
_Ife Brown' x F_1	66	54	120	1:1	1.091	0.25 – 0.50
Wc Ibadan-1 x F_1	36	-	36			
F_2	269	75	344	3:1	1.876	0.10 – 0.25

Source: Aliboh *et al.* (1996)

Table 2: Inheritance of pod dehiscence in crosses between wild and cultivated cowpea

Cross and Generation	№ of Plants		Total Plants	Proposed ratio	X^2	P
	Dehiscent	Non–dehiscent				
'Ife BPC' x Wc Ibadan-10						
_Ife BPC'	-	16	16			
WC Ibadan-10	16	-	16			
F_1	16	-	16			
_Ife BPC' x F_1	11	12	23	1:1	0.830	0.25 – 0.50
Wc Ibadan-10 x F_1	24	-	24			
F_2	104	40	144	3:1	0.593	0.25 – 0.50
'Ife Brown' x Wc Ibadan-1						
_Ife Brown'	-	36	36			
Wc Ibadan-1	27	-	27			
F_1	29	-	29			
_Ife Brown' x F_1	57	63	120	1:1	0.300	0.50 – 0.75
Wc Ibadan-1 x F_1	36	-	36			
F_2	252	92	344	3:1	0.558	0.25 – 0.50

Source: Aliboh *et al.* (1996)

Table 3: Inheritance of dry pod colour in crosses between wild and cultivated cowpea

Cross and Generation	№ of Plants		Total Plants	Proposed ratio	X^2	P
	Black colour	Straw Colour				
'Ife BPC' x Wc Ibadan-10						
_Ife BPC‘	-	16	16			
WC Ibadan-10	16	-	16			
F_1	16	-	16			
_Ife BPC‘ x F_1	13	10	23	1:1	0.416	0.50 – 0.75
Wc Ibadan-10 x F_1	24	-	24			
F_2	115	29	144	3:1	1.815	0.10 – 0.25
'Ife Brown' x Wc Ibadan-1						
_Ife Brown‘	-	36	36			
Wc Ibadan-1	27	-	27			
F_1	29	-	29			
_Ife Brown‘ x F_1	55	65	120	1:1	0.833	0.25 – 0.50
Wc Ibadan-1 x F_1	36	-	36			
F_2	248	96	344	3:1	1.550	0.10 – 0.25

Source: Aliboh *et al.* (1996)

Using backcross and F_2 joint segregation data, these 12 loci were assigned to five linkage groups out of the eleven linkage groups possible in cowpea (Figure 3). Of the 45 F_2 and backcross linkage tests between gene pairs in this study, 22 suggested independence while 23 indicated linkage (Table 4).

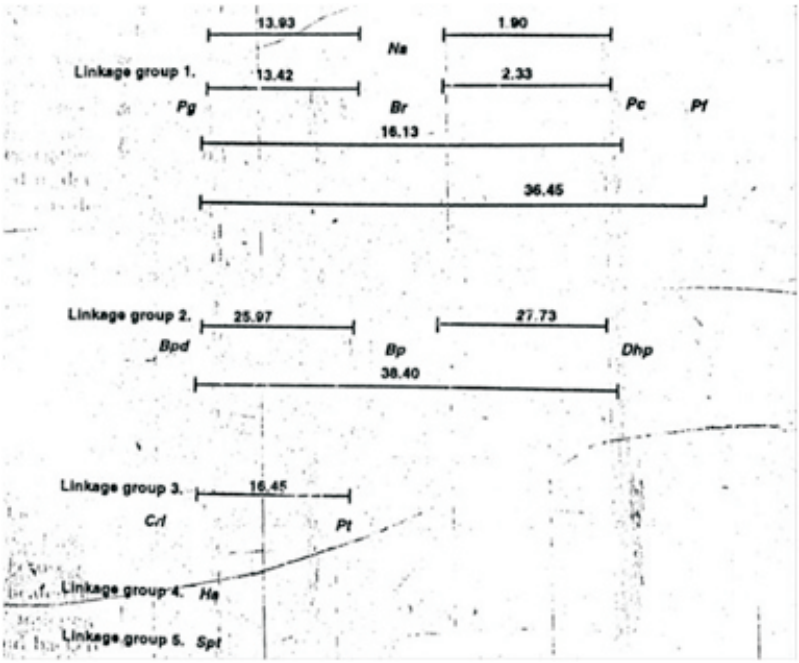


Figure 3: Cowpea gene order and map distances from F2 population

Table 4: Allelic constitution, F2 and backcross progeny distribution, calculated recombination values and map distances of linked traits in cowpea

Alleles	Generation	Number of Plants					X^2 linkage*	Recombination % and SE	Map Distance MU and SE	Linkage Phase
		A	b	c	d	Total				
Pg pg Bpd bpd	F_2	558	1153	200	39	950	3.00	45.23 ± 2.56	74.58 ± 2.56	C
	BC	99	97	96	87	379	0.14	49.08 ± 2.57	116.98 ± 2.57	C
Pg pg Pf pf	F_2	601	203	0	68	872	163.55*	31.12 ± 3.02	36.45 ± 3.02	C
	BC	171	0	0	149	320	320.00*		≥	C
Bpd bpd Pf pf	F_2	518	182	136	36	872	1.89	46.08 ± 2.64	79.98 ± 2.65	C
	BC	87	76	86	71	320	0.06	49.38 ± 2.79	126.92 ± 2.80	C
Bpd bpd Bp bp	F_2	650	126	79	120	975	163.02*	25.07 ± 2.96	27.56 ± 2.97	C
	BC	95	24	16	120	255	119.62*	15.69 ± 2.27	16.24 ± 2.28	C
Bpd bpd Dhp dhp	F_2	583	197	85	110	975	70.18*	34.38 ± 2.78	42.17 ± 2.79	C
	BC	99	46	14	96	255	78.21*	23.53 ± 2.65	25.54 ± 2.66	C
Bpd bpd Pc pc	F_2	612	151	133	63	259	13.73*	40.61 ± 2.66	56.67 ± 2.66	C
	BC	79	40	50	86	255	22.28*	35.29 ± 2.99	43.94 ± 3.00	C
Bp bp Dhp dhp	F_2	618	112	86	159	975	224.46*	22.26 ± 3.01	23.93 ± 3.02	C
	BC	72	64	28	91	255	23.03*	36.08 ± 3.00	45.55 ± 3.01	C
Bp bp Pc pc	F_2	572	149	145	93	959	32.14*	37.77 ± 2.73	49.27 ± 2.73	C
	BC	78	33	51	93	255	30.46*	32.94 ± 2.94	39.53 ± 2.95	C
Dhp dhp Pc pc	F_2	561	149	151	98	959	30.45*	35.71 ± 2.56	37.13 ± 2.56	C
Ha ha Pt pt	F_2	348	144	147	39	678	4.72*	43.94 ± 3.07	68.52 ± 3.07	C
Ha ha Bpd bpd	F_2	341	143	135	49	668	0.55	48.31 ± 2.95	101.58 ± 2.9	C
	BC	75	81	72	82	310	0.05	49.35 ± 2.84	125.74 ± 2.84	C
Pt pt Bpd bpd	F_2	352	130	121	66	669	4.50*	44.22 ± 3.08	69.78 ± 3.08	C
Pg pg Pt pt	F_2	148	578	76	172	974	10.99*	42.51 ± 2.59	62.84 ± 2.60	C
Pg pg Crl crl	F_2	518	204	194	58	974	2.61	46.19 ± 2.50	80.72 ± 2.51	C
Pg pg Spt spt	F_2	548	176	186	64	974	0.17	49.04 ± 2.43	115.91 ± 2.43	C
Pg pg Br br	F_2	491	230	4	238	963	90.12*	13.11 ± 3.15	13.42 ± 3.16	C

Pg pg Pc pc	F_2	511	220	227	5	963	76.78*	15.59 ± 3.13	16.13 ±3.13	C
Pg pg Na na	F_2	502	226	231	4	963	84.13*	13.58 ± 3.15	13.93 ± 3.15	C
Pt pt Crl crl	F_2	497	255	216	6	974	85.0*	15.88 ± 3.10	16.45 ± 3.11	C
Pt pt Br br	F_2	553	197	175	38	963	6.38*	43.15 ± 2.59	65.25 ± 2.60	C
Pt pt Pc pc	F_2	556	193	174	40	963	4.54*	44.32 ± 2.56	70.24 ± 2.57	C
	BC	30	32	31	31	124	0.03*	49.19 ± 4.49	120.19 ± 4.50	C
Pt pt Na na	F_2	557	188	179	39	963	5.05*	44.02 ± 2.57	68.88 ± 2.57	C
	BC	31	31	37	25	124	1.17	45.16 ± 4.47	74.47 ± 4.48	C
Crl crl Spt spt	F_2	549	162	185	78	974	4.88*	45.07 ± 2.53	73.98 ± 2.53	C
Spt spt Na Na	F_2	547	182	164	70	963	2.24	46.55 ± 2.51	83.29 ± 2.51	R
Crl crl Na Na	F_2	551	166	188	58	963	0.02	49.71 ± 2.42	146.00 ± 2.45	R
Crl crl Br br	F_2	534	171	194	64	963	0.03	49.62 ± 2.43	139.22 ± 2.43	R
Spt spt Br br	F_2	544	183	180	56	963	0.20	48.90 ± 2.44	112.47 ± 2.44	R
Spt spt Pc pc	F_2	551	174	180	58	963	0.20	48.22 ± 2.43	110.78 ± 2.44	R
Br br Pc pc	F_2	716	9	13	225	963	847.87*	2.33 ± 3.22	2.33 ± 3.22	C
	BC	56	0	0	68	124	124.00*			C
Br br Na na	F_2	773	0	0	230	963	965.00*			C
	BC	56	0	0	68	124	124.00*			C
Pc pc Na na	F_2	719	12	6	226	963	868.15*	1.90 ± 3.82	1.90 ± 0.23	C
	BC	56	0	0	68	124	124.00*			C

*P≤ 0.05

a _ dominant at both loci A-B-

b _ dominant at the first locus, recessive at the second locus A-bb

c _ recessive at the first locus, dominant at the second locus aaB-

d _ recessive at both loci aabb.

Source: Kehinde *et al.* (1997)

Prior to the initiation of this study, we did not come across any published work that gave a precise linkage map of cowpea which could serve as a basis for further study.

The inheritance of seed coat texture in cowpea was investigated by studying the crosses involving seven accessions. This trait is of vital importance in cowpea improvement in the areas of cookability and consumer acceptability. It can also be used as a marker. In two of the four crosses, the seed coat texture was found to be under monogenic inheritance. In the other two crosses, the trait was found to be controlled by two genes with complementary effect, giving a segregation ratio of 9 smooth : 7 rough for F_2 and 1 smooth : 3 rough for backcross generation (Kehinde and Ayo–Vaughan, 1999).

In a study to determine the extent of inter–specific crossability between *Abelmoschus esculentus* and *Abelmoschus caillei*, hybridizations were randomly carried out between four varieties of *A. caillei* and two varieties of *A. esculentus.* Results indicated that successful intraspecific hybridization between *A. caillei* is high (87%) while interspecific crosses, though possible, had low success rate (29%). However, seeds obtained from intraspecific and interspecific hybridization had high seed germination percentages (98% and 92%), respectively (Kehinde, 2001).

The segregation patterns of genes governing the expression of pigmentation on vegetative parts; flower; fresh pod; and dry pod, were studied in cowpea (Kehinde, 2001). For flower colour, dry pod colour and pigmentation on vegetative parts, monogenic gene action was involved while for fresh pod colour, complementary gene action was observed.

In year 2000 and 2001, we made crosses between two accessions of *Abelmoschus caillei* with high genetic variability to generate F_1, F_2 and backcross generations to study inheritance of pod and seed

yield characters (Adeniji and Kehinde, 2003). Generation Mean Analysis revealed that additive gene effects were positive and they significantly accounted for pod and seed yield characters. Dominance × Dominance gene effects were significantly positive for seeds per pod, ridges per pod and mature pod length, indicating the presence of epistatic gene action (Tables 5 and 6). The high narrow sense heritability estimates recorded for 100 seed weight, seeds/pod and ridges/pod suggested that early generation selection would be effective for pod and seed yield improvement.

Similarly, eight parental accessions of *Abelmoschus caillei* were hybridized and the resulting F_1, F_2 and backcross generations, including the parental lines were evaluated at the lowland ecology of FUNAAB. The objective was to study the mode of inheritance and genetic control of pigmentation on stem, pods, petioles, peduncle, leaf vein and calyx, pubescence on pods, peduncles and stem, as well as pod orientation. The eight accessions varied for these characters. The results indicated a monogenic pattern of inheritance for pigmentation on the vegetative parts while a duplicate recessive gene action (9:7), conditions inheritance of pubescence on the stem, peduncle and pods.

Table 5: Gene effects using sic parameter models on mean of parents, F_1, F_2 and backcrosses in West African Okra

	Seed/pod	100-seed weight	Pods/plant	Ridges/pod	Seed weight	Seeds/ridge	Mature pod Length
M	77.53±0.42	498±0.22	10.03±0.19	7.75±0.13	152.27±0.48	9.72±0.10	11.18±0.18
a	39.16±0.14	0.03±0.06	3.21±0.12	70.26±0.10	1.93±0.07	0.80±0.06	1.02±0.22
d	-17.83±1.67	-1.58±0.61	40.58±0.98	-1.40±0.39	-109.79±2.03	0.40±0.45	-6.66±0.20
aa	-15.12±2.03	-1.34±0.03	10.39±0.25	-0.92±0.59	-92.94±2.21	1.24±0.48	-5.28±0.74
ad	24.75±0.80	-0.20±0.01	51.69±0.35	-0.75±0.24	261.1±0.58	0.04±0.01	-0.80±0.27
dd	21.55±3.79	1.50±1.30	-45.78±1.20	2.14±0.91	-139.56±2.48	-5.11±0.85	7.15±0.44

M _ Population mean; a _ additive gene; d _ dominance gene; aa _ additive x additive gene; dd _ dominance x dominance gene; ad _ additive x dominance gene; Source: Adeniji andKehinde (2003)

Table 6: Components of genetic variation for seven characters computed for six generations in West African Okra

Character	E	D	H	$\sqrt{H_1/D}$	H_b	H_n
Ridges/pod	0.38	1.54±1.09	0.84±1.09	0.74	89	57
Seeds/ridge	0.84	1.66±0.88	-0.28±0.96	n.a	58	51
Weight of 100 seeds	0.15	0.88±0.67	0.05±0.56	0.21	84	73
Pod length	0.68	2.02±1.20	1.68±1.24	0.51	97	48
Seed weight	18.76	45.74±6.89	15.86±0.75	0.41	54	49
Seeds/pod	3.39	28.94±4.06	9.38±4.34	0.57	91	69
Pods/plant	2.78	1.82±4.04	7.76±2.23	2.06	64	16

n.a _ not available; H_b _ broad-sense heritability; H_n _ narrow-sense heritability
Source: Adeniji and Kehinde (2003)

The inheritance of pod orientation conforms to duplicate gene action (15:1).

The introduction of pure lines and hybrids of okra with improved length and width of edible pods into the cropping system, necessitated studies on the combining ability and genetic components of different accessions.

Seven parents and their 21 F_1 hybrids were evaluated. Results indicated that the mean squares due to General Combining Ability (GCA) and Specific Combining Ability (SCA) for length and width of pods were significant (Figures 4 and 5). The estimated variance due to SCA was greater than GCA variance for length and width of pods at edible stage. Four of the parents used were identified as best combiners. Both oligogenic and polygenic actions were observed in the study. Conclusively, there was an empirical superiority of the possibilities of evolving pure lines and hybrid okra with improved length and width into the cropping system.

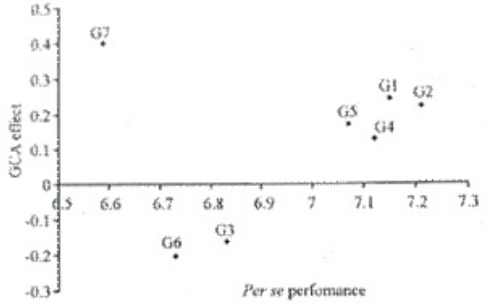


Figure 4: Relationship between GCA effect and per se performance for mature pod length of okra

Source: Adeniji and Kehinde (2003)

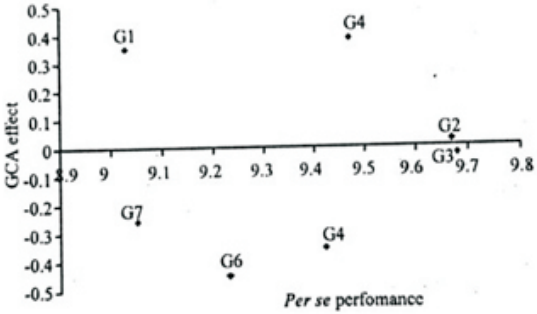
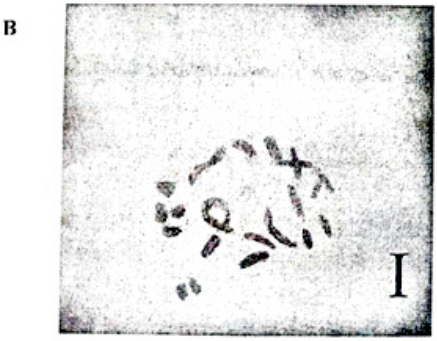


Figure 5: Relationship between GCA effect and per se performance for mature pod width of okra

Source: Adeniji and Kehinde (2003)

Accession L6 (2n = 44) Polyploid

A. Metaphase in Accession L6 with 2n _ 44 chromosomes



Accession DL99/71 (2n _ 22) Diploid

Plate 2: Metaphase chromosomes of *C. lanatus*
B. Late prophase in Accession L6 with 2n _ 44 chromosomes
Scale line represents 1.0 μm

3.2 Assessing Genetic Diversity in Crop Species

A study was conducted to determine the diversity present in 18 West African okra (*Abelmoschus caillei*) accessions using 10 morphological characters. Metroglyph analysis classified the accessions into seven groups (Figure 6). The overlapping and

discrete nature of the range of index score among the seven groups suggested that some genotypes shared similar morphological variation (Table 7).

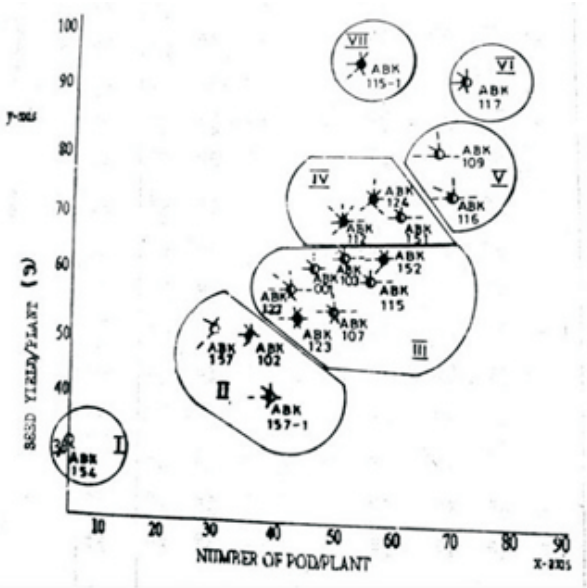


Figure 6: Scatter diagram in metroglyph analysis

Table 7: Frequency distribution of index score and the average index score of the 7 groups of okra genotypes studied

Group	Genotype (s)	Distribution of Index Score	Average Index Score
I	ABK 154	11	11
II	ABK 157, ABK 102, ABK 157-1	13–15	13.7
III	ABK 001, ABK 103, ABK 152, ABK 115, ABK 107, ABK 123, ABK 128	14–22	17.43
IV	ABK 124, ABK 151, ABK 112	15–21	19.0
V	ABK 116, ABK 109	16–17	16.5
VI	ABK 117	14	14
VII	ABK 115-1	15	15

Source: Ogunseye *et al.* (1999)

In another study, we sought to identify the major characters responsible for the variation in 20 accessions of melon egusi using Principal Component Analysis (PCA) and Single Linkage Cluster Analysis (SLCA) to classify their variation pattern (Idehen *et al.*, 2007). The first three principal components accounted for 76.33% and 78.70% of the total variation in the early and late seasons respectively (Table 8). SLCA summarized the relationships among the accessions at various levels of similarity into a dendrogram while the accessions were sorted into six distinct groups (Figure 7). The study identified accession L4 as early maturing and high yielding, thus becoming an obvious parent for hybridization whenever breeding for early maturity is the objective. Similarly, the phylogenetic diversity and relationships among fifty melon egusi accessions were measured using 25 Simple Sequence Repeat (SSR) markers (Idehen *et al.*, 2012).

Table 8: Eigen values and percentage of total variation accounted by the first four principal component axes of the ordination of _egusi' melon accessions in both seasons

Principal axis	Season	Eigen value	Total variation accounted for (%)	Cumulative Percentage
I	ES	4.83	34.56	34.56
	LS	5.25	37.48	37.48
II	ES	4.23	30.28	64.84
	LS	3.31	23.66	61.14
III	ES	1.60	11.50	76.33
	LS	2.46	17.56	78.70
IV	ES	0.97	6.91	83.24
	LS	1.10	0.09	86.56

ES – Early Season

ES – Late Season

Source: Idehen *et al.* (2007)

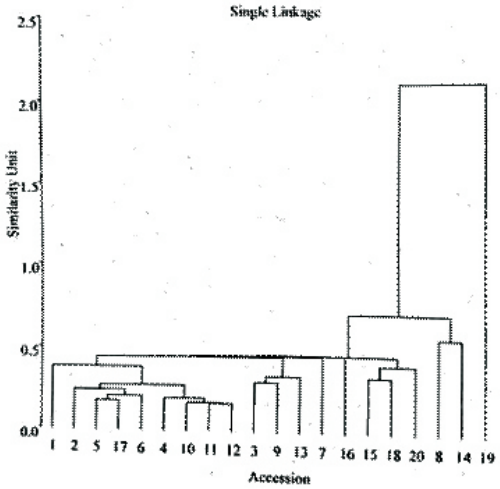


Figure 7: Dendrogram resulting from Single Linkage Cluster Analysis (SLCA) of twenty accessions of _egusi' melon

A total of 49 bands were scored, of which 42 of them were polymorphic, accounting for 93.60% of the polymorphic loci. The Polymorphic Information Content (PIC) value ranged from 0.36 to 0.80 (Table 9). UPGMA cluster analysis revealed five distinct groups (Table 10). This study identified promising genotypes for early flowering and high yield in melon breeding programmes, while revealing extensive range of genetic diversity represented in the melon accessions.

Principal Component Analysis (PCA) was carried out on pooled Sequence Related Amplified Polymorphism (SRAP) and Simple Sequence Repeat (SSR) markers and three–dimension plot is shown in Figure 8. We observed a high level of allelic diversity and polymorphism of SRAP and SSR markers which were due to the extensive range of genetic diversity present in the — melon egusi accessions. However, SSR markers revealed higher levels of genetic polymorphism than did the SRAP markers.

Table 9: Number of alleles, polymorphism and polymorphism information content (PIC) of 25 simple sequence repeat (SSR) primers

Primer name	Total number of bands	Polymorphic bands	Polymorphism (%)	№ of alleles	PIC
SSR-00119	1	1	100	2	0.80
SSR-00163	2	2	100	3	0.45
SSR-00251	1	1	100	1	0.75
SSR-00358	1	1	100	2	0.62
SSR-02585	1	1	100	1	0.64
SSR-02764	3	3	100	3	0.54
SSR-03484	2	2	100	3	0.58
SSR-04083	2	2	100	3	0.62
SSR-04584	1	1	100	2	0.60
SSR-04831	4	4	100	2	0.54
SSR-05195	2	2	100	2	0.82
SSR-05753	1	1	100	1	0.78
SSR-07523	5	5	100	3	0.40
SSR-10464	1	1	100	1	0.60
SSR-11080	4	4	100	4	0.58
SSR-11343	1	1	100	1	0.72
SSR-12414	1	1	100	2	0.56
SSR-12767	3	1	33	3	0.68
SSR-15877	1	1	100	2	0.54
SSR-16500	1	1	100	1	0.36
SSR-16749	1	1	100	1	0.72
SSR-21760	2	1	50	2	0.70
SSR-22498	1	1	100	1	0.68
SSR-28284	5	2	40	5	0.54
SSR-28958	2	1	50	2	0.62
Mean	1.96	1.68	93.60		0.61
Total	49	42	-		-

PIC _ Polymorphism information content
Source: Idehen *et al.* (2012)

Table 10: Distinguishing morphological features of each group of accessions

	Growth Habit	Leaf shape	Flower colour	Seed shape	Seed coat Colour	Days to flowering	Fruit weight (g)	Fruit size (cm)	Seed yield (kg/ha)
Group I	Climbing	Ovate	W	FO	DB/C	34.25b	596b	34.50a	1018.83b
Group II	Climbing	Ovate	W	FO	DB	36.20a	671a	33.80a	1426.66a
Group III	Trailing	Serrated	Y	FE	DB	32.00c	274d	34.50a	607.33c
Group IV	Trailing	Serrated	Y	FE	DB	33.56bc	545c	33.89a	1083.11b
Group V	Trailing	Serrated	Y/W	FE	DB/LB	32.67b	571b	33.97a	1182.02b
Mean						33.73	52.80	33.90	1066.73
SE (±)						0.43	36.20	0.25	73.96

SE: standard error; W: white; Y: yellow; FO: Flattened ovoid; FE:Flattened elliptic; DB: dark brown; C: cream; LB:: light brown

Source: Idehen *et al.* (2012)

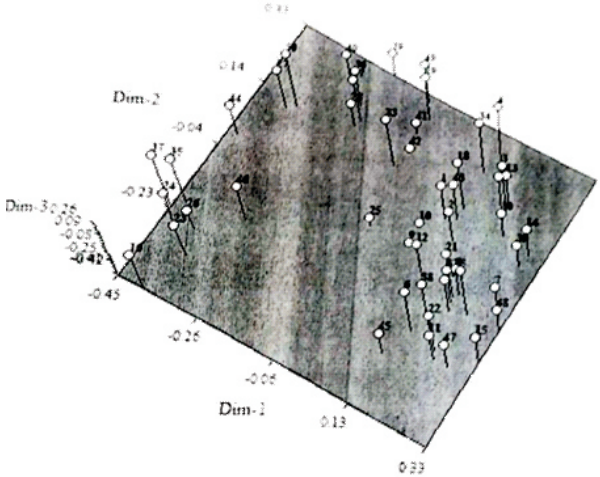


Figure 8: Three–dimension (3D) plot of 50 ‗egusi' melon accessions based on pooled Sequence Related Amplified Polymorphism (SRAP) and Simple Sequence Repeat (SSR) markers

The germination and regeneration of the different ―egusi‖ melon seed types carried out on Murashige and Skooge (MS) medium supplemented with antibiotics showed that one of the accessions (A22) had a high survival rate which will make it a useful material for regeneration and for subsequent transformation (Plate 3).

Plate 3: Cotyledon explants 12 days after planting in MS medium supplemented with growth hormone

Morphological classification of genetic diversity in 29 accessions of cultivated okra (*Abelmoschus esculentus* (L.) Moench.) was carried out using PCA and SLCA (Nwagburuka *et al.*, 2011). The first four principal axes accounted for over 60% of the total variation among the 18 characters describing the accessions. While PCA classified the accessions into six clusters, SLCA grouped them into five clusters. In order to further ascertain the level of diversity present within the 29 accessions, which were collected from different agro– ecological zones of Nigeria, genomic DNA from young apical were extracted and analyzed by the Random Amplified Polymorphic DNA (RAPD) technique (Nwagburuka *et al.*, 2011). Eighty four (84) amplified products and 53 RAPD bands were scored with an average of 61.4% of them revealing polymorphism across accessions.

The dendrogram revealed five distinct clusters. The result of the RAPD analysis revealed that the use of 24ng concentration of DNA produced better results in terms of DNA reproducibility. This observation will reduce the limitations of DNA reproducibility in PCR due to small DNA concentration. It could also help in minimizing the cost of running this analysis since DNA concentration as low as 24ng will produce reasonable results. Diversity studies using molecular markers establish much more distinct relationships between accessions than morphological methods which are based mainly on phenotypic expressions that are subject to environmental influences.

The African yam bean (*Sphenostylis stenocarpa* Hochst. Ex. A. Rich) is a tuberous legume crop indigenous to tropical Africa. Its prominence and genetic resources have been declining, thereby necessitating urgent research efforts to prevent imminent extinction. Genetic divergence in 80 genotypes, mostly indigenous to Nigeria was examined by Principal Component Analysis (PCA) and hierarchical cluster analysis involving 62 qualitative and quantitative characters (Adewale *et al.*, 2018). The

total genetic variation observed among genotypes was explained by 61 axes of the PCA, with the first three axes accounting for 40.37% of total variation (Table 11).

The hierarchical cluster analysis classified all the genotypes into groups on the basis of average distance between clusters at 1.00 point of inflection. It was observed that tuber, pod, seed and pigmentation characteristics were important components of the wide genetic variability between AYB genotypes.

Table 11: Variation distribution into the Principal component axes

PC Axes	Eigen value	Proportion (%)	Cumulative (%)
1	13.3109420	21.47	21.47
2	7.0944429	11.44	32.91
3	4.6255553	07.46	40.37
4	3.8935068	06.28	46.65
5	3.2930736	05.31	51.96
6	2.4417454	03.94	55.90
7	2.2137639	03.57	59.47
8	2.1108651	03.40	62.88
9	1.9164305	03.09	65.97
10	1.7138740	02.76	68.73
11	1.6365908	02.64	71.37
12	1.4841373	02.36	73.77
13	1.3738688	02.22	75.98
14	1.1616688	01.87	77.86
15	1.1408514	01.84	79.70

In a bid to ensure the cultivation of tea (*Camellia sinensis* (L.). O. Kuntze) beyond the upland ecologies ofNigeria, GGE biplot methodology was used to analyze yield data of 34 genotypes in three environments to identify high yielding, stable and adapted genotypes (Figure 9) (Olaniyi *et al.*, 2019). The three environments were: Ibadan (rain forest); Mambilla (mountain forest); and Mayoselbe (woodland forest) over a period of 2 years. Genotypes C143, NGC 18, C357 and C318 were the best high yielding and most stable across all the tested environments, suggesting that they are suitable for these environments (Figure 10). NGC 40, NGC 19, and NGC 15 adapted well to Ibadan environment while NGC 46 and NGC 8 adapted to the Mambilla environment. However, it was concluded that Mambilla environment represented the best (ideal) environment for tea cultivation in Nigeria, while Ibadan was the most discriminating environment and Mayoselbe was the most representative environment.

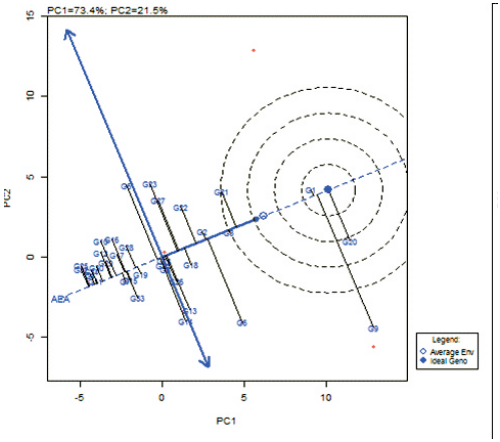


Figure 9: GGE Biplot of mean performance and stability of 34 tea genotypes across the test environments

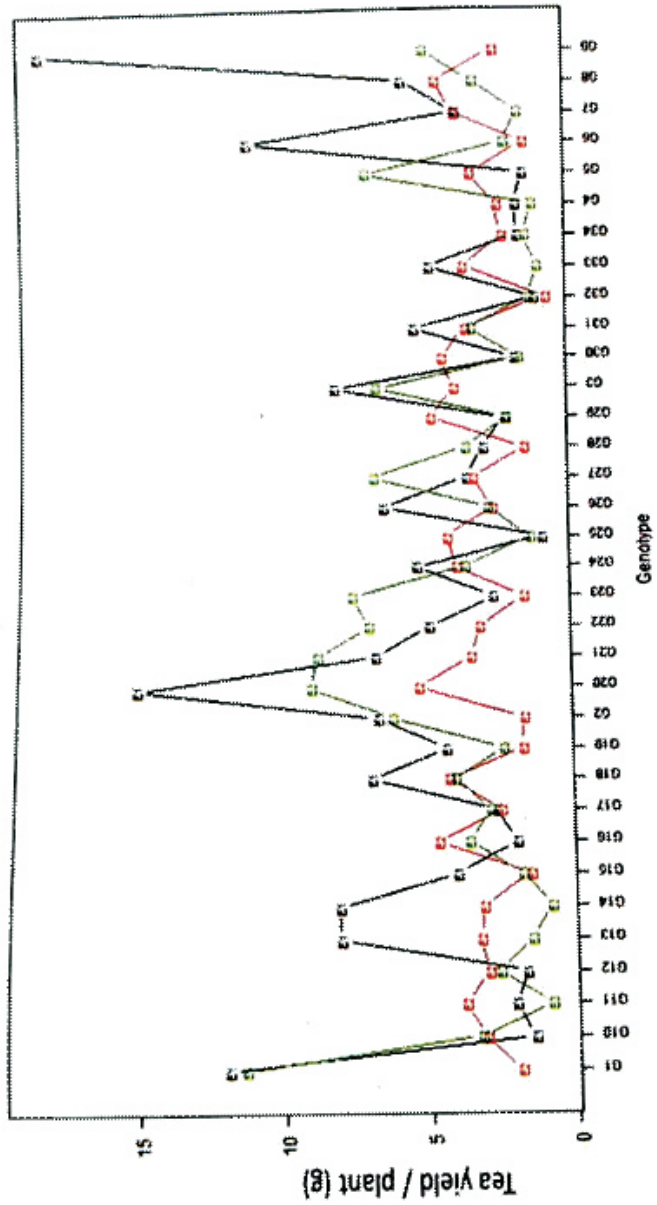


Figure 10: Yield response plot of 34 tea genotypes in 3 environments

Caffeine, protein and crude content are major constituents in tea. These substances are naturally occurring in tea leaves and significant variations were observed in the genotypes with respect to the environments under study, which indicated that the genotypes accumulated these components differently in different environments (Figure 11). The correlation coefficient among protein, caffeine and crude fibre showed that protein is highly and positively correlated with crude fibre and caffeine (Table 12).

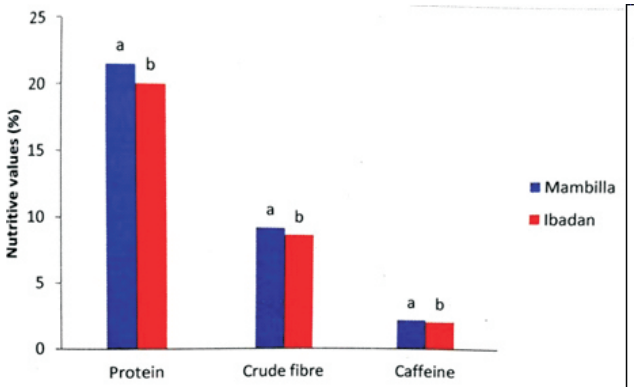


Figure 11 : Protein, crude fibre and caffeine contents as determined by the environments

Table 12: Correlation coefficient of 3 proximate analyses of tea

	Protein	Crude fibre	Caffeine
Protein	1.00	0.30**	0.34**
Crude Fibre		1.00	0.23**
Caffeine			1.00

*, ** significant differences at 0.05 and 0.01 level of probability respectively

4.0 Conclusion

Lack of knowledge of the genetic diversity inherent in a crop germplasm will lead to limited progress in the improvement of the crop. Our studies of several indigenous crop species (Melon, Okra, West African Okra, African Yam Bean and Tea) revealed large diversity and a broad genetic base in these crops, implying a great genetic potential in their utilisation. Using morphological and molecular characterization techniques, we classified accessions of these crops into distinct clusters with considerable difference and high levels of polymorphism between the groups. We also identified some promising genotypes with traits like early maturity, high seed yield, high adaptability to specific environments, suitable growth habits etc. This has facilitated the maintenance and further acquisition of germplasm resources, as well as the incorporation of specific genes governing desired traits for the development of improved crop varieties.

Also we carried out experiments aimed at enabling a better understanding of the gene systems operating in the expression of many morphological and yield traits. The results from heritability and genetic analysis studies indicated the extent to which characters can be transmitted from one generation to another generation. They also served as valuable tools that can be used to predict the magnitude of genetic gain that will follow selection of these characters. Of course, the major remarkable features of both natural selection and artificial selection (as carried out during genetic and plant breeding procedures) is that while some traits maintain continuity from generation to generation, others experience discontinuity and fail to progress from one generation to another generation.

5.0 Recommendations

1. There must be adequate funding and sustained efforts for plant genetic resources exploration, collection, characterization and conservation in Nigeria, for both cultivated species and their wild relatives.

2. Relevant authorities and agencies should ensure regular review of existing national legislations backing plant genetic resources conservation and utilization. Concerted efforts must also be made to enforce these laws.

3. Federal and State governments need to demonstrate sincere commitment towards research activities by increasing the funding made available to universities and research institutes.

4. There is a need to bridge the gap between university researchers and scientist at the National Research Institutes with a view to enhancing research outputs in the agricultural value chain which will ensure food security in the country.

5. The existing synergy and collaboration between the Institute for Food Security, EnvironmentalResources and Agricultural Research (IFSERAR); Agricultural Media Resources and Extension Centre (AMREC) and relevant colleges in FUNAAB should be further strengthened so as to carry out demand–driven, farmer–centred and problem–solving researches that will justify the existence of our university.

6. Our university (FUNAAB) should also continue to develop human capacity and material resources in biotechnology which should be deployed towards promoting agricultural research and food production in our catchment areas.

7. Nigeria must not shy away from the cultivation and use of Genetically Modified (GM) crops. Concerned regulatory authorities should however, ensure that such crops meet biosafety standards.

8. Sustained efforts should be made to mitigate the current negative effects of climate change at National and local levels in order to enhance agricultural research and production activities.

6.0 Acknowledgements

Mr. Vice-Chancellor sir, I am a not a self–made man. In the course of my sojourn in life a lot of people, too numerous to mention, have contributed to my progress. However, my greatest appreciation goes to my maker and heavenly Father (Jehovah Almighty); my Saviour and Master (the Lord Jesus Christ) and my Helper and Strengthener (the Holy Spirit). I am what I am today by the Grace of God. All the glory be to God.

My gratitude goes to all my teachers at every level of my academic pursuit — St. Peters (Ang.) Primary School, Ake, Abeokuta; Abeokuta Grammar School; Ogun State Polytechnic (now Moshood Abiola Polytechnic) (for my _A' Level) and the University of Ibadan (for my degree certificates). They taught, encouraged, molded and mentored me to become who I am today. As many as they are, special mention must be made of my ―academic father‖ who instilled in me the virtues of humility, hardwork, punctuality, honesty and moderation. I am talking of no other person other than Prof. Iyiola Fawole. He took me in as my final year project supervisor, trained me for the M. Sc. research work and released me to the labour market after he thoroughly supervised my Ph.D. thesis. I am deeply grateful to him. May he live long to reap the fruits of his labour. I am also grateful to a worthy teacher and mentor, Prof. Timothy Olurotimi Tayo, who brought me to UNAAB. He is an epitome of discipline, hardwork and focused intellectual pursuit. Thank you sir.

Of course, the Pioneer Vice Chancellor of this University, Prof. Nurudeen Olorunnimbe Adedipe, who taught me at the University of Ibadan and interviewed me for my appointment here. He is a thoroughbred academic and administrator and he encouraged me to develop as a budding academic. I also appreciate the other former Vice Chancellors — Prof. Julius Okojie, Late Prof. Israel Adu, Prof. Oluwafemi Balogun, Prof. Olusola Oyewole as well as the former acting Vice Chancellors — Prof. Ishola Adamson and Prof. Ade Enikuomehin (a brother and friend). I thank them for the opportunities they gave me to serve this University. However, Mr. Vice Chancellor sir, please permit me to accord special recognition and thanks to Prof. Oluwafemi Olaiya Balogun during whose tenure I had the most opportunities to be my best and contribute my best so far to the development of this University. I am also very grateful to our current Vice Chancellor, Prof. Felix Kolawole Salako, who is both a loving brother and worthy leader. He is so passionate and committed to the development of our University as attested to by the giant strides and achievements recorded thus far. Thank you for the opportunities you gave to me and may the Lord continue to strengthen you sir.

At this juncture, I must also appreciate the immediate past Vice Chancellor of Lagos State University (LASU), Ojo, Lagos Prof. Olanrewaju Adigun Fagbohun (SAN, NPOM). He gave me the opportunity not only to have my sabbatical leave at LASU, but also appointed me as the pioneer Ag. Dean of the School of Agriculture, Lagos State University. He gave my team and I at the school all the support we needed and this culminated in unprecedented infrastructural development and full accreditation of the National Universities Commission for our programme, in just about 2 years ofestablishment. He is such a pragmatic and transformative leader.

I will like to appreciate the goodwill that I have received from the entire academic, technical and administrative staff of this

University. Space constraint will not allow me to list everyone. Special thanks go to the Dean of my College, Prof. J. J. Atungwu; my dear friend and the immediate past Dean, Prof. M. O. Atayese; my Head of Department and a friend of 35 years, Prof. (Mrs) M. A. Ayo-Vaughan; all the academic staff of the Department of Plant Breeding and Seed Technology, especially ―our most senior‖, Prof. O. J. Ariyo; all the academic and non–teaching staff of COLPLANT. Special mention must be made of some senior colleagues whom we have worked together in this University and who have impacted me positively. They include: Prof. M. T. Adetunji; Prof. S. T. O. Lagoke; Prof. S. O. Afolami; Prof. E. B. Oguntona; Prof. (Mrs). Daisy Eruvbetine; Prof. C. F. I. Onwuka; Prof. T. A. Arowolo; Prof. and Prof. (Mrs) Eromosele; Prof. Tope Popoola; Prof Sam Oluwalana; Prof. Tunde Ajayi. I also appreciate thespecial friendship of Prof. J. J. Atungwu, Prof. F. I. Adeosun and Dr. R. A. Sobayo (a.k.a. the FUNAAB– LASUSOA team).

To my numerous former and present research students (both undergraduates and postgraduates), thank you for your dedication and hardwork including your contributions to some of the research results presented in this lecture. Special mention must be made of my past doctoral students: Prof. C. C. Nwagburuka (BABCOCK University); Dr. Adewale Adeniji and Dr. Babawale Daniel (both of FUOYE); Dr. O. O. Olaniyi (CRIN); Dr. E. O. Idehen (FUNAAB). My special appreciation goes to Prof. (Mrs.) H. A. Bodunde, Chairperson and members of FUNAAB Publications Committee for her efforts in editing the manuscript of this lecture and also to Mr. Ayodeji Famogbiele for his editorial assistance.

Mr. Vice Chancellor sir, being an ardent believer in and a disciple of the Lord Jesus Christ, I must appreciate my spiritual leaders. Top among them is my Pastor, spiritual coach and mentor, bible teacher, brother, confidant and a man after God's heart, Revd. Akintunde Joshua Amosun. He has been all of the above to me

since 1996 when we met and I am blessed to have him in my life. His wife, (Revd. Mrs. Kemi Amosun), who also happens to be my Pastor and sister, is well appreciated for her support and encouragement all these years. I also appreciate every member of Rock Foundation Church, Abeokuta for their love, prayers and support. Sincere appreciation also goes to my Lords spiritual, Bishop Samuel Oludele Ogundeji (Lord Bishop of Egba West Anglican Diocese); Bishop Emmanuel Oludaisi Adekunle (Lord Bishop of Egba Anglican Diocese); Venerable (Dr.) A. Ayoade (Vicar, Holy Trinity Anglican Church, Gbagura, Abeokuta) and other ministers of the gospel who have been of significant blessings to me and my family. I thank members of the Abeokuta Club and Egba Science Education Foundation (ESEF) for their love and support.

The Kehinde Dynasty in Gbagura land, Abeokuta is such a large one and I have enjoyed tremendous goodwill and brotherhood among them. On a lighter note, this is not surprising since it was claimed that I am a "re-incarnation" of one of their progenitors and a strong pillar in the dynasty who was also my grandfather — Chief Christopher Emmanuel Kehinde, the former Ekerin of Egba Christians. I came into the world a few months after he died, hence the name given to me Babatunde; though that didn't prevent my dad from beating me when I was young.

The first grandchild of Chief C. E. Kehinde is Emeritus Professor Olufunmilayo Ayoka Adebambo. She it was who prevailed upon me to change my course of study from Agricultural Economics (which I chose as first option in JAMB admission) to Agricultural Biology in order to study Plant Breeding and Genetics. She also prevailed upon me not to leave the University of Ibadan until I bagged the Ph.D. degree. Thank you ma for your foresight. May you live long to reap the fruits of your labour. Special appreciation also goes to Bashorun Festus Oladiji Kehinde (Balogun Idere, Gbagura); my other uncles, aunties, cousins, nephews and nieces.

Worthy of deep gratitude are my siblings: Mrs. Olufunmilayo Lawal; Pastor (Mrs) Oluyemisi Bolarinwa–Odunayo and Dr. Gbenga Kehinde.
I also appreciate my age-long friends: Pharm. Badejo Ayinde, Pastor Yomi Adeyemi, and Prof. A. B. Idowu (Vice-Chancellor, Samuel Adegboyega University).

My sincere appreciation must go to the patriarch who should ordinarily be my father–in–law but has assumed the role of my father — Prince Ezekiel Ajibade Aderibigbe of Arowomole, Ogbomoso. Daddy, thank you for holding forth and being there for us all the time. May the Lord grant you long life. I also thank Pastor Olayinka Bolarinwa–Odunayo and all my wife's siblings, both home and abroad.

I equally appreciate all members of my mother's family, the Isiyemi Royal Family of Isale Awori, Atan–Ota in Ogun State. Special thanks go to Princess Mosunmola Adeosun (Nee Isiyemi); Princess Bunmi Ligali (Nee Isiyemi) and Prince Adesanya Isiyemi.

To the vehicles who brought me into this world: my father, late Chief Samuel Olayinka Kehinde (former Balogun of Gbagura Christians) and mother, late Chief (Mrs) Elizabeth Olanrewaju Kehinde (the former Iya Ijo of Holy Trinity Anglican Church, Gbagura, Abeokuta), thank you for all your labour of love and care. You cherished education and endeavoured to give us quality education and proper moral and spiritual upbringing. We shall continue to remember you with fond memories. May your gentle souls continue to rest in peace.

In the year 1992, while on academic sojourn at the University of Ibadan, I came across a young intelligent and innocent soul by the name Iyabode Adekemi Aderibigbe. Sparks flew, hearts blended, the Lord intervened and by November 02, 1996 we became

husband and wife. Thus began a journey that has been a blessing to me in every area of my life. She has been a strong pillar of support and very understanding. Prof (Mrs) Iyabode Adekemi Kehinde, Professor of Plant Pathology, Federal University of Agriculture, Abeokuta, I doff my hat for you. I thank God for the angels that God has blessed us with Comrade OreOluwa Faith (current President, Association of Veterinary Medicine Students, FUNAAB); IbukunOluwa Joy; and IreOluwa Peace.

Mr. Vice-Chancellor sir, Principal Officers of the University, distinguished colleagues, invited guests, ladies and gentlemen, greatest FUNAABITES, I thank you most sincerely for your patience and attention. God bless you.

Please join me to sing this song:

HYMN: GREAT IS THY FAITHFULNESS

Great is Thy faithfulness O God my Father, There is no
shadow of turning with Thee;
Thou changest not Thy compassions they fail not,
As Thou hast been Thou forever will be.

Great is Thy faithfulness, Great is Thy faithfulness,
Morning by morning new mercies I see;
And all I have needed Thy hand hath provided,
Great is Thy faithfulness.

Summer and winter and springtime and harvest,
Sun, moon, and stars in their courses above;
Join with all nature in manifold witness,
To Thy great faithfulness, mercy and love.

Great is Thy faithfulness, Great is Thy faithfulness,
Morning by morning new mercies I see;

And all I have needed Thy hand hath provided,
Great is Thy faithfulness

Pardon for sin, and a peace that endureth,
Thine own dear presence to cheer and to guide;
Strength for today and bright hope for tomorrow,
Blessings all mine, with ten thousand beside.

Great is Thy faithfulness, Great is Thy faithfulness,
Morning by morning new mercies I see;
And all I have needed Thy hand hath provided,
Great is Thy faithfulness.

7.0 References

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