UNIVERSITY OF ILORIN

THE TWO HUNDRED AND TWENTY FIRST (221ST)
INAUGURAL LECTURE

"CHROMOSOME AND ITS DYNAMICITY FOR CLASSIFICATION AND FOOD SECURITY"

BY

PROFESSOR OBA TOYIN MUSTAPHA
B.SC., M.Sc., Ph.D. (Ilorin), MBA (Kano)
DEPARTMENT OF PLANT BIOLOGY,
FACULTY OF LIFE SCIENCES,
UNIVERSITY OF ILORIN, ILORIN, NIGERIA

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The Vice Chancellor

Professor Wahab Olasupo Egbewole SAN
LL.B (Hons) (Ife); B.L (Lagos); LL.M (Ife); Ph.D. (Ilorin);
FCArb; Fspsp

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PROFESSOR OBA TOYIN MUSTAPHA
B.SC., M.Sc., Ph.D. (Ilorin), MBA (Kano)
PROFESSOR OF CYTOGENETICS AND BIOSYSTEMATICS
DEPARTMENT OF PLANT BIOLOGY,
UNIVERSITY OF ILORIN, ILORIN, NIGERIA

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All Non-Teaching Staff,
My lords spiritual and temporal,
Distinguished students of Plant Biology,
Gentlemen of the Print and Electronic Media,
Distinguished invited guests, friends and relations
Great Unilorites, Ladies and Gentlemen.

Preamble

Mr. Vice-Chancellor Sir, kindly permit me to appreciate the Almighty Allah for the privilege He granted me to be here today. All knowledge belongs to Allah, the Creator of Heaven and Earth who gives man part of this knowledge for the benefit of humanity. With profound gratitude to Almighty Allah, I consider it a great honour and privilege to present the 221st Inaugural Lecture of the University of Ilorin. Today's inaugural lecture "**Chromosome and Its Dynamicity for Classification and Food Security"** is the second in the Department of Plant Biology that was carved out of the defunct Department of Biological Sciences in 2014. The advent of the gentleman

standing before you today into Cytogenetics and Biosystematics was prompted by Professors V. L. A. Yoloye of blessed memory and S. O. Oyewole. I was lured into this aspect of Biology by these men when one of them, Prof. Yoloye, gave an attachment of job offer as an Assistant Lecturer in the Department of Biological Sciences on completion of my M. Sc. programme because Prof. Oyewole was the only Geneticist in the Department then. My interest was in Plant Physiology as a result of interesting and cordial relationship I had with Professor E. O. Etejere during my undergraduate days. As God would have it then, Prof Etejere was in Canada on Sabbatical leave. The rest is history for here I am today.

Mr. Vice-Chancellor Sir, I will like to, once again, appreciate Almighty Allah for using these three people, Alhaji Ahmad Olayiwola Kamal, Prof. Shuaib Oba Abdulraheem and Alhaji Saka Abdulkareem in my journey of life. Alh. A. O. Kamal (may Allah grant him Alijanat Fridous) was instrumental to my secondary School education while Prof. Abdulraheem and Alh. Abdulkareem were instrumental to my being in academic.

Introduction

Classification is a natural occupation of man. Classifying organisms based on similarities helps to provide order to the thousands of living organisms on earth. The urge to classify plants has been with man since he first set his foot on this planet, borne of a need to know what he should eat, avoid, use as cures for ailments and utilize for his shelter. Initially, this information was accumulated and stored in the human brain and passed on to generations verbally in dialects restricted to small communities. Slowly, man learnt to put his knowledge in writing (black and white) for others to share and improve upon. We have now reached a stage whereby a vast amount of information can be conveniently stored and utilized for far- reaching conclusions aimed at developing ideal systems of classification, which depict the putative relationships between organisms.

Chromosomes

Nucleus is the store-house of almost all genetic information needed for the functioning of a cell/organism. It also governs the development of almost all the traits of an organism by providing the information necessary for the syntheses of various structural and functional proteins. At the interphase stage of cell division, the nucleus contains mainly granules. In eukaryotes and prokaryotes, deoxyribonucleic acid (DNA) serves as the molecule storing genetic information. In viruses, either DNA or ribonucleic acid (RNA) serves this function. DNA, while single-stranded in a few viruses, is usually a double-stranded molecule organized as a double helix. Contained in each DNA molecule are hereditary units called genes. The gene is the functional unit of heredity. In chemical terms, it is a linear array of nucleotides which are the chemical building blocks of DNA and RNA. A more sophisticated approach is to consider it as an informational storage unit capable of undergoing replication, mutation, and expression. These genes are part of a larger element called chromosomes.

Chromosomes are rod-shaped, dark stained (because they contain nucleic acids) bodies seen during metaphase stage of mitosis when cells are stained with a suitable basic dye and viewed under a light microscope (Fig.1) They were given the name chromosome (chroma = colour + soma = body) due to their marked affinity for basic dyes.

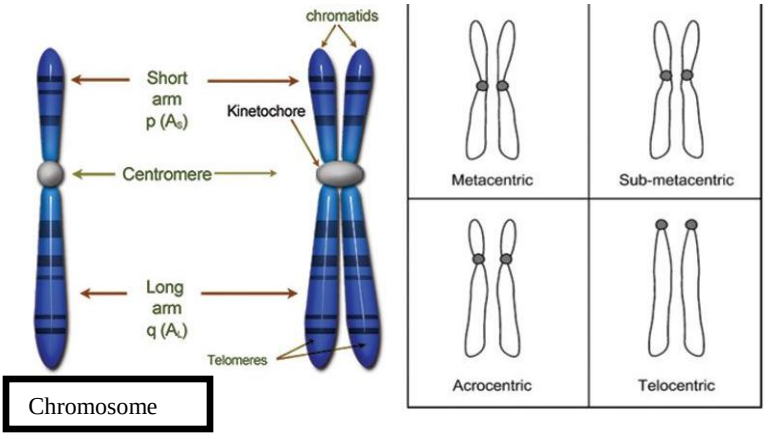


Fig.1: **Chromosome structures showing different positions of the centromere**

Each species has a definite, and, generally, a constant somatic and gametic chromosome number. Somatic chromosome number is the number of chromosomes found in body cells, more specifically, meristematic tissue of a species and is represented by 2n. Ordinarily, somatic cells contain two copies of each chromosome (except sex chromosomes). The two copies of a chromosome are identical in morphology, gene content and gene order, and are known as homologous chromosomes. Gametic chromosome number is precisely one half of the somatic number (one copy of each of the different chromosomes of that species) and is represented by n.

The size of chromosomes shows a remarkable variation depending upon the stage of cell division. Chromosomes are generally studied and measured during mitotic metaphase when they are very thick, quite short and well spread in the cell. In addition, chromosome size is markedly affected by the type of pretreatment given to cells. Cells pretreated with certain chemicals, e.g. colchicine, 8-hydroxyquinoline etc. show relatively shorter chromosomes at metaphase than do untreated cells.

Each metaphase chromosome appears to be longitudinally divided into two identical parts each of which is known as chromatid. The two chromatids of a chromosome are held together at a point called centromere. In most species, each chromosome has a single centromere in a fixed position which does not change except due to structural chromosome aberrations. Therefore, the position of the centromere serves as an important landmark in the identification of different chromosomes of a species. In most species one chromosome has a single centromere (primary constriction). Such chromosomes are termed as monocentric. Some species have more than one centromere and they are termed polycentric. In both monocentric and polycentric chromosomes, the centromeric property is confined to one or more definite points of the chromosomes so that such centromeres are referred to as localized. However, in many insects, homopteran and hemipteran insects, the centromeric activity is non-localized and spread over the entire chromosome length. Such centromeres are known as diffuse centromeres.

The two ends of a chromosome are known as telomeres. Telomeres are highly stable and they do not fuse or unite with telomeres of other chromosomes. But when damaged or removed due to chromosome breakage, the damage chromosome ends are highly unstable and they readily fuse with broken ends of other chromosomes.

In some chromosomes, a second constriction, in addition to that due to centromere (the primary constriction), is also present and is known as secondary constriction. Chromosomes having secondary constriction are called satellite chromosomes or sat-chromosomes. The position of secondary constriction in sat-chromosomes is fixed and remains constant.

The general morphology, (size of chromosomes, position of centromeres, presence of secondary constrictions and size of satellite bodies) of the somatic chromosome complement of an individual constitute its karyotype. Karyotypes are presented by arranging the chromosomes of somatic complement in a

descending order of size keeping their centromeres in a straight line. All the normal members of a species have an identical karyotype. Therefore, the karyotype of a normal somatic cell of a normal individual represents the karyotype of the concerned species. Cytotaxonomy is the classification of organisms using comparative studies of chromosomes during mitosis. Cytotaxonomy uses the characteristics of cellular structures to classify organisms. In cytotaxonomy, the chromosomal configuration of an organism is the most widely used parameter to infer the relationship between two organisms. The inference of species relationships is based on the assumption that closely related species share similar characteristics in their chromosomal setup (karyotype).

Chemistry of the chromosome

The material of which chromosomes are composed is called chromatin. Chromatin is grouped into two classes based on its stainability with basic dyes during various stages of cell cycle. Heterochromatin normally stains darkly while euchromatin is usually lightly stained. Heterochromatin appears to be more densely packed than euchromatin. Heterochromatic regions of chromosomes are generally inactive and they replicate later than euchromatin.

The chromosome in all eukaryotic organisms is chemically the same. Chemically, all eukaryotic chromosomes consist of two types of biological macromolecules: nucleic acids and proteins. The nucleic acid (DNA) and a class of basic protein called histones are present in approximately the same proportion (by weight) in each chromosome. The histone proteins are homogenous and are of five types: H1, H2A, H2B, H3 and H4 and they always occur in molar ratios 1:2:2:2:2 respectively in all eukaryotic chromosomes. Every eukaryotic chromosome contains only one molecule of DNA and the histone proteins form the backbone of each chromosome (Fig.2). The DNA molecule and the histone proteins are intricately associated to form the nucleoprotein called the chromosome. Both of them are

consistent qualitatively and quantitatively in every chromosome. The other nucleic acid, RNA, and other proteins which are non-histones vary in amount between different organisms. Their presence and amount depend on the metabolic state of each cell, the specific function of the cell, and the environmental condition of the organism in question. The DNA molecule is specifically wound round the histone backbone and this is architecturally packaged by coiling and super coiling to form what is seen as the discrete organelle during the process of cell division. Hence, while the function of the histone protein is specific as the carrier of the genetic material DNA, the non-histones only serves as binding and packaging material for the chromosome. Thus, what makes the difference between one chromosome and another is the language of inheritance coded on its DNA molecule. This means that for the complement of chromosomes in any specific cell, the language of inheritance in a particular chromosome is specific and it is the same for all the cells of any particular organism, and the same for all organisms of the same species, barring any accident of nature. Each species of organism is therefore special (Oyewole, 2002).

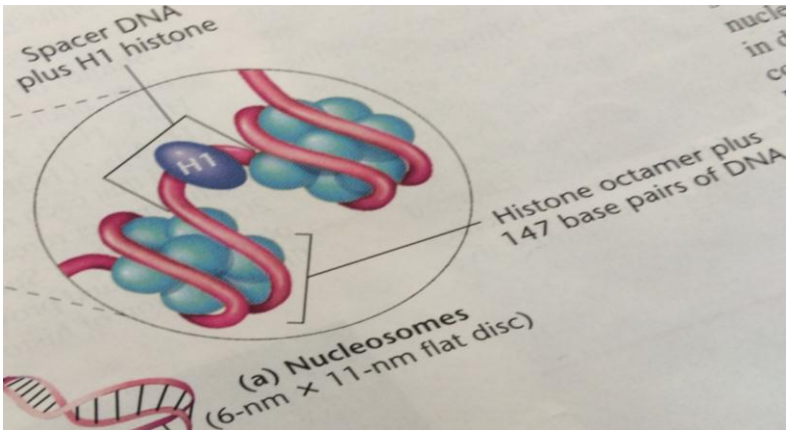


Fig. 2: Nucleosomes

Cytogenetics

From the first establishment of the chromosome theory of heredity, information derived from the study of nuclear cytology has contributed to the understanding of genetics. Indeed, the intimate relationships of the two disciplines led to such adjustments in the conceptual framework of both that the area of contact has for long been called cytogenetics. Cytogenetics consists of the use of chromosomal techniques to obtain genetical information and the use of genetics to illuminate chromosomal behaviour; and consequently, of the study of the interrelationships of cytology and genetics. Thus, in many organisms, both plant and animal, cytogenetics has occupied a central position in the development of our understanding of inheritance. Indeed, it is fair to say that our improved comprehension of the genetics of higher plants, particularly of polyploidy species, is owed in considerable measure to the contribution of cytogenetics.

The science of cytogenetics is based on the fact that the hereditary material of an organism (prokaryotes and eukaryotes) is ordered into one or more chromosomes. By means of a wide variety of physical, chemical, and biological techniques, it has been possible to examine the structure and function of these organelles, and to correlate chromosomal characteristics with patterns of genetic function and of phenotypic inheritance and distribution. Such an ordered arrangement of heritable material possesses obvious advantages. As greater and greater degrees of complexity of structure and behaviour were introduced into the biological world through evolutionary change, and as increased multicellularity was accompanied by cell and organ differentiation, an increasing number of genetic units, both structural and regulatory, were required to provide the information necessary to specify and control that complexity during the process of growth and development (Swanson, *et. al*. 1981).

The basic tenet of cytogenetics is the genetic continuity of life, conservation of species through reproduction and origin

of diversity as expressed by individual. Genetic continuity is enriched by variation. Hence, life reproduces to conserve life and changes to produce diversity (Fig. 3).

Systematics

Systematics is the study and description of variation in organisms, the investigation of causes and consequences of this variation, and the manipulation of the data obtained to produce a system of classification. Various systematic activities are directed towards the singular goal of constructing an

Fig. 3. Diversity in cowpea seeds

ideal system of classification that necessitates the procedures of identification, description, nomenclature and constructing affinities.

The activities of plant systematic are basic to all other biological sciences and in turn depend on the same for any additional information that might prove useful in constructing a

classification. These activities are directed towards the following aims.

- provide a convenient method of identification and communication. A workable classification having the taxa arranged in hierarchy, detailed and diagnostic descriptions are essential for identification;
- provide inventory of the world's flora;
- direct evolution at work: to reconstruct the evolutionary history of the plant kingdom, determining the sequence of evolutionary change and character modification;
- provide a system of classification that depicts the evolution within the group; and
- provide an integration of all available information. To gather information from all the fields of study, analysing this information using statistical procedures with the help of computers, providing a synthesis of this information and developing a classification based on overall similarity.

Systematists use today's technology to classify plants based on evolutionary relationships that can be identified through molecular sciences. With this new technology, plant classification continues to evolve. Plants are occasionally moved from one classification to another or names are slightly changed to reflect new knowledge.

Concept of Biosystematics

Taxonomy may be defined as the study and description of the variation of organisms, the investigation of the causes and consequences of this variation, and the manipulation of the data obtained to produce a system of classification. Such a definition is wider than that which is sometimes given, and has intentionally been drawn up to coincide with the meaning of the term systematics. In fact, the two terms are nowadays commonly used synonymously. It should, however, be realized that some authors prefer to differentiate between them, in which

case systematics has more or less the broad definition given above, and taxonomy is restricted to the study of classification.

Attempts are often made to differentiate between different facets or lines of approach to taxonomy. A distinction might be made between **experimental taxonomy** or **biosystematics** and **orthodox** or classical **taxonomy**. Experimental taxonomy does not simply imply the use of experimental procedures, but is the taxonomic study of organisms from the standpoint of populations rather than individuals, and of the evolutionary processes which occur within populations. Hence the term biosystematics is preferable. It is, inevitably, largely concerned with genetic, cytological and ecological aspects of taxonomy and must involve studies in the field and experimental garden, whereas orthodox taxonomy more often relies on morphological and anatomical data and can be carried out to a large degree in the herbarium and laboratory. Biosystematics may therefore be considered as the taxonomic application of the discipline known as **genecology** – the study of the genotypic and phenotypic variation of species in relation to the environment in which they occur. It is unfortunate that the term biosystematics has been widened by some taxonomists to cover virtually any taxonomic activity not pursued in the herbarium or almost any newly acquired technique. It should be emphasized that it is not the nature of the data used, be they morphological, cytological or chemical, but the use to which they are put which differentiates between classical taxonomy and biosystematics. However, it must be equally stressed that these two fields are not separate and opposing, but rather are closely interacting, complementary approaches to taxonomy, without either of which taxonomy is incomplete.

The need for some system of classification is absolute, for it is only by first naming organisms and then grouping them in recognizable categories that one can begin to sort out and understand the vast array which exists (Stace, 1989; Clarke and Lee, 2019). This requirement is not confined to taxonomists, or even to biologists, for living organisms are part of the everyday

life of all humans. Thus, it is not surprising that classification is a process which mankind naturally and instinctively carry out, and which has been carried out from the very beginning, for the accurate recognition (identification) of food, predators, mates, fuel, building materials, etc. essential for his survival. At the purely practical level, biologists must know what organisms they are working with before they can pass information about them to other people. Experiments cannot be repeated unless the organisms used are correctly identified.

Considering the numbers of kinds of plants known, it is obvious that the problem of classifying them all is enormous. Almost 300,000 species of green plants are currently recognised, in addition to over 100,000 fungi, a few thousand bacteria and other microscopic organisms which some biologists would classify as plants.

Need for Scientific Names

Scientific names formulated in Latin are preferred over vernacular or common names since the later pose a number of challenges (Singh, 2009).

1. Vernacular names are not available for all the species known to man.
2. Vernacular names are restricted in their usage i.e they are not universal in their application.
3. Common names usually do not provide information indicating family or generic relationship.
4. Frequently, especially in widely distributed plants, many common names may exist for the same species in the same language in the same or different localities.
5. Often two or more unrelated species are known by the same common name.

Scientific names, on the other hand, are treated as Latin regardless of their origin. This is because Latin is a dead language and as such meanings and interpretation are not subject

to changes unlike English and other languages. In addition, Latin is specific and exact in meaning.

My Research Activities

Mr. Vice-Chancellor Sir, over the years, I have beamed my research (on classification) light on the family Liliaceae (the Lilies). I consider myself lucky to have chosen members of the family as my research materials just like Mendel was lucky to have chosen *Pisum sativum.* This is because the study of karyotypes is particularly rewarding in such families as Liliaceae and Amaryllidaceae where large chromosomes and frequent bimodality in size within the complements made possible the determination of the progress of the chromosome change and its consequences. The monocotyledonous family Liliaceae is one of the largest of the angiosperm families with representatives all over the world and in all conceivable ecological niches. The conservative view of its phylogeny holds that it is one of the less advanced families of the monocotyledons. Most of its members are perennial herbaceous geophytes that have found use as ornamental garden plants. Hence very little interest has been generated by this group of plants except among gardeners and other forms of naturalists. The taxonomy of its members has therefore suffered neglect from taxonomists and biosystematists. The apparent similarity in the morphology of its representatives has left the family in taxonomic and nomenclatural confusion.

Apart from my efforts while I was conducting my undergraduate project work, my interest in scientific research was spurred during my National Youth Service Corps (NYSC) programme in Cocoa Research Institute of Nigeria (CRIN). In CRIN, at that time, everything one needed to conduct good research work was provided. It was at CRIN I made up my mind to go into academic.

Mr. Vice-Chancellor Sir, we can appreciate the impression of beauty created by an ingenious and logical organization of things. The goals of a biosystematist are to relate living organisms into natural schemes representing their

relationship to each other through evolutionary descent. He must think analytically and dynamically in terms of evolutionary process; and synthetically and comprehensively in terms of present relationships. This is no meagre challenge. The question now is how to go about discovering natural relationships. The approach is to accumulate all data possible about organisms. Data may be accumulated from morphological and ecological studies. Other areas are Chemistry, Genetics and Cytology.

Mr. Vice-Chancellor Sir, I employed more of genetic and cytological studies in my research to establish relationships. This is because virtually every morphological or physiological feature of an organism is gene controlled and genes are units of inheritance in evolution. Genetics is one of the most powerful biosystematics tools. The approach is to perform crosses to prove or disprove some theory of relationships. Crosses may be made in all possible combinations and permutations of several species and subspecies within a genus. Biosystematists have become deeply involved in cytological studies, particularly of the chromosomes. These studies provide one good example of clear-cut species differences at the cellular level. Chromosome number is studied in preparations of dividing cells, usually from root tips or from pollen mother cells. Sometimes, chromosome morphology is valuable in biosystematic studies. Most commonly, chromosome lengths are examined and relative distances between positions of the centromeres are tabulated (Oyewole and Mustapha 1990). The number and type of chromosome aberrations present at meiosis may also be important.

Researches on Biosystematics

Mr. Vice-Chancellor Sir, my research under classification started with *Pancratium hirtum.* Apart from the taxonomic studies carried out by Morton (1965) on *Pancratium hirtum* and *Pancratium trianthum*, there was little information on aspects of population of *P. hirtum* A. Chev (Amarylidaceae) in Nigeria. Representatives of this species were observed to

demonstrate minor but obvious morphological differences. Mustapha, (1986) examined the effect of using basic dye staining of the nucleolus in populations of *P. hirtum* in an attempt to determine variation in the population with a view to confirming whether the obvious morphological differences observed were genetically established. Nucleoli in all the groups examined stained dark brown, the nucleus an ochraceous yellow and the cytoplasm pale yellow (Plate 1). They all appeared to be homogenous.

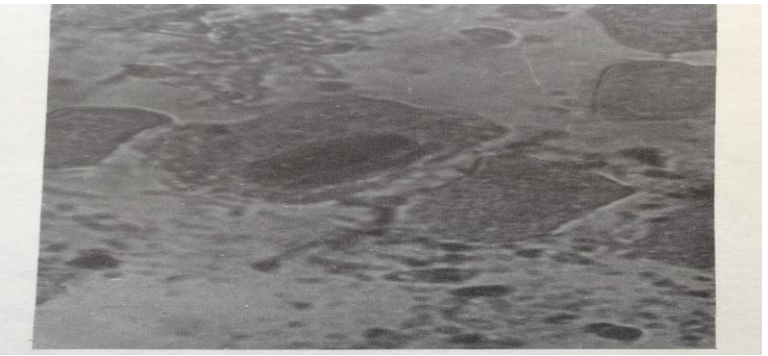


Plate1: Silver impregnation of root tips of *P. hirtum*

Mr. Vice-Chancellor Sir, having confirmed that the populations of *P. hirtum* are homogenous, Oyewole and Mustapha (1990) decided to go a step further by looking into the karyotype analysis of the groups with the view to resolving taxonomic relationship among various groups and to supplement or complement the observed morphological differences in an attempt to rationalize its taxonomy. Chromosomal length in each group varies as well as the total length of the chromatin material (Plate 2).

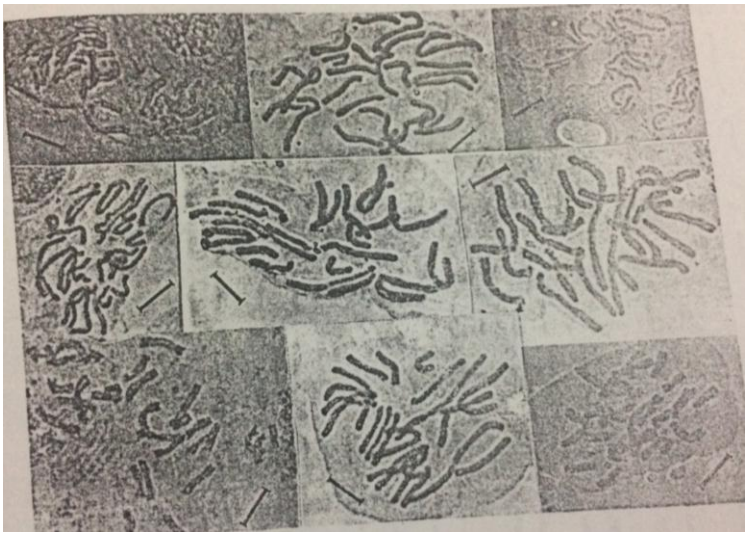


Plate 2: Metaphase chromosomes of *P. hirtum*

Despite the outward similarity of karyotypic configuration of the nine groups and the constancy in chromosome numbers (2n=22), there was evidence that a number of centromeric shifts have occurred in their separate evolutionary histories (Table 1). Karyotype differentiation (Plate 3) in our work was believed to have involved

i. loss of chromosome segments from certain members of the complements, thus rendering homologous members dissimilar in length and morphology;
ii. variation in the length of chromatin per compliment;
iii. most probably, chromosome changes involving rearrangement of genes and /or gene-blocks in translocations and inversions; and
iv. natural hybridizations between different cytotypes.

All the groups were found to be characterized by general conservatisms in karyotype evolution. It was concluded that the species is dynamic and the taxon can be regarded as complex of sibs

Table1: Centromeric location differentiation

Centromeric location differentiation

Taxa	M	m	sm	st	t	T
C_1	-	3	1	1	6	-
C_2	-	3	1	-	7	-
C_3	-	3	1	-	6	1
C_4	-	3	1	1	6	-
C_5	-	4	1	-	6	-
C_s	-	3	1	1	6	-
C_h	-	3	2	2	3	1
C_f	-	3	-	1	6	1
C_n	-	3	2	1	5	-

T = Terminal point
t = Terminal region
st = Subterminal region
sm = Submedian region
m = Median region
M = Median point

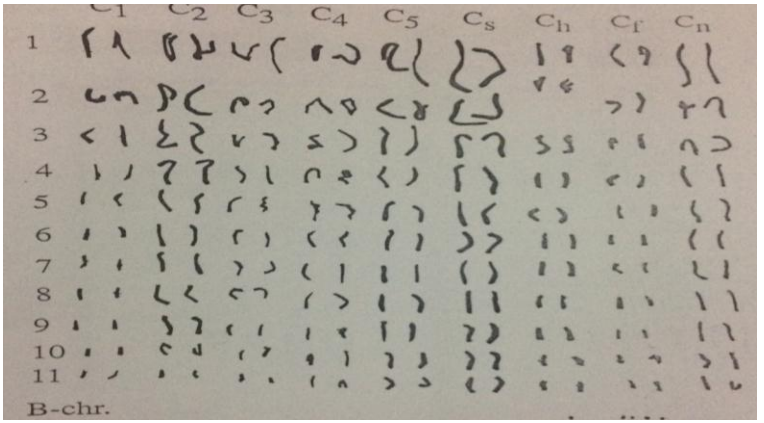


Plate 3: Karyotype of *P. hirtum*

Mr. Vice-Chancellor Sir, *Urginea indica* (Roxb) Kunths is one of the four species recognized in the last revision of the Family (Hepper, 1968). *U. indica* is widespread in the central segment of Nigeria. It occurs in different ecological niches and various soil types within the savanna region and show variety of morphological forms. In view of the fact that *U. indica* complex is dynamic, I had every reason to believe that samples of wild populations (from various part of Nigeria) will continue to reveal the inadequacy of the existing taxonomy of the genus and hence the need for its revision. To make it a comprehensive study and in line with the standard procedure of biosystematics, I employed various aspects of biology- ecology, morphology, anatomy and cytology in considering the cytogenetic relationship and probable mode of evolution of *U. indica* complex.

Ecological studies were carried out on the various population (samples) collected so as to establish relationships between the genetic composition of the populations and their environments. The studies showed that factors such as weather, temperature and soil play important roles in the distribution and form of growth of *U. indica* complex (Mustapha, 1996).

Floral morphological variation and foliar anatomical features (Plate 4) were also examined (Mustapha, 1997; 2000). Six groups were recognized after taking majority of the characters into consideration. The six groups fall into two more or less distinct morphological alliances consisting of groups A, B and C and on one side and groups E and F on the other side. Group D links both alliances through C and E (Table 2). Those two groups also correlated with ecological preference of the taxa. The foliar anatomical investigation revealed differences in the features of leaf epidermis and leaf anatomy correlated with ecological variations in the groups. Their differences, therefore, represent genetic variations among the different taxa within the framework of their ancestry. This therefore, established that the differences observed mean that evolutionary line of the complex diverged after each group found itself in different ecological

niches and as such developed adaptive structures in such ecological habitats.

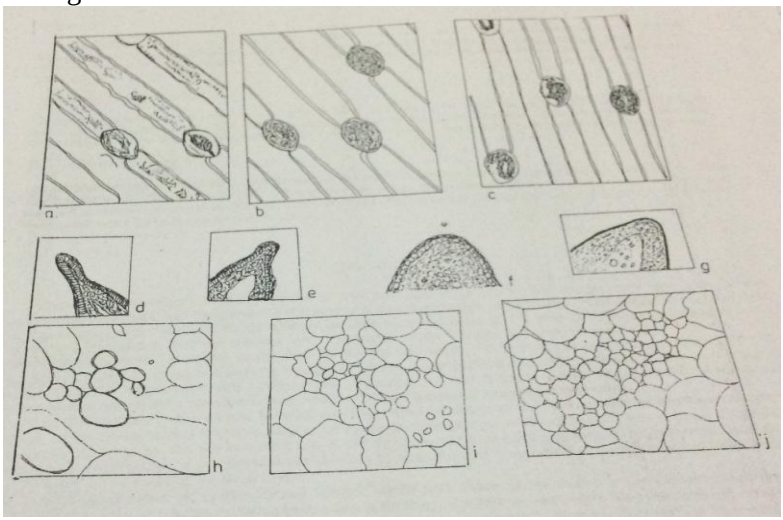


Plate 4: Foliar anatomical features of *U. indica*

Top row: a, b and c show epidermal cell pattern of groups A, D and F respectively

Middle row: d, e, f and g show leaf margin sections of groups A, B, E and F respectively

Bottom row: h, I and J show vein structures of groups B, C and D respectively

Table 2: Character variability for taxa and groups of *U. indica*

CHARACTERS	TAXA	GROUPS					
		A	B	C	D	E	F
1. Leaf length	18.70*	0.53	2.10*	1.30	2.40	1.21	0.85
2. Leaf width	2.10*	1.03	2.72*	2.87*	2.71*	1.33	1.17
3. Leaf Index	26.90*	1.25	2.34*	2.16*	4.32*	1.96*	1.59
4. Pedicel length	4.40*	0.17	1.78	1.59	0.62	0.79	4.58*
5. Peduncle length	79.40*	1.05	0.88	2.91*	0.63	0.54	2.79
6. Tepal length	3.20*	0.33	0.58	0.71	0.44	0.62	0.27
7. Tepal width	5.13*	0.18	0.80	1.73	0.78	1.01	1.13
8. Filament length	0.42	0.18	0.55	4.19*	0.64	0.12	0.41
9. Anther length	0.63	0.05	1.21	0.77	0.30	0.62	1.25
10. Stamen length	0.59	0.12	0.24	0.31	0.39	0.36	0.72
11. Pistil length	0.67	0.20	0.79	0.74	0.49	0.54	1.18
12. Ovary length	1.45	0.08	0.82	0.58	0.41	0.15	2.16*
13. Style length	1.12	0.23	0.74	0.68	0.68	0.21	0.37
14. No. of flowers	3.54*	1.39	1.72	0.79	1.75	1.56	4.39*
15. No. of leaves	2.51*	1.02	1.26	2.92*	2.22*	2.05*	1.75

*At 5% (0.05) level, r ≥ 1.960 shows significant variability.

Mr. Vice-Chancellor Sir, in the quest for gathering more evidence from other sources, a study was carried out on intraspecific variation in the karyotype of *U. indica* complex (Mustapha, 2000). The study revealed that the mitotic divisions were normal and endomitosis was observed in all the groups. Counts of 2n = 20 chromosomes were obtained. More than one karyotypes were observed for all the groups leading to formation of 16 cytotypes. The study also revealed that morphological variation in these groups is more obvious than in chromosome morphology indicating that chromosome repatterning may have been mild, involving only small segment in gene/gene-block rearrangement. Hence the taxon is taken to comprise a stable

polymorphism in which the different forms have attained genetic stability.

Pooling together all findings from areas of study considered, I was able to recognize, through taxonomic treatment of the complex, three distinct taxa in the areas of distribution of the species in Nigeria (Plate 5). The three taxa were recognizable on equal taxonomic levels of subspecies. The subspecies are *Urginea indica* ssp. *indica, Urginea indica* ssp *augustifolia* and *U. indica* spp *tenuifolia* (Oyewole and Mustapha, 2000).

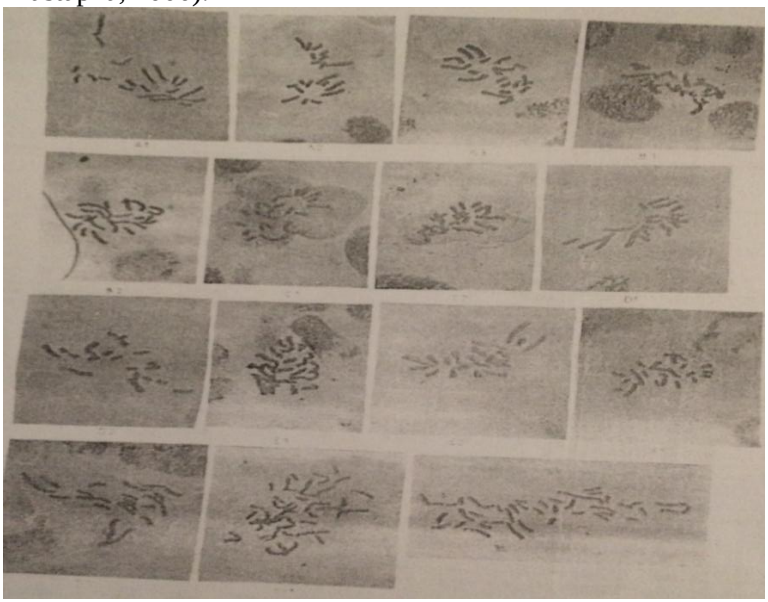


Plate 5: Photomicrograph showing metaphase somatic chromosomes of *U. indica.* (i) and (ii) show endomitosis in C_1 and B_2 respectively.

Research on Molecular Biosystematics

Mr. Vice-Chancellor Sir, early attempts at molecular systematics were also termed as chemotaxonomy and made use of proteins, enzymes, carbohydrate, and other macromolecules that were separated and characterized using techniques such as

chromatography. These have been replaced in recent times largely by DNA sequencing, which produce the exact sequences of nucleotides or bases in either DNA or RNA segments extracted using different techniques. These are considered superior for evolutionary studies since the actions of evolution are ultimately reflected in the genetic sequences.

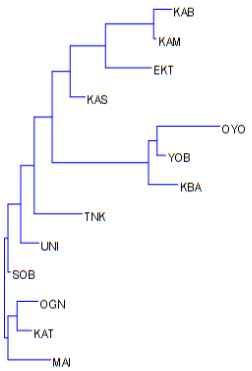
The task of identifying and describing new species has been significantly facilitated by DNA barcodes. The incorporation of sequence data has brought about a total turn around in the field of phylogenetics (Pagel, 1999). DNA Barcoding is based on the assumption that a short standard sequence can differentiate individual of a species since genetic variation between species exceeds that within species (Hajibabaei *et al.,* 2007; Chaudhary and Dantum, 2011).

There are some controversial conclusions drawn from orthodox taxonomic studies of *Dipcadi filamentosum* Medik. Morton (1961) classified it as a separate species while Hepper (1968) in his revision of the plant taxa lumped it between *D. tacazzeanum* and *D. longifolium*. Hence, we assessed the genetic diversity on the basis of data generated by different molecular markers which provides a means of rapid analysis of germplasm that often corroborates phenotypic data (Abdulkareem *et al.*, 2018a).

Our finding revealed that the similarity matrix for morphological, anatomical**,** phytochemical and proximate analysis ranged between 94% and 95% while that of molecular markers was 77%. Sequencing of the plant revealed that the sequence length is 607bp and 26 barcodes sequences (standard). The Pairwise Genetic Distance of all populations were between 0.003 and 0.041 and the Transition and Transverse bias of the nucleotides were between 3.1501 and 18.6998 ATCG ratio. BLAST similarity percentage gave a range of 98% - 99% showing that all the samples considered were *D. filamentosum* and had a common evolutionary relationship and hence should not be lumped together with *D. longifolium.* The absence of the sequence on the National Centre for Biotechnology Information

database proved the sequence generated to be correct. Cluster analysis separated the populations into three main groups with eight varieties (Fig. 4a-b).

Our studies (Abdulkareem *et al.,* 2018b) revealed that use of DNA barcoding for the taxonomic identification of the genetic sequence of the Nigerian populations of *D. filamentosum* has helped to recover the species and resolve the controversy of its classification. Also, the absence of this FASTA sequence of *D. filamentosum* on the NCBI data bank shows that this is a pioneer study on this Nigerian species of the plant (Fig. 5). Furthermore, our study established that the phylogenetic methods that were applied in the description, identification and genetic diversity studies of the species of *D. filamentosum* using the *rbcL* primer had provided a comprehensive molecular marker based study for the genus *Dipcadi* in Nigeria (Abdulkareem and Mustapha 2019).



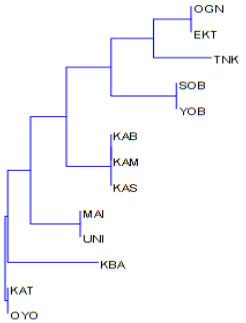


Fig. 4 a **Fig. 4b**

Fig. 4a-b: Neighbour joining clustering (Jaccard) of 13 populations of *D. filamentosum* using RAPD markers (left) and ISSR marker (right).

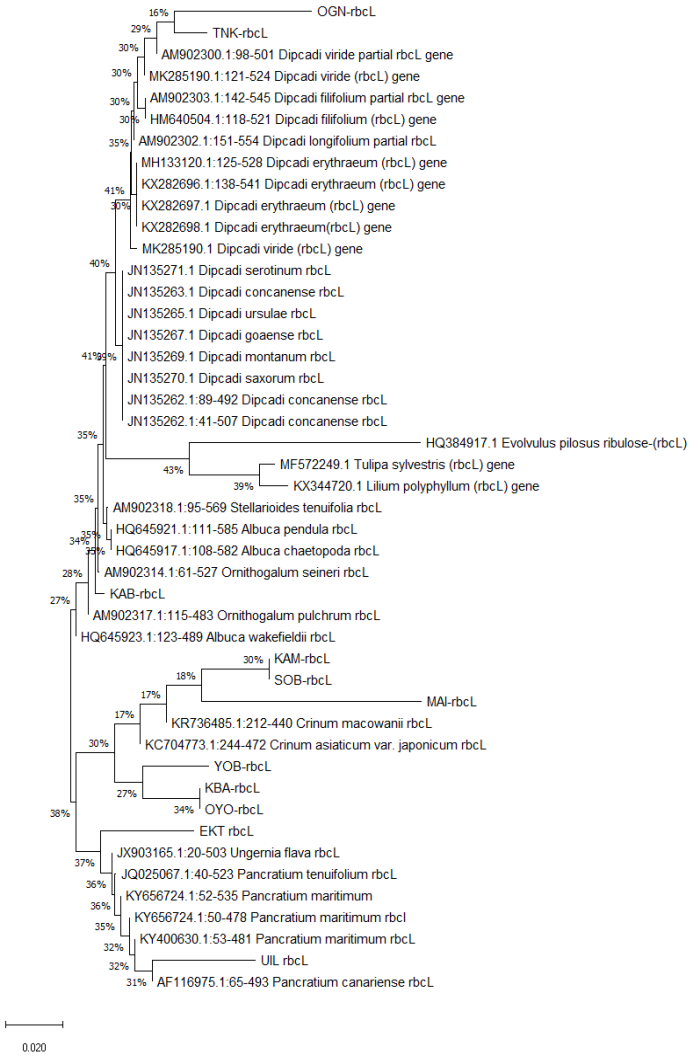


Fig. 5: DNA Barcoding of the Populations of *D. filamentosum*

Though, sufficient information is available on some plant families in Nigeria (Osuji and Owei, 2010; Popoola et al., 2011) by virtue of the major cytological surveys, cytological studies on the plant family Lamiaceae in Esan's land is scanty. Furthermore, most of the previous reports were aimed at ascertaining the chromosome numbers of these plants and not their karyology. We carried out a study on ethnobotanical and cytomorphology of Lamiaceae (Fig 6 a-f). in Esan Land, Edo State, Nigeria.

The plants showed variability in terms of chromosome number and base numbers (Plates 6 and 7; Table 3). Majority of the members were diploids. The chromosomes of some species were found to have satellites. Through the study we were able to document baseline data on morphology and karyotype of the plants. Information such as ploidy levels, chromosome base number, chromosome numbers (interchromosomal and intrachromosomal assymentry) in the karyotype gave useful information about the evolutionary trend (Fig. 7) and status of the plants which is important to breeders who may want to improve the medicinal qualities of those plants. Also, chromosome number of *Clerodendrum incisum* (2n=4x=48) was reported for the first time in the work.

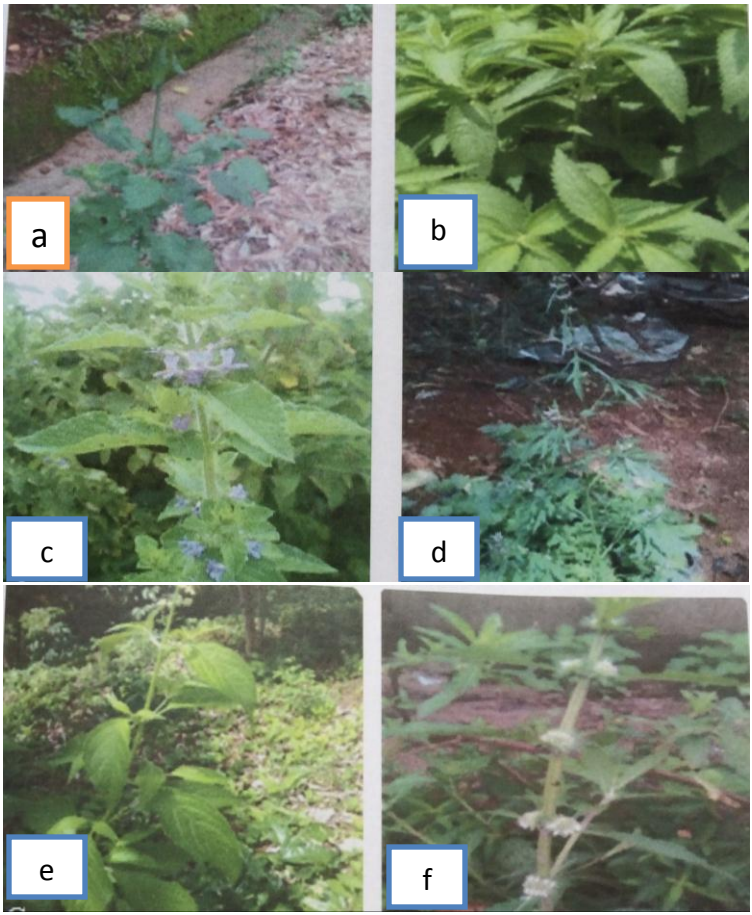


Fig. 6 a-f: Morphological description of members of family Lamiaceae.

Key: a= *H. opposita*, b= *H. lanceolata*, c= H. *suaveolens*, d= *L. sibricus*, e= *L. nepetifolia*, f= *L. martinicensis*

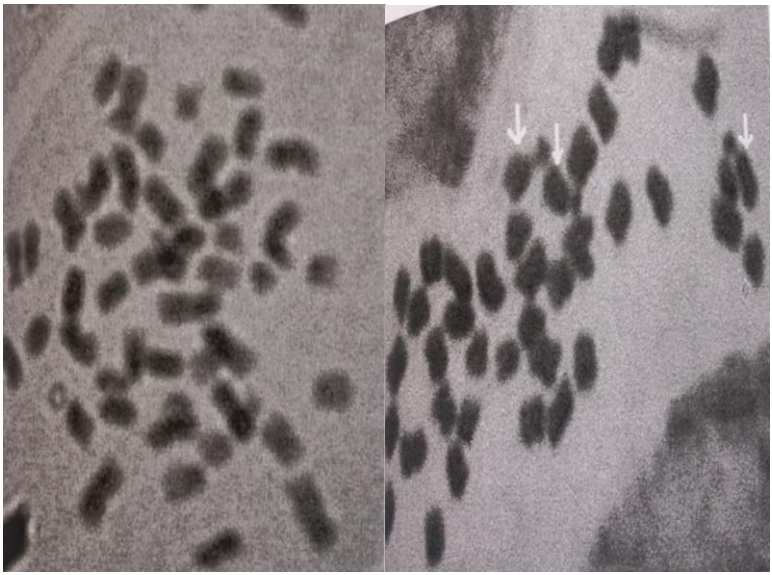


Plate 6: Somatic chromosomes (2n=48) of *C. incisum* (left) and *O. gratissimum* (2n=40) with white arrow indicates chromosomes with satellites (right)

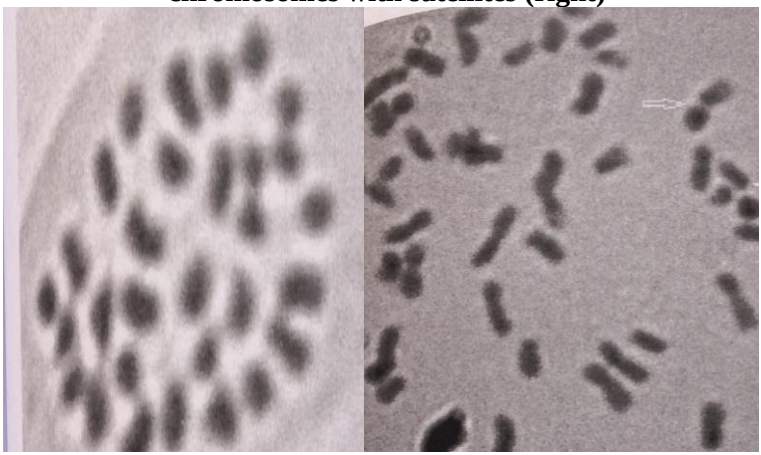


Plate 7: Somatic chromosomes (2n=30) of *B. polystachyon (left) and C. splendens* (2n=48) with white arrow indicate two chromosomes with satellites (right

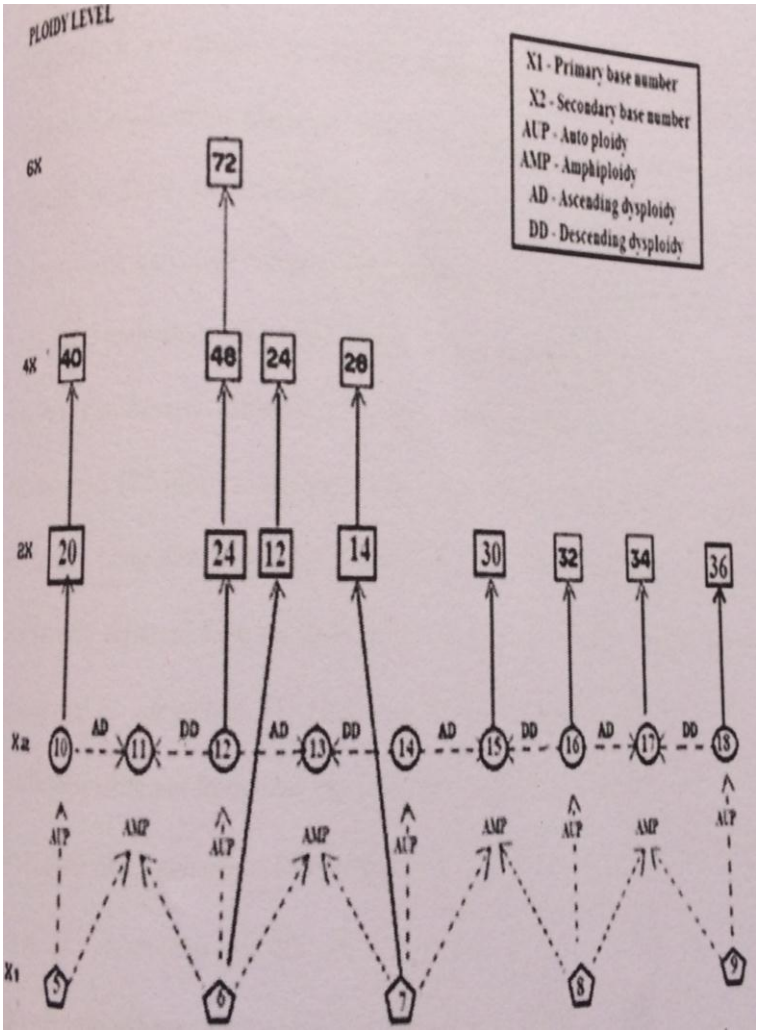


Fig. 7: The probable evolution of chromosome numbers in species of Lamiaceae

Table 3: Chromosome number and other features of members of Lamiaceae

S/No	Name of Taxa	Chromosome number (2n)	Primary base number x1	Secondary base number x 2	Ploidy level	No of satellites
1	*Aeollanthus Pubescens*	34	8	17	2x	-
2	*Basilicum Polystachyon*	30	7	15	2x	-
3	*Clenrodendrum incisum*	48	6	12	4x	-
4	*Clenrodendrum. Splendens*	46	6	12	4x	2
5	*Coleus. blumet*	48	6	12	4x	-
6	*C. scutellarioides*	48	6	12	4x	-
7	*Hoslundia. apposita*	24	6	-	4x	2
8	*Hyptis. Lanceolata*	32	8	16	2x	2
9	*H. suaveolens*	28	7	-	4x	2
10	*Leonorus sibricus*	20	5	10	2x	1
11	*L. nepetifolia*	24	6	12	2x	-
12	*L. matinicensis*	28	7	14	2x	-
13	*Mentha piperita*	72	6	12	6x	-
14	*Ocimum africanum*	48	6	12	4x	4
15	*O. Basilicum*	48	6	12	4x	2
16	*O. canum*	24	6	12	2x	1
17	*O. gratissimum*	40	5	10	4x	3
18	*O. Kilimandscharium*	76	6	13	6x	-
19	*O. tenniflorum*	36	9	18	2x	-
20	*Platostoma africanum*	12	6	-	2x	-
21	*P. hallii*	34	8	17	2x	-
22	*Solenostemon monostachyus subsp monostachyus*	14	7	-	28	1
23	*S. monostachyus subsp perenis*	28	7	-	48	2

Research on *Chlorophytum*

Chlorophytum plants are well known for their wide usage in the tropical and subtropical regions of Africa. In spite of their importance, species in the genus are often confused. Sardassi *et al.* (2006), attributed taxonomic difficulty in the genus to misidentification of its species. Abdul *et al.* (2014), believed that restricted distribution and remote habitats of the species, short seasonal flowering and fruiting period, identification keys with overlapping characters among others are responsible for difficulty encountered in identifying species in the genus.

Bearing this in mind, we investigated comprehensive biosystematic studies of the genus. At the end of the study, we were able to provide a broad base means of identifying the species in the genus through descriptive taxonomic key provided. We also, through the study, uncovered an unidentified species of *Chlorophytum* and named it *C. sabiense* which may have probably been lumped with unrelated group in the past (Omokanye *et al.,* 2021).

Food security

Food security according to Food and Agricultural Organization (FAO) is achieved when it is ensured that all people at all times, have physical, social and economic access to sufficient, safe and nutritious food which meets their dietary needs and food preference for an active and healthy life (FAO, 2000).

Mr. Vice-Chancellor Sir, my first contribution to knowledge was in 1986 after I was appointed as an Assistant Lecturer in Bayero University, Kano. The work was more or less in Plant Physiology but relevant in enhancing food security. It was from my first-degree final year project report. We observed that the plant, *Adansonia digitata,* is of high economic importance but it is sparsely distributed. Physiological and biochemical studies were therefore carried out to find out the reason for its sparse distribution. It was found that *Adansonia digitata* seeds and growing seedlings are equipped with the necessary food reserves for a healthy and rapid growth. The low population density of this species was attributed to seed coat dormancy exhibited by the seeds and the annual savanna bush fires which burn off the young seedlings. Since the seed coat problem can be overcome by acid scarification (Etejere and Osatimehin, 1984), we recommended that raising the young seedlings in nurseries and adequate protection from environmental hazards after transplanting in the field would enhance population density and distribution of the species (Etejere *et al.,* 1986).

Research on *Abelmoschus*

Basic physiology and genetic research on Okro crop productivity revealed that yield potential is rather high and not yet fully exploited. Furthermore, a rich gene pool with regard to both genomic and plasmonic factors have not been fully utilized for the purposeful and efficient enhancement of crop productivity. In 1999, our team was engaged in finding the range of variability, phenetic relationship and combining ability among the available varieties so as to facilitate maintenance and further expansion of germplasm resources in Okro (Oyewole *et al*, 1999). The study which was carried out during pronounced water stress involved twelve varieties of Okro (Table 4).

Table 4: Correlation between fruit character and the varieties

ITEMS	MOSN 10-CH	EF	IL	NLF 9-CH	MFSN	JK	SLF	OLF	EAH	FD	BS	EDE
Correlation between FW and FL	* +0.44	*** +0.87	*** +0.76	*** +0.85	*** +0.87	*** +0.94	*** +0.86	*** +0.61	n.s +0.30	** * -0.76	*** +0.72	n.s +0.25
Correlation between FW and FSL	** +0.53	n.s -0.09	** +0.59	*** +0.46	n.s +0.34	n.s +0.34	* +0.56	n.s 0.35	n.s +0.18	n.s -0.25	** +0.56	* +0.60
Correlation between FW and number of seeds per fruit	*** +0.91	*** -0.90	*** +0.97	*** +0.81	*** 0.93	*** 0.93	*** +0.95	*** +0.79	*** +0.81	** * -0.82	*** 0.94	** +0.74
Correlation between FL and number of seeds per fruit	* +0.48	n.s -0.01	*** +0.75	** 0.59	n.s +0.22	n.s +0.42	** +0.73	n.s +0.01	n.s +0.41	* 0.33	n.s +0.08	n.s 0.18
Correlation between FL and number of seeds per fruit	** +0.52	*** -0.94	*** +0.76	** +0.61	*** +0.91	*** +0.78	*** +0.94	*** +0.71	n.s 0.23	** * -0.96	*** +0.75	n.s +0.49
Correlation between FSL and number of seeds per fruit	n.s +0.39	n.s -0.04	** +0.56	** +0.55	n.s 0.17	n.s 0.41	* +0.54	n.s -0.03	n.s -0.31	n.s 0.34	** 0.50	n.s +0.27

*=significant at 10% , **=significant at 5%, ***= significant at 1%, ns= not significant, (+)=positive correlation and (-)= negative correlation, Key: FW= fruit weight; FTL= fruit stalk length; FL= Fruit length

(MOSN 10-CH, EF OKRO, IL OKRO, NLF9 CH, BS OKRO, EAH OKRO, EDE, MFSN, SLF, JK and OLF. After various crosses were evaluated, OLF, BS and JK were recommended for selection when the breeder's aim is to breed for drought resistant varieties especially in the sub arid regions.

Research on Root-Knot Nematode

Low and inconsistent yields of cowpeas in the tropical farming system are partly due to insect pests and environmental factors. In addition to these factors, plants parasitic nematodes also serve as constraints to cowpea production. As a result of this, Mustapha *et al.* (2000) examined Root-Knot nematode resistance in cowpea (*Vigna unguiculata* (L.) Walp). The study, which was as a result of my collaboration with International Institute of Tropical Agriculture (IITA), was carried out at IITA Research farm in Kano station during the dry season in plots heavily infested with nematodes (*Meloidogyne* species). Twenty-one cowpea varieties were used for the study. The overall effect of the Root-knot nematode on growth and yield parameters in the 21 cowpea varieties showed that seedlings of highly susceptible varieties were galled early and died prematurely which may have been due to arrest of materials for translocation from the roots to the shoots by the galls. Those that survived suffered less competition for essential growth requirements and the activity of the nematodes might have been curtailed in the root so that normal growth and development persisted. The heritability values for the number of eggs/plant was 61.8% establishing that the number of eggs/plant is a good index to differentiate resistant varieties from susceptible ones and is not affected much by the environment. The resistant varieties were virtually free of galls and permitted very little egg development (Table 5).

Table 5: Correlation coefficients between growth and yield characteristics and parameters measuring nematode infection

Growth and yield parameter	Root weight (g)	No. of galls/plant	Gall index	No. of eggs/plant	Susceptibility index
Days to flowering	-0.14	0.13	0.10	0.22	0.20
Canopy height	-0.26	-0.43	-0.37	-0.37	-0.39
Canopy spread	0.08	0.09	-0.08	0.22	0.17
No. of branches	-0.23	-0.19	-0.23	-0.13	-0.18
No. of pod/plant	0.12	0.05	0.02	0.10	0.09
No. of seed/pod	0.13	-0.08	-0.13	0.02	-0.11
100 – seed weight (g)	0.09	0.19	0.20	0.13	0.09
Seed yield/plant (g)	0.08	0.05	0.02	0.09	0.03
straw yield/plant (g)	-0.19	-0.11	-0.5	0.03	-0.07
Harvest index	0.13	0.05	0.02	0.05	-0.05
Yield (kg/ha)	-0.33	-0.29	-0.21	-0.29	-0.27

Research on *Vigna*

Mr. Vice-Chancellor Sir, in a similar study, genetic variability among cultivars of cowpea (*V. unguiculata* (L.) Walp) using morpho-agronomic traits and nutritional composition was examined (Animasaun *et al.*, 2015). Results of the study showed that substantial variation existed in the characters evaluated to warrant selection of promising genotypes in terms of yield and nutritional values for further improvement. The cultivars, from principal components analysis were divided (Table 6) into two broad genetic groups (A and B). Group A consists of two

clusters whose members showed low performance in terms of economic traits and group B comprises two clusters of superior cultivars for most of the traits studied (Fig.8). Variability as expressed in the studied cultivars could be useful for understanding genetic diversity of selection of cultivars with novelty in vegetative growth, yield and nutritional composition in the process of breeding programme and crop production.

Table 6: Eigen vectors and percentage explained variation by the first three principal components of morpho-agronomic traits and nutritional composition of ten cultivars of Cowpea

Components	Prin 1	Prin 2	Prin 3
Eigen value variance	11.453	9.909	5.940
Individual percentage (%)	26.634	23.045	13.815
Cumulative percentage (%)	26.634	49.679	63.493
Eigenvectors*	SGM (0.851)	LL(2WAS) (0.903)	NL(6WAS) (0.850)
	NDF (-0.871)	LB(2WAS) (0.922)	DPW (-0.809)
	FC/P (0.827)	LL(6WAS) (0.911)	NBM (0.773)
	PL (0.866)	LB(6WAS) (0.943)	NB(6WAS) (0.798)
	NSP (0.849)	LLM (0.866)	NL(2WAS) (0.646)
	SPP (0.948)	LBM (0.934)	FC (0.672)

SGM = Stem girth at maturity, NDF = Number of days to flowering, FC/P = Flower Clusters/Plant, PL = Peducle Length, NSP = Number of seeds/Pods, SPP =Seeds per Plant, LL(2WAS) = Leaf Length at 2 weeks after sowing, LB(2WAS) = Leaf Breath 2 weeks after sowing, LL(6WAS) = Leaf Length at 6 weeks after sowing, LB(6WAS) = Leaf Breath 6 weeks after sowing, LLW = Leaf Length at Maturity, LBM = Leaf breath at maturity, NL(6WAS) = Number of Leaves at 6 weeks after sowing, DPW = Dried pod weight, NBM = Number of branches at maturity, NB(6WAS) = Number of branches at 6 weeks after sowing, NL(2WAS) = Number of leaves at 2 weeks after sowing.

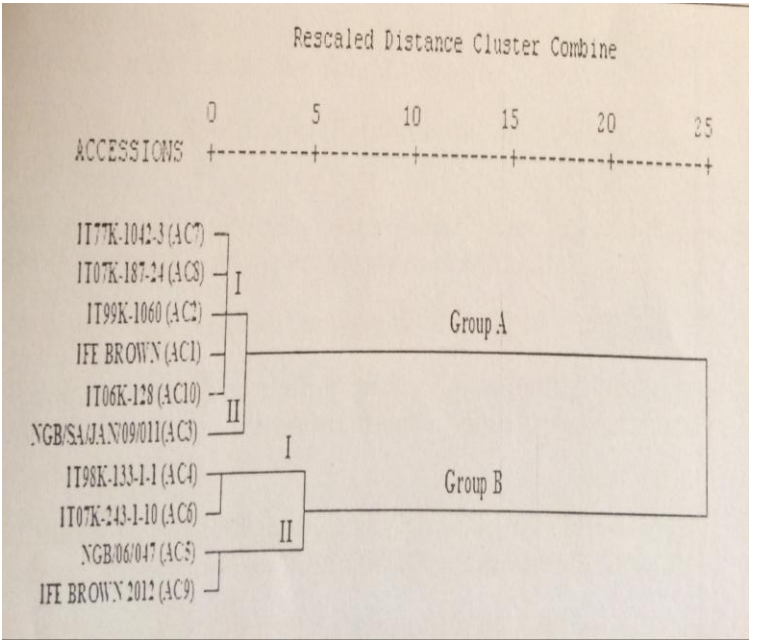


Fig. 8: Dendrogram for the clusters of Groups A and B

Abdulkareem and Mustapha (2014), also examined the performance of cowpea varieties for yield and yield components in Ilorin, Kwara State, Nigeria. Eleven varieties, which were obtained from IITA, Ibadan, were used for the study. The study demonstrated that varieties differed significantly for cowpea yield and yield components. In earlier study, Alege and Mustapha (2007) evaluated 16 cowpea varieties at Ilorin for yield attributes. The results revealed existence of genetic variability among all the varieties for traits investigated. Five varieties, IT 97K-461-4, IT 99K-529-1, IT 99K-429-2, IT99K-1122 and IT 98k-506-1 were recommended for cultivation in this part of the country (Table 7).

Table7: Yield components in 16 cowpea varieties

S/NO	Varieties	Pod number Per plant	Pod length	Pod diameter	Seed per pod
1	IT99K-316.2	8.0 ± 0.71^{bc}	12.22 ± 1.36^{b}	2.54 ± 0.17^{bc}	10.2 ± 2.59^{bcd}
2	IT97K-568.18	10.4 ± 1.81^{ab}	14.66 ± 0.91^{ab}	2.24 ±0.21^{defg}	11.4 ± 2.41^{bc}
3	IT96K-610	11.0 ± 3.16^{ab}	12.70 ± 1.45 ^{bcd}	2.20 ± 0.13 ^{defg}	9.0 ± 2.34 ^{bcd}
4	IT98K-506.1	8.0 ± 2.65^{bc}	15.1 ± 0.43^{a+}	2.28 ± 0.21^{defg}	10.8 ± 2.17^{bc}
5	IT98K-491.4	11 ± 4.71^{ab}	11.78 ± 1.86^{d}	2.12 ± 0.13 ^{fg}	6.8 ± 0.84^{cd}
6	IT98K-491.7	7.2 ± 2.59^{bc}	12.72 ±0.92^{bcd}	2.36 ±0.29 ^{defg}	12.8 ±1.92^{b}
7	IT99K-1060	9.6 ±1.94 ^{bc}	12.98 ± 1.19 ^{bcd}	2.16 ± 0.18 efg	9.0 ±2.34cde
8	IT00K-898-5	8.4 ±2.07^{bc}	12.50 ±1.98 ^{cd}	2.18 ± 0.16 efg	5.8 ±0.84e +
9	IT97K-461-4	12.6 ±3.36^{a+}	12.02 ±1.08 ^{d}	2.52 ±0.13c^{b}	8.4 ±1.81^{cde}
10	IT00K-1150	10.2 ±3.11^{ab}	11.96 ±1.05 ^{d}	2.22 ± 0.16d^{efg}	9.8 ±1.78^{bcd}
11	IT98K-205-8	9.4 ±1.67^{ab}	14.26 ±1.05 ^{abc}	2.40 ±0.19^{cde}	8.8 ±2.16^{cde}
12	IT99K-429-2	10.6 ±3.58 ^{ab}	11.22 ±1.76 ^{d}	2.44±0.29^{cd}	10.6 ±3.51 ^{cb}
13	IT99K-529-2	8.6 ±2.41^{ab}	14.36 ± 2.76 ^{abc}	2.92 ±0.11^{a+}	11.8 ±2.39^{bc}
14	IT00K-901-5-	10.2 ± 1.92 ^{ab}	11.88 ± 1.37 ^{d}	2.02 ± 0.11^{g}	11.0 ± 4.06 ^{bc}
15	IT98K-126-4	11.0 ± 3.74 ^{ab}	14.50 ± 0.84 ^{ab}	2.20 ± 0.10 ^{defg}	10.2 ± 2.49 ^{bcd}
16	IT99K-1122	6.0 ± 1.22 ^{c*}	14.50 ± 0.83 ^{ba}	2.20 ± 0.10 ^{defg}	16.8 ±1.30 $^{a+}$
	FLSD	3.68	1.81	2.49	3.14

Means within the same column followed by the same letters did not differ significantly at $p<0.05$

Research on *Striga*

Mr. Vice-Chancellor Sir ,*Striga hermonthica* (Del Benth.) presents the largest biological constraint to the major food crops in Africa, including cereals and legumes. Two thirds of the 73 million hectares devoted to cereal production in Africa are severely attacked by *Striga* with the greatest damage occurring in Sahelian and Savannah zones. *Striga* is the most parasitic weed species on a world scale. Heavily infested farms are abandoned and occasional migration of farming communities due to *Striga* infestation has been reported (Obilana and Ramaiah, 1992). In term of monetary value, *Striga* caused yield loss of between 28 and 87 million dollars annually in West Africa (Obilana, 1983). Considering the importance of the root parasitic *Striga* as a constraint to pearl millet production in Nigeria, Aladele and Mustapha (2003) in another collaborative work with International Crops Research Institute for the Semi Arid Tropics (ICRISAT) screened 100 pearl millet accessions of West African origin. The accessions were evaluated and scaled down to 22 during year 2000 main season at Babura (Jigawa State) and Maiduguri (Bornu State) in the Sahel ecological zone of Nigeria. Twenty were selected for their low *Striga* count per square meter and two were selected for their susceptibility (Table 8).

Research on *Pennisetum*

Despite the economic importance of pearl millet, its production is often limited by incidence of Downey mildew and smut diseases. This consequently reduced the yield. In this regards, Mustapha and Mustapha (2007), studied the incidence

Table 8: Mean Striga count per square metre at four locations in Nigeria

Variety	Babura	Maiduguri	Bagauda	Minjibir	Mean
DMR12	0.889	0.000	0.111	0.111	0.278
DMR15	0.056	0.000	0.000	0.000	0.014
DMR36-1	0.111	0.000	0.167	0.000	0.069
DMR68	0.056	0.000	0.278	0.000	0.083
ExBornu	0.000	0.056	0.000	0.000	0.014
G.I.14-9	3.278	0.000	0.056	0.167	0.875
G.I.334-2	2.667	0.000	0.000	0.056	0.681
GERO254	0.056	0.500	0.056	0.000	0.153
ICMV88102	0.222	0.000	0.000	0.000	0.056
ICMV89102	0.111	0.000	0.056	0.056	0.065
ICMV91116	0.111	0.000	0.167	0.000	0.065
ICMV94105	0.111	0.056	0.167	0.000	0.083
IKMPI	0.278	0.111	0.167	0.000	0.139
ISMP2	0.222	0.000	0.111	0.111	0.111
LCIC9702	0.222	0.000	0.111	0.000	0.083
LCIMCB11	0.111	0.000	0.056	0.000	0.042
LCICMB3	0.389	0.056	0.056	0.111	0.153
LCICMB6	0.167	0.000	0.000	0.000	0.042
LGP	0.056	0.000	0.167	0.000	0.056
MOURI	0.056	0.000	0.167	0.056	0.069
OKASHANA	0.222	0.000	0.111	0.222	0.139
PURDUE	0.111	0.000	0.111	0.000	0.056
Mean	0.432	0.035	0.096	0.040	0.151
CV%	314	546	196	182	449
Std Deviation	1.106	0.1576	0.037	0.0961	0.4785
LSD 5%	2.233	0.3181	0.073	0.1917	0.9464
Fvalue	1.17^{ns}	0.94^{ns}	1.24	2.45^{ns}	0.98^{ns}

of the two diseases on three improved varieties that were collected from Lake Chad Research Institute (LCRI) Maiduguri and one local variety INMV 55 collected from a local farm in Kano. The study was carried out in Kabuga Area of Kano State for two growing seasons with the view to identify the varieties that are most adapted and suitable as far as severity of diseases is concerned. Our work established that for Downey mildew, local varieties were less susceptible when compared to the improved varieties. Conversely, the improved varieties were found to be resistant to smut disease when compared the local one.

Research on Mutagens

Mr. Vice-Chancellor Sir, geneticists sometimes begin their analysis of genes by examining spontaneous, naturally occurring mutations. However, mutations are rare in nature and researchers need to induce mutations in organisms of interest in order to increase the chance of detecting a relevant mutant. The goal of mutagenesis is to create one mutation at random in the genome of each individual in the experimental population, so that one gene product is disrupted in each individual, leaving the rest of the genome as wild type. During genetic analyses, researchers use a wide range of different mutagens, depending on the type of mutation desired. Ionizing radiation can be used to create chromosome breaks, deletion and translocations. In contrast, chemical mutagens can cause base-pair changes. With these mutagens, a range of mild to severe mutant phenotype can be generated.

Among the dominant cultivated grass family (Poaceae) of the tropical and subtropical regions is *Digitaria. D. exilis* (Haller) is the most important member of a diverse group of wild and domesticated *Digitaria* species native to the savannas of West Africa where it is called Acha . Although Acha is important for its organoleptic qualities, its production is faced with a number of challenges out of which grain yield is the most significant (Morakinyo and Awojobi 1991). Currently, the genetic improvement of Acha centers on germplasm collection and morpho-agronomic characterization with the objective of broadening the crop gene pool. In recent times, chemical mutagens have become important tool in crop improvement. These mutagens are used to induce variability and extended gene pool from which crop disease resistance, high yield and fortified nutrients are produced (Chowdhary and Tah, 2011). In view of the fact that very little information was available on the improvement of *D. exilis* by mutagenesis, Animasaun *et al*. (2014) examined the effect of different doses of nitrous acid on the growth characteristics of the crop to create variability on which selection could be based for the purpose of breeding and

improvement. *D. exilis* seeds obtained from National Cereal Research Institute (NCRI), Moor Plantation, Ibadan were divided into four separate groups and were treated with freshly prepared nitrous acid of 0.1 M for varying times of 2, 4, 6 and 8hrs. Data obtained for different parameters indicated that a shorter time of treatment of 4hrs produced significant variability and desirable effects on the crop. Generally, for all the characters evaluated, 4hrs treatment consistently produced optimal effect on the crop (Table 9).

Table 9: Quantitative (characters at maturity) of nitrous acid treated D. *exilis*

Table 9: Quantitative (characters at maturity) of nitrous acid treated D. *exilis*

Treatments (hr)	NLT	LL (cm)	NPT	IL(cm)	LSL (cm)	LB (cm)	NDM
2	13.89± 1.08^{b}	14.29± 1.03^{b}	6.20± 0.37^{d}	5.1± 0.79^{bc}	6.56± 0.68^{a}	0.70± 0.02^{b}	88.80± 3.78^{a}
4	15.46+ 1.90^{a}	18.09+ 1.40^{a}	6.60+0.60^{ab}	5.74+ 0.84^{b}	5.48+0.48^{abc}	0.78+ 0.02^{a}	83.40+ 4.85^{c}
6	12.94+ 0.46^{bc}	11.51+ 0.96^{c}	5.80+ 0.86^{c}	5.40+ 0.35^{bc}	6.04+ 0.80^{b}	0.70+ 0.03^{b}	84.00+4.03^{bc}
8	12.03+ 0.81^{c}	12.03+ 1.04^{c}	5.40+ 0.81^{c}	5.14+ 0.61^{c}	4.62+ 0.75^{c}	0.56+ 0.04^{c}	84.60+4.00^{bc}
Control	15.18± 2.04^{a}	15.28± 1.15^{ab}	7.20± 0.58^{a}	6.10± 0.44^{a}	6.42± 0.26^{a}	0.76± 0.13^{a}	92.60± 4.12^{a}

Values with same alphabet are not significantly different (P=0.005) along the column.NLT= Number of leaf/tiller, LL= Leaf length, NPT= Node/Plant/tiller, IL= Internode length,LSL= Leaf sheath length, LB= Leaf breadth, NDM= Number days to maturity.

Realizing the effect of chemical mutagens on *D. exilis* Animasaun *et al.* (2014) were spurred to also assess the effects of application of gamma radiation from ^{60}Co source on growth characteristics of the crop. Seeds of *D. exilis* obtained from NCRI, Badegi, Niger State were exposed to Gamma-radiation at Sheda Science Technology Complex (NTC SHESTCO) Abuja, Nigeria. The study established that ionizing radiation mutagenesis could be routinely used to generate genetic variability for breeding of improved crops. In order to increase the likelihood of inducing distinct type of genetic variation in the

crop, gamma ray of 80Gy radiation which consistently produced the optimal effect was recommended for adoption (Fig.9).

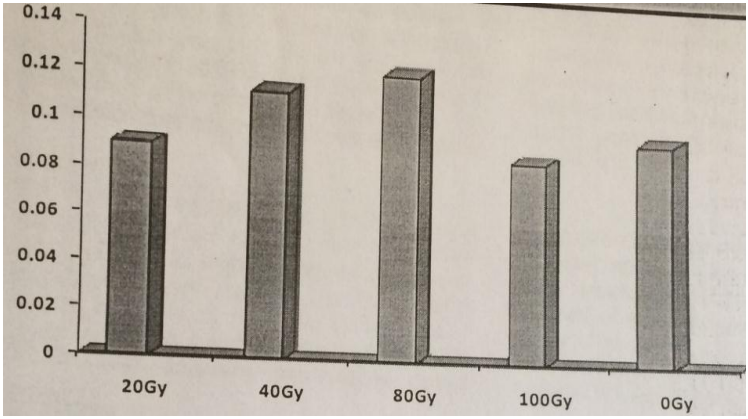


Fig.9: 100-seed weight of M_1 progeny of *D. exilis* exposed to different gamma radiation

Tomato (*Solanum lycopersicon*) is a crop grown worldwide not only for its edible fruit but also for its nutritional values for the wellbeing of mankind. Chemical mutagenesis had been established as an effective and important tool for improving crop yield. However, the response of plant to this mutagenic chemical varies from plant species to another and it is often dose dependent.

Mustapha, in collaboration with other researchers, used sodium azide to induce genetic variability in three accessions of tomato collected from National Centre for Genetic Resources and Biotechnology (NACGRAB) Ibadan, Nigeria (Abdulkareem *et al.,* 2017). Our study established that concentration of sodium azide as low as 1 mM can effectively trigger traits that can help increase farmers turnover in term of marketable fruit yield in all the accession studied (Table 10).

Table 10: Floral and fruit characteristics of sodium azide effect on *S. lycopersicon*

Variety	Treatment(mM)	Number of flowers per plant	Fruit number per plant	Fruit weight per plant
Tropimech	0	2.00[b]	12.00[a]	12.86[a]
	1	10.00[a]	3.50[b]	8.73[b]
	2	0.00	0.00	0.00
	4	4.00[c]	1.50[bc]	2.33[c]
NGB01302	0	2.00a	8.00[a]	0.00
	1	0.00	0.00	1.01[b]
	2	0.50[b]	1.00[b]	0.61[b]
	4	3.50[a]	1.00[b]	9.85[a]
	0	3.00[a]	6.00[a]	7.45[a]
Tima	1	0.00	0.00	0.00
	2	0.00	0.00	0.00
	4	0.00	0.00	0.00

Means with the same letter along a column are not significantly different.

In another work, Mustapha and Abdulkareem (2015) examined the effect of ultraviolet (UV-C) radiation 245 nm on yield and growth of tomato. We were able to establish that tomato fruit yield can be enhanced if the seeds are irradiated for 30 mins (Table 11). We also established that treated seeds matured early when compared to untreated seeds.

Table 11: Floral and fruit characteristics of UV effect on *S. lycopersicon*

Parameters	0	10	20	30 min	40	50	60
No. of flower	18.00	13.20	13.61	17.10	12.26	15.26	13.59
No. of fruit per plant	10.05	8.44	6.22	12.00	5.56	7.20	5.11
Fruit weight	32.43	29.63	33.75	39.79	30.4	30.87	18.87
Fruit length	2.00	2.30	2.33	3.7	1.73	2.23	1.97
Fruit diameter	4.00	2.92	2.45	3.02	1.92	2.40	1.50

Research on Shelf-life of *Solanum*

Fungal spoilage of tomato fruits is common during postharvest activities. Fungal spoilage ravages the fruits and plays a contributory role in postharvest losses of tomato. In the quest for prolonging the shelf-life of tomato fruits, Garuba *et al*. (2018) evaluated the efficacy of interaction of three botanical preservatives and three storage structures. The study revealed that pot-in-pot refrigerator, irrespective of the preservatives, gave the best results in terms of enhancing the shelf life of tomato fruits without compromising its quality

Conclusion

Mr. Vice-chancellor Sir, distinguished ladies and gentlemen, I have within the past forty-five minutes or thereabout delved on chromosome as a tool for classification and food security. A major achievement in the study of chromosome science is the understanding of its dynamicity, replacing the concept of its uniformity and monotonous behaviour. Allelic diversity and heterozygosity occur through mutation (either naturally or artificial) and permit the generation of novel phenotypic variation. It is therefore, pertinent to explore these changes to identify and name plants. This lecture has also highlighted how these changes could be used for crop improvement. If Nigeria must grow her economy, our leaders must address the issue of sustainable food security by providing enabling environment for a top-notch research on chromosome behaviour.

Recommendations

Mr. Vice-chancellor Sir, it has become a customary feature for inaugural lecturers to make some recommendations in line with the theme of the lecture. I wish to make the following brief submissions by way of recommendations

i. There is need to encourage and adopt molecular marker assisted breeding to accelerate yield as it offers tremendous potentials to enhance productivity. For

proper and reliable identification of plants, advance molecular study using barcoding is proposed as the best way of resolving taxonomic difficulties or confusions.

ii. Scientific names of plants being the keys to their literature, Biologists should endeavour to familiarise themselves with scientific names of plants for better understanding of biodiversity.

iii. From experience, students are shying away from Biosystematics for the simple reason of lack of understanding the concept. To avoid shortage of Biosystematists, they should be encouraged to go into Biosystematics aspect of Plant Biology. Plant Cytogenetists and Biosystematists should be motivated to make biosystematics more appealing to students.

iv. The University should endeavour to establish a Molecular Biology Laboratory in the Department of Plant Biology to augment the service rendered by Central Research Laboratory of our better by far University.

v. Government should evolve a policy that will create a synergy between Universities and Industries. This will go a long way to make them benefit from researches carried out in the Universities to avoid such report from gathering dust on the shelves. To boost crop performance, extension workers should encourage and educate farmers to use developed varieties produced as a result of researches in the Universities and other research institutes.

vi. Biosystematics laboratories in the Universities in the country should be equipped with state of the art equipment to make preparation of metaphase chromosomes easier for students.

vii. Research Institutes owned by the Federal Government should be well funded to enhance sustainable food security.

viii. Adequate gene banks of crop species should be maintained and constantly updated with new materials to avoid extinction of endangered species.

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