UNIVERSITY OF PORT HARCOURT

TAXONOMIC COMPLEXITIES AND MOLECULAR DIVERSITY: ANCIENT AND MODERN

An Inaugural Lecture

By

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ORDER OF PROCEEDINGS

2.45P.M.   GUESTS ARE SEATED

3.00P.M.   ACADEMIC PROCESSION BEGINS

The procession shall enter the Ebitimi Banigo Auditorium, University Park, and the Congregation shall stand as the procession enters the hall in the following order:

ACADEMIC OFFICER
PROFESSORS
DEANS OF FACULTIES/SCHOOL
DEAN, SCHOOL OF GRADUATE STUDIES
PROVOST, COLLEGE OF HEALTH SCIENCES
LECTURER
AG. REGISTRAR
DEPUTY VICE-CHANCELLOR (RESEARCH & DEVELOPMENT)
DEPUTY VICE-CHANCELLOR (ACADEMIC)
DEPUTY VICE-CHANCELLOR (ADMINISTRATION)
VICE CHANCELLOR

After the Vice-Chancellor has ascended the dais, the congregation shall remain standing for the University of Port Harcourt Anthem.

The congregation shall thereafter resume their seats.

THE VICE-CHANCELLOR'S OPENING REMARKS.

The Ag. Registrar shall rise, cap, invite the Vice-Chancellor to make his opening remarks and introduce the Lecturer.

The Lecturer shall remain standing during the Introduction.

THE INAUGURAL LECTURE

The Lecturer shall step on the rostrum, cap and deliver his Inaugural Lecture. After the lecture, he shall step towards the Vice-Chancellor, cap and deliver a copy of the Inaugural Lecture to the Vice-Chancellor and resume his seat. The Vice-Chancellor shall present the document to the Registrar.

CLOSING
The Ag. Registrar shall rise, cap and invite the Vice-Chancellor to make his Closing Remarks.

THE VICE-CHANCELLOR'S CLOSING REMARKS.
The Vice-Chancellor shall then rise, cap and make his Closing Remarks. The Congregation shall rise for the University of Port Harcourt Anthem and remain standing as the Academic [Honour] Procession retreats in the following order:

VICE CHANCELLOR
DEPUTY VICE-CHANCELLOR (ADMINISTRATION)
DEPUTY VICE-CHANCELLOR (ACADEMIC)
DEPUTY VICE-CHANCELLOR (RESEARCH & DEVELOPMENT)
AG. REGISTRAR
LECTURER
PROVOST, COLLEGE OF HEALTH SCIENCES
DEAN, SCHOOL OF GRADUATE STUDIES
DEANS OF FACULTIES/SCHOOL
PROFESSORS
ACADEMIC OFFICER

ACKNOWLEDGEMENTS

fellowships transformed my research and teaching, and eventually distinguished me in plant biotechnology.

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Mr. Vice Chancellor, this journey is indeed a long one and many have played roles that cannot be overlooked. Permit me Sir, to acknowledge the spiritual roles of Ven. Dr. S.T. Nbete and The Rt. Rev. Mba N. Idika. These have stood in the gap for my family. To Bro. Aham (Aham Eke-Ejelam, SAN) and my friend, Aham Ucheobi, thanks for all your support and encouragement through these years.

Without students, lecturers have no job, and probably, I will not be standing here to give this lecture. Therefore, I appreciate all my students especially those I supervised their dissertations and theses including Drs. B.A. Odogwu, C. Ekeke, E. Roberts Inala, F. Obianefo, T.N. Udeagbala, F. Awala, A. Chukwu, and S. Chuku from Plant Science & Biotechnology, and Drs. C.U. Nebo, K.C. Nwogbidi, and U.B. Uzodinma, L.T. Daniel-Bille, Sally Bonn, and M.P. Solomon from Institute of Natural Resources, Environment & Sustainable Development. I learnt so much working with these former students.

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1.0. Introduction

Mr. Vice Chancellor and distinguished audience, I shall begin this lecture with a quote from Onofeghara (1986). Professor Francis A. Onofeghara, the first Professor in the Department of Botany (now Plant Science & Biotechnology), University of Port Harcourt while delivering the third inaugural lecture of the University stated that "***An inaugural lecture is an academic exercise, an occasion to survey one's field, to explain what it is one does, to demonstrate its relevance and to place one's contributions in their proper perspective. It provides an opportunity for one to tell his mixed audience what he claims to profess***." Mr. Vice Chancellor, this quote from the late academic sage and Professor of Botany is inspirational and offers guidance on how a professorial inaugural lecture should be framed. I hope that I am able to follow the lead of late Professor Onofeghara in effectively conveying the relevance of my field of study, not only to the academic community in this esteemed institution, but also to society as a whole.

1.1. God, the Originator of Names and the first Plant Taxonomist

Mr. Vice Chancellor and distinguished audience, I shall commence by reminding us that plants emerged directly from the spoken words of God, the Supreme Creator. The Holy Bible provides this golden proclamation:

- Then God said, "Let the land produce ***vegetation***: seed-bearing ***plants*** and ***trees*** on the land that bear fruit with seed in it, according to their ***various kinds***." And it was so. The land produced vegetation: ***plants*** bearing seed according to their ***kinds*** and ***trees*** bearing fruit with seed in it according to their ***kinds***. And God saw that it was good – Genesis 1: 11 – 12.

In the above golden proclamation lies the origin of diversity of plants on earth. In Genesis 2: 9, God the taxonomist, named

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the first two trees: *Tree of Life* and *Tree of Knowledge of Good and Evil*. These names were the first names given to an organism to differentiate it from other organisms. This was before God created man and gave the first man the name **Adam**. While God showed his attachment to plants by naming the first two plants, **He** handed over the naming of "animals and all birds of the air" to **Adam** – Genesis 2: 19 – 20.

The diversity of plants therefore began with the conscious use by God of the words *plants* and *trees* and *their various kinds* not *plant* and *tree*. Figuratively, God signified the different types of *plants* and *trees* (*their various kinds*) with specific characteristics as seen in the world today. In these lie the **origin** of **diversity** of *plants* and of course, **animals** (Plate 1).

Plants are found almost everywhere. They thrive in aquatic, terrestrial and mountainous environments. They are the only organisms that manufacture food and feed other organisms on earth through **photosynthesis**, a complex biochemical process that harnesses the energy of the sun. In addition, plants provide uncountable and diverse medicine for man and animals, clothing, shelter, purifies and decorates man's environment with unusual beauty, and are crucial in man's economy. God was methodical in the process of creation. **He** created *water* and the *land* before *plants*. Both *water* and *land* provide functional habitats for *plants* and their diversities, hence the need to have created them first. Immediately after the creation of *plants*, came sunlight, an enabler of photosynthesis, the food manufacturing machinery. Thus, food, clothing, shelter, and medicine all from plants, were "ready" before God proceeded with creating the animals that live in water and on land, birds of the air and even the first human being in **Adam**.

Mr. Vice Chancellor and distinguished audience, the point of all this is that God is the first **plant taxonomist** and the originator of the concept of diversity in plants. If the concept of plant diversity and the origin of plant names can be traced to God's word as written in the Holy scriptures, then taxonomy is indeed an **ancient science**.

Plate 1: *The Garden of Eden* by Jan Brueghel the Elder and Pieter Paul Rubens, c. 1615, depicting both domestic and exotic wild animals such as tigers, parrots, and ostriches co-existing with different trees

1.2. A World Without Names is Complex and Confusing

Mr. Vice Chancellor, imagine that, as we processed into this auditorium to start this inaugural lecture, there were no names or means of identifying those of you seated at the podium. Imagine that titles such as Vice Chancellor, Deputy Vice Chancellor, and Registrar were non-existent. Certainly, this would present us with a confusing and complex situation. It would be even more confusing and complex if the Principal

Officers and individuals in the audience were all called "man". Such a confusing scenario can occur when the Public Relations Officer, who is simply called "man", picks up the microphone to introduce the Vice Chancellor who is also referred to as "man". Because everyone in the auditorium is called "man", anyone can come up to the podium to give the opening remarks reserved for the Vice Chancellor. This example emphasizes an important point I would like to make in this lecture: *without a name there is no identity*. Providing or giving identity by way of a unique name to every living organism, which as noted earlier was started by God in the Old Testament of the Holy Bible, is the major thrust of the science of taxonomy. The name of any living or non-living object is given based on certain attributes and characteristics. Thus, the name Vice Chancellor, identifies a certain person based on certain attributes. It is an identity.

The microphone in my hand is named so based on certain attributes. It is different from the loudspeaker, amplifier, projector and screen. The country Nigeria is different from Ghana, Togo is different from Senegal, and so on. Nations of the world differ from each other based on certain attributes. Their names identify them and tell you the part of the world where they are located. Imagine a world without names of countries and one where continents are unnamed. Imagine that no names are given for climatological variations in the earth such as temperate or tropical. How can a building where books are kept be located if the building is not named "library" to differentiate it from a hospital, supermarket or restaurant? Of course, libraries, hospitals, supermarkets and restaurants are housed in buildings that are designed differently. Such differences in building design reflect certain attributes for which they derive their names. How can you have books in a library that are not sorted into categories and titles, or a

supermarket without clearly defined sections and specific names for each product? Have you wondered what *barcodes* are on every product in a supermarket? They help name and identify a product based on its unique attributes and corresponding price. Imagine a restaurant in which food choices in the menu are unnamed, or your kitchen, where granulated sugar and salt are unlabeled. Imagine chemicals on a laboratory table without names – water, hydrochloric acid, sulphuric acid, amongst others – all in amber bottles on the laboratory rack or chemical store without names. No doubt, that will be suicide. From a geologist's perspective, rocks and stones are not the same. Objects within these broad categories have specific names based on certain characteristics. The international trade of precious stones requires proficiency in naming and characterizing stones. Without such proficiency, the risk of misclassifying a precious stone becomes greater, which in turn could reduce the true value of that stone.

The importance of naming is also important in human morphology and anatomy. For example, every part of the body has a name. The head, eye, ear and nose are all names. Every bone has a name. You cannot refer to ulna as radius, fibula as tibia or humerus as femur. In plant morphology, a root is not called a stem, or leaf a flower. Xylem and phloem are names and mean different things. The names, which are based on certain attributes, characteristics and functions (Plates 2 & 3), must be used appropriately or else confusion sets in. What if bones, parts of plants, and organs of animals did not have names?

Without a name and names, we will certainly have a chaotic, complex and confusing world. Taxonomy minimizes chaos and resolves complexities and confusion. **What then is Taxonomy?**

Plate 2: Parts of a Plant

Plate 3: Parts of a Human
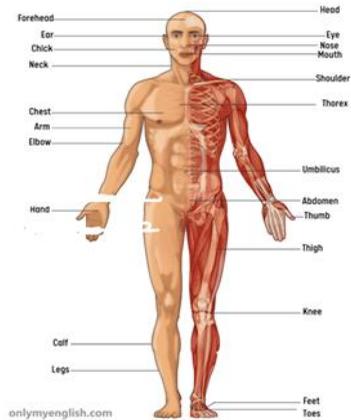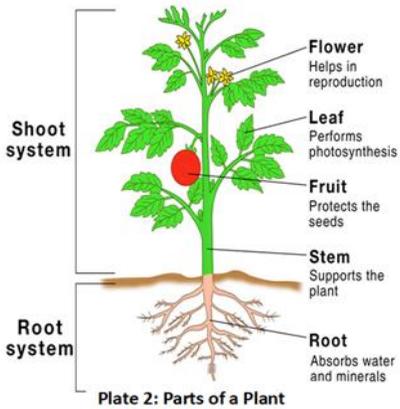
1.3. Definition and Explanation of Taxonomy and Taxonomic Terms

Taxonomy is coined from two Greek words, namely, *taxis* (meaning arrangement) and *nomos* (meaning rules or laws). It is the study of the 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 classification (Stace, 1989). Plate 4 provides an example of variation in plants.

Mr. Vice Chancellor and distinguished audience, implicit in the definition of taxonomy is the fact that the science is not simply the naming of organisms. It is unfortunate that some scientists from other disciplines have over the years, reduced the significance of the science of taxonomy to a simple exercise of naming organisms. In reality, this is not the case. Taxonomists possess knowledge that enables a better understanding of life and the processes that sustain it. A taxonomist must not only be able to describe, but also

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understand and explain the underlying factors that lead to the variation of organisms. Such factors include morphological, ecological, phytogeographical, physiological, anatomical, genetic, phytochemical and palynological attributes. A taxonomist must be broadly trained in field and laboratory experimentation, have capacity to conduct investigations and understand how the aforementioned factors, which are called lines of taxonomic evidence, bring about variation in organisms. It is the data generated from such investigations that are used in the classification and eventual naming of organisms. Taxonomy is therefore dependent on results obtained from a broad range of investigations and studies from other scientific disciplines, to generate data applied in classification. A taxonomist must possess a good background knowledge of scientific disciplines that provide data for the classification and naming of organisms. In most cases, a taxonomist is a seasoned professional in one or more of these disciplines. As such Vice Chancellor Sir, a taxonomist is figuratively "*jack of all trades*, *master of them all"*. This point is further elaborated in Figure 1. The common axiom amongst taxonomist is that "*taxonomy is synthetic*", which means that taxonomy has no data of its own, but derives her data for classification and naming from other scientific disciplines. Herein lies the complexities of the science of taxonomy and its practitioners. What can be more complex and tasking than for one discipline to raise experts who depend on information and knowledge from several other disciplines to impact knowledge?

Systematics – This is the scientific study of the kinds and diversity of organisms, and of any and all relationships between them (Simpson, 1961). Systematics was recognized as a more inclusive field of study concerned with understanding the diversity, naming, classification and evolution of

organisms. It is noteworthy that the scope of taxonomy has broadened in recent years such that taxonomy and systematics are now synonymous.

Plate 4: Diversity of Plants
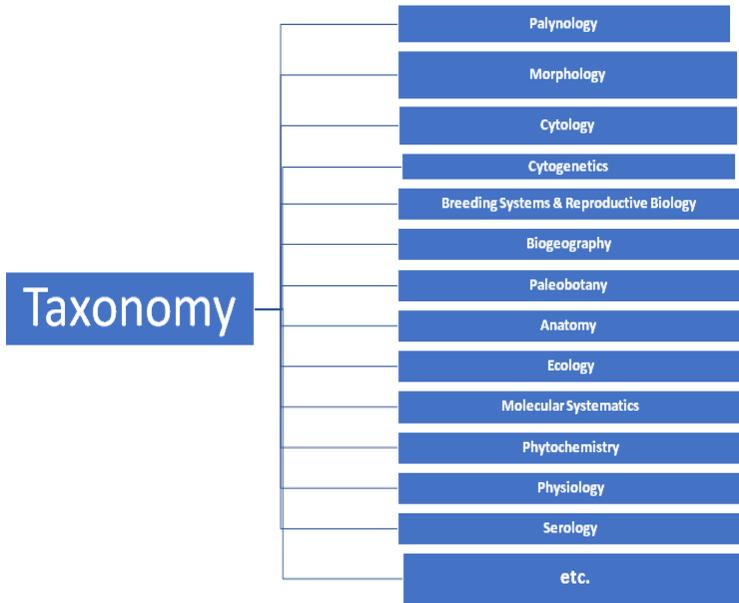
Figure 1: Lines of Taxonomic Evidence or Sources of Taxonomic Data

Classification – This is the production of a logical system of categories, each containing any number of organisms, which allows easier reference to its components. More simply stated, classification is the ordering of organisms into groups or sets based on their relationships. An example for a layman or non-taxonomist is the setting in a supermarket (Plate 5).

In supermarkets, the shelves, which represent taxonomic categories or groups, bear name tags covering a broad product area such as toiletries. This broad product category will certainly contain individual products with shared characteristics. For the purpose of this presentation, I will compare supermarket products to organisms. These individual products (organisms), which may be 10 to 50 types or more, bear specific names and have similarities that form the basis for which they are grouped. Grouping products facilitates

easier reference. Sometimes, partitions are provided on the shelves to ensure that the more closely related or the same products, stay together. Classifying goods in a supermarket into product categories and providing products with specific names makes shopping easier.

Plate 5: The shelves in a supermarket is a logical system of categories depicting classification. Each shelf, which for the purpose of this presentation is like a taxonomic category or group, contains several products. Typically, the shelves house similar products and are stacked together for easier reference.

The example of grouping products in a supermarket based on common characteristics is similar to the role that classification plays in taxonomy. By logically grouping organisms together based on their shared (i.e., relatedness) characteristics, classification provides the data and paves the way for the correct naming of organisms.

Identification or **determination** – This is the naming of an organism by reference to an already existing classification system.

Nomenclature - This is the study of the system and methods of naming organisms, and the construction, interpretation and application of the regulations governing the system. The regulations governing the system is provided by the International Code of Nomenclature for Algae, Fungi, and Plants (ICN) published by the International Association of Plant Taxonomy (IAPT).

Taxon (plural, taxa) - is any taxonomic grouping, such as a phylum, a family or a species. It is a useful general term that indicates the rank of a group and the organisms contained within that group.

A **description** of a taxon is a statement of its characteristics, which constitutes the definition of that taxon.

Characters are attributes that contribute to a taxonomic description. These attributes are known as taxonomic or systematic characters.

Name is a word or set of words by which a person or thing is known, addressed, or referred to.

Biodiversity (**Biological Diversity**) – This is the totality of all species, animals and microorganisms and the ecosystem and ecological processes which drives all natural system (Ndukwu, 2012). It is the variety and variability among the living organisms (plants, animals and microorganisms) from all terrestrial ecosystems, and the ecological complex of which

they are part, and this includes the diversity within the species, between the species and of the ecosystem (UNCED, 1992).

3.0. The Need for and Importance of Taxonomy

Mr. Vice Chancellor and distinguished audience, the need for and importance of taxonomy can be inferred from its main aim, which is to identify, characterize, classify, and give specific names to all the living organisms according to their characteristics. The underlisted are among the reasons why taxonomy is important and needed in human endeavours:

i.   "The urge to classify is a fundamental human instinct; like the predisposition to sin, it accompanies us into the world at birth and stays with us to the end" (Hopwood, 1959).

ii. Taxonomy is the knowledge base for understanding the diversity of life on earth and the interrelationships among different groups of organisms.

iii. Taxonomy is both the '*queen*' and '*servant*' of biology and related disciplines (Figure 1). Taxonomy is a 'queen' in the sense that it rises above all other fields of biological and scientific research. All other biological/scientific research fields requiring the establishment or improvement of a classificatory system depend on it. Taxonomy is a 'servant' because one of its primary functions is to provide basic services on the identity and probable close relatives of organisms. The services offered by taxonomy are most impactful to those conducting research in biology and other related areas. For instance, genetics, conventional and molecular breeding and biochemical studies that play important roles in plant improvement (agricultural and horticultural crop plants, medicinal plants, amongst others), require that researchers in these fields establish the identity and natural relationships of the plants they are working on. It is common knowledge in breeding that wild relatives of crop plants provide a rich source of disease resistant,

desirable and novel genes. Relying on taxonomic information to identify these wild relatives so they can be used in the improvement of crop plants, is a continuous science (Subhojit *et.al.,* 2013; Patil *et. al.,* 2014; Agbagwa *et.al.,* 2015; Patil *et. al.,* 2015; Agbagwa *et.al.,* 2018).

iv. A taxonomist is required to describe each organism and be able to characterize it morphologically. A taxonomist gives an organism a name so that others may recognize it and distinguish it from a host of similar organisms.

v.   Research conducted on an unnamed organism is an effort in futility. Without any information on the identity of an organism, any results on this organism would be erroneous. Thus, taxonomy is the foundation of the various scientific disciplines dealing with organisms. As a matter of fact, you must know the identity of an organism before you can communicate information about that organism.

vi. As shown in **Table 1,** over seven million species of plants and animals live on the planet (Chapman, 2009). When you add groups as lichens, algae, mushrooms, and microorganisms such as bacteria, which recent classification schemes do not consider as plants or animals, the earth is estimated to have 11.3 million species. However, less than 1.5 million organisms have been identified with specific names. With regard to plants, it is estimated that there are 390,900 different plant species, which have been identified and known to science. In 2019, botanists registered 1,942 newly named species of vascular plants on the International Plant Names Index. These newly named plant species were mainly flowering plants, ferns and gymnosperms. Mycologists, on the other hand, recorded 1,886 novel fungi on the equivalent Index Fungorum (Antonelli, *et.al*., 2020). From the southeastern part of Nigeria, Agbagwa and Ndukwu (2004) characterized, identified and reported a new species of

Gnetum. Furthermore, Agbagwa and Okoli (2007) characterized, identified and reported a new species of *Abrus*. The number of unidentified species keeps increasing, leading to more work for taxonomists.

Table 1: Estimates of the total number of living plant and animal species on earth (Chapman, 2009)

Category	Species	Totals
Vertebrate Animals		
Mammals	5,500	
Birds	10,000	
Reptiles	10,000	
Amphibians	15,000	
Fishes	40,000	
Total Vertebrates		80,500
Invertebrate Animals		
Insects	5,000,000	
Arachnids	600,000	
Molluscs	200,000	
Crustaceans	150,000	
Echinoderms	14,000	
Others	791,830	
Total Invertebrates		6,755,830
Plants		
Flowering plants (angiosperms)	352,000	
Conifers (gymnosperms)	1,050	
Ferns and horsetails	15,000	
Mosses	22,750	
Total Plants		390,800
TOTAL SPECIES		7,227,130

vii. In 2015, the Royal Botanic Garden (RBG) Kew reported that 2,034 new plant species were discovered. The report warned that 21% of plants are at risk of extinction due to threats from climate change, habitat loss, disease and invasive species. It also stated *inter alia,* "It's really important to know how many plant species there are, where they are and the relationship between the groups, because plants are absolutely fundamental to our well-being. They provide us with our food, our fuel, our medicines - even controlling our climate."

viii. Taxonomists can save the world from confusion by correctly identifying organisms, by providing an accurate number of species on earth, by increasing awareness of the threats of extinction, and by documenting species that have gone extinct.

ix. Plants are important in themselves and directly determine the diversity of many other taxonomic groups by providing shelter, food and defense.

x. Biodiversity and taxonomy- Biodiversity is declining at an unprecedented rate because of human activities. Therefore, decisions must now be taken to reverse this trend. How do decision-makers decide where to establish protected areas if they do not know what is being protected? How can regulators identify and combat harmful invasive species if they cannot distinguish them from native species? How do developing countries ensure that they reap the benefits of the use of their biological diversity, if they do not know the biological diversity that is being used? How will researchers know, which new plants and animals have potential use for the pharmaceutical industry? How will new plants, animals and microorganisms that benefit the food and beverage industry be discovered? Taxonomy provides a basic understanding about the components of biodiversity,

which in turn is necessary for effective decision making about conservation and the sustainable use of natural resources.

xi. Taxonomy is the foundation of all the various scientific disciplines dealing with organisms. It guides policy and regulatory bodies in making informed decisions on conservation strategies and provides pivotal services for many industries such as agriculture and the production of pharmaceuticals. Taxonomy also supports poverty alleviation, combating disease and environmental sustainability by directly or indirectly supporting eight of the seventeen Sustainable Development Goals (SDG) namely: SDG 1 (No Poverty), SDG 2 (Zero Hunger), SDG 3 (Good Health and Wellbeing, SDG 11 (Sustainable Cities and Communities), SDG 12 (Responsible Consumption and Production), SDG 13 (Climate Action), SDG 14 (Life Below Water), and SDG 15 (Life on Land).

xii. Taxonomy establishes a reference system for the naming of organisms.

4.0. Taxonomy: A Brief Historical Perspective

Mr. Vice Chancellor, we have established that there is a great diversity of organisms on earth. We have also established that variations amongst organisms although complex, is fascinating. Such complexity requires the need for a robust classification system. Every scientific field and subject, has a history. Taxonomy has a history. Therefore, permit me to present an abridgement of the history of the science of taxonomy.

4.1. Folk Taxonomy and Common Names

We noted earlier that "*the urge to classify is a fundamental human instinct that accompanies us into the world at birth*".

Also, "God created us in His own image (Genesis 1: 27)" meaning that the ingenuity of God is in man to tackle complexities like the issue of naming organisms. Thus, in early civilizations, man applied ingenuity and sharp instinct, and recognized, which plants could be used as food, which to use as fuel, which to use as shelter, which was poisonous and which could compete with crops (i.e., weeds). Each tribe or community developed folk names for plants and animals based on certain characteristics and properties that were well known to them. Those names are known as folk names, while the practice of naming is called folk taxonomy. Folk taxonomy is therefore a vernacular naming system and is considered as a prescientific classification. Generally, common names are the English equivalent of folk names. **Tree of Life** (*'ēṣ haḥayyīm* – Eitz Chaim) and **Tree of Knowledge of Good and Evil** (ʕesʕ hadaʕaθ tˤov wɔrɔʕ) were the first folk names ever used for organisms.

Folk taxonomy for plants was based on three things: (i) uses, (ii) perceived relationship, e.g., taste and smell, and (iii) cultural importance. It is noteworthy that external appearance (i.e., morphology) played roles in folk taxonomy. However, folk taxonomy depended more on smell, taste, nutritional values and uses of the plant. An important feature of folk taxonomy was that the name given to members of a group showed easily identifiable characteristics of the group. Although folk taxonomy is regarded as prescientific, folk names of plants and animals are still in use today and will continue to be used by ethnic groups and tribes as a means of identification. Common examples of the naming system in folk taxonomy are shown in Table 2.

Table 2: Examples of Folk Taxonomy

	Folk Name		Common Name (English)	Scientific Name	Family
	Igbo name	Yoruba name			
1	Ebele	Igiigba	Calabash Tree	*Crescentia cujete*L.	Bignoniaceae
2	Ebele	Igba	Calabash Plant	*Lagenaria siceraria*(Molina) Standl.	Cucurbitaceae
3	Ube	Pia	Pear	*Dacryodes edulis* H.J. Lam.	Burseraceae
4	Ube bekee	Pia oyinbo	Avocado pear	*Persea americana* Mill.	Lauraceae
5	Nmimi	Ata igbere	Pepper fruit	*Dennettiatripetala* Bak. F	Annonaceae
6	Ose	Ata	Pepper	*Capsicum frutescens* L.	Solanaceae
7.	Uziza	Ata iyere	Pepper plant (black pepper)	*Piper nigrum*	Piperaceae
8	Uziza	Ata iyere	Pepper plant (black pepper)	*Piper guineense*	Piperaceae
9	Oseoji	Ataare	Alligator pepper	*Aframomummelegueta*K. Schum	Zingeberaceae
10	Ukwa	Afon	Breadfruit	*Artocarpus communis* J.R.Forst. &G.Forst.	Moraceae
11	Ukwa	Afon	Breadfruit, wild jackfruit	*Treculia Africana*Decne.	Moraceae
12	Oji	Obi	Kola	*Cola acuminate* (P Beauv.) Schott. &Endl.	(Sterculiaceae) Malvaceae
13	Oji	Obi	Kola	*Cola nitida*(Vent.) Schott. &Endl.	(Sterculiaceae) Malvaceae
14	Ngwo	Ogoro	Raffia	*Raphia hookeri*G.Mann&H.Wendl.	Arecaceae
15	Ngwo	Ogoro	Raffia	*Raphia vinifera*P.Beauv.	Arecaceae
16	Oroma, afufa	Osan	*Orange	*Citrus sinensis* (L.) Osbeck.	Rutaceae
17	Udara	Agbalumo	Star apple	*Chrysophyllum albidum* G. Don	Sapotaceae
18	Opo	Ogedeagbaga	Plantain	*Musa paradisiaca* L.	Musaceae
19	Aku bekee	Agbon	Coconut	*Cocos nucifera* L.	Arecaceae
20	Mangolo	Mangoro	Mango	*Mangifera indica* L.	Anacardiaceae
21	Afufa, anara	Igba	Garden egg	*Solanum melongena* L.	Solanaceae
22	Nkwu	Igiope	Oil Palm Tree	*Elaeisguineensis* Jacq.	Arecaceae
23	Okwuru	Ila	Okra, Ladies' finger	*Abelmoschus esculentus* (L.) Moench.	Malvaceae
24	Ji	Isu	Yam	*Dioscorea*L.	Dioscoreaceae
25	Ji-apu	Ege or Gbaguda	Cassava	*Manihot esculenta*Crantz.	Euphorbiaceae
26	Ahuekere	Epa	Groundnut	*Arachis hypogea* L.	Fabaceae
27	Nkwaba	Opeoyinbo	Pineapple	*Ananas comosus* (L.) Merr.	Bromeliaceae

*Orange is a common name for several fruits from different citrus plants

Folk names and by extension folk taxonomy, still find use and relevance today. For example, books classifying herbs, shrubs and trees based on their uses, sizes and habits, are still common to this day. Folk taxonomy as a classification system, however, is greatly encumbered by the following:

i.   Folk names come in one language representing a particular ethnic group or tribe as shown in Table 2. They are not universal. Thus, each species has a name given to it by every ethnic group or tribe, which is different from that of another ethnic group or tribe. For instance, the word ube, the Igbo name for *Dacryodes edulis*, means completely nothing to a Hausa, Yoruba or native Indian. It is even possible that within the aforementioned tribes, the word ube may exist, but the term refers to a different plant, animal or inanimate object. Therefore, the word ube means nothing to a non-Igbo person. This implies that ube does not confer identity to the species concerned. As such, the whole essence of a name is eroded. A taxonomical name should identify an organism universally. The palm wine trees *Raphia hookeri* and *Raphia hookeri* are both known with the same common name, raffia (Table 2). In Igbo, they are both called *ngwo*, *ogoro* in Yoruba and *ukot* in Efik. This further buttress the inconsistencies in folk names.

ii.   Several instances exist where two or more unrelated plants are known by the same folk or common name (Table 2, Plate 6).

iii.   Often in one ethnic group or tribe, a single species may have two or more folk names applied either in the same or different localities. This is the case with *Musa paradisiaca* (i.e., plantain) and *Dialium guineense* (i.e., velvet tamarind) among the Igbos.

iv. There are several species that do not even have folk or common names. Folk taxonomy provides names for just a handful of plants mostly food crops, fruits and vegetables.

v. Folk and common names usually do not provide information indicating family or generic relationships (Table 2). For example, the calabash tree and calabash plant belong to different families but are both called calabash. The same can be said for the different pears and peppers, e.g., pepper, pepper fruit, pepper plant, alligator pepper (Plate 6b).

vi. As a result of the above, folk and common names lack predictivity.

Plate 6a: showing unrelated plants known by the similar common name (a) *Crescentia cujete* (calabash tree) Bignoniaceae; (b) *Lagenaria siceraria* (calabash) Cucurbitaceae

Because folk taxonomy lacks predictivity, a globally-accepted system of classification is required. The need for a universally-accepted system is further necessitated by the millions of organisms that need to be classified, identified and named. In the case of naming plants, information on a specific plant or group of plants in one locality, region, country and even over an entire continent, demands a universally accepted system of classification. This classification system should be **predictive** in assigning a name to an organism similar to a fingerprint in the case of human beings. Ideally, a plant named *Dacryodes edulis* in Nigeria, will refer to the same plant in Congo, India, and elsewhere in the world.

Plate 6b: showing unrelated plants known by the similar common name (a) *Piper guineense* (black pepper) **Piperaceae**; (b) *Dennettia tripetala* (pepper fruit) **Annonaceae**; (c) *Capsicum frutescens* (pepper) (**Solanaceae**); (d) *Aframomum melegueta* (alligator pepper) (**Zingerberaceae**).

4.2. Concept of Predictivity

The **Concept of Predictivity** in **Taxonomy** suggests that a name given to an organism, or a group of organisms, based on certain characteristic features, should be the same anywhere in the world. The name given to an organism should allow anyone to recognize relatives of that organism including those members that have yet to be assigned a name. Stace (1989) in reviewing this important concept in taxonomy, drew attention to the lack of predictivity of the *Sexual System*, a plant classification system put forward by Linnaeus (1735). This classification system, which then became almost universally accepted, simply depended on the number of stamens in each flower, and classified all known plants into 24 classes. This classification system was simple, popular and easy to use in identifying plants because it was based primarily on a single character. The use of a single character such as stamen can be compared to the use of taste as a character. The use of a single character, such as stamen, can be compared with the use of taste, shape or size as a character, as applied in folk taxonomy and the classification of inanimate objects. The Linnaean Sexual System ended when it was discovered that unrelated plants were classified into same groups when only stamen characteristics were considered. To this point, Stace (1989) stated "*In the class Diandria (two stamens), for example, may be found (amongst others) the genera Circaea, Salvia and Anthoxanthum. Nowadays these genera are placed in three quite different families (*Onagraceae, Lamiaceae and Poaceae *respectively), the remainder of each of which appeared in Linnaeus' scheme in separate classes (*Octandria, Didynamia and Triandria*). In other words, a plant belonging to the* Diandria *had, by definition, two stamens; but nothing else is implied or can be deduced about the plant. It might be an enchanter's nightshade, a sage or a grass. On the other hand, if one discovers that a plant belongs to the grass family*

*(*Poaceae*), one can immediately infer a great deal of information about it—its peculiar floral morphology and anatomy, its unique seed structure and many other general anatomical, cytological and chemical characteristics. These inferences are likely to prove well-founded, even in respect of a grass not previously investigated, because virtually all grasses possess a basic uniformity, which applies equally to undiscovered and to fully studied species. Thus, the very statement that a plant belongs to the* Poaceae*, if correct, automatically predicts many features that will be applicable to that plant. A classification, which enables one to carry out this operation successfully, is a predictive classification, and predictivity is one of the most obvious criteria that can be used to assess how good a classification is*" (Plate 7 - examples of Poaceae). Classification systems relying on one or a few characters are regarded as artificial systems or artificial classification. Because the Linnaean sexual system relies solely on stamen characteristics, it is considered an artificial system. Such systems have low predictivity. By contrast, natural classifications that are based on many characters and different lines of taxonomic evidence, are highly predictive (Agbagwa, 1997 on *Cucurbita*; 2002 on *Abrus*; Ekeke *et.al.,* 2014 on *Combretum*).

Plate 7: *Predictivity* depicted in different general of Poaceae (grasses). a) *Zea mays* (maize); b) *Saccharum officinarum* (sugar cane); c) *Oryza sativa* (rice); d) *Panicum maximum* (elephant grass); e) *Sorghum arundinaceum* (wild sorghum); f) *Acroceras zizanioides* (oat grass). Notice similar leaf and inflorescence morphology all through

Mr. Vice Chancellor and distinguished audience, the word **character** has been mentioned several times throughout this lecture, but it has not been properly defined within the context of taxonomy. Character or taxonomic character is defined as "any attribute of form, structure, physiology or behaviour, which is considered separately from the whole organism for a

particular purpose such as comparison, identification, or interpretation" (Davis and Heywood, 1967). In more general terms, "any expressed attribute" of the organism that can be measured, counted, or otherwise assessed may be called a character. ***Character***, ***character-state***, and ***characteristic*** have often been used interchangeably. This should be discouraged as much as possible because while character is the particular attribute that the taxonomist considers and uses for classification purposes, the various expressions of each character are called character-states. This concept is demonstrated in Table 3. A character may have different character-states. A character-state exclusive to a particular taxon (i.e., species, genus, etc.) is *characteristic* to that taxon/group. One example supporting the concept of character-state is in the Arecaceae (i.e., Palm family or Palmae) where a large quantity of clear liquid in fruit endosperm is *characteristic* to *Cocos nucifera* (coconut) (Plate 8a). This clear liquid is called coconut water. Another example of character-state can be found within the Fabaceae (Leguminosae). Papilionaceous corolla (Plate 8b) is *characteristic* to the subfamily Papilionoidea. According to Sivarajan and Robson (1991), "bladders and pitchers are *characteristic* to the insectivorous taxa, *Utricularia* and *Nepenthes,* respectively" (Plate 8c and d). While *Utricularia* belongs to the Lentibulariaceae, *Nepenthes* is of the monotypic family Nepenthaceae. Due to these specific characteristics, these species and or their relatives can be identified anywhere and anytime.

Table 3: Character in Taxonomy

	Character	Character-state
1	Habit	Climbing, decumbent, herb, shrub, tree, etc.
2	Leaf type	Simple, compound, cauline, peltate, etc.
3	Leaf arrangement	Alternate, opposite, whorled
4	Leaf apices	Acute, acuminate, obtuse, truncate, etc.
5	Leaf surface	Glabrous, pubescent (glandular, ciliate, etc.)
6	Inflorescence	Axillary, bract, head, terminal, spike, etc.
7	Floral symmetry	Regular, zygomorphic, asymmetric
8	Placentation	Axile, basal, parietal, free central, etc.
9	Fruit type	Simple, aggregate, multiple
10	Seed shape	Flat, fusiform, ovoid, spheroid, etc.

As stated earlier, character in organisms, can be measured, counted or assessed in different ways. Characters that can be measured or counted are referred to as *quantitative characters*. Some examples of quantitative characters in plants are leaf size (length and width), number of stomata per leaf surface, number of stamens, fruit size, number of seeds, length and number of trichomes and number of vascular bundles (Agbagwa and Ndukwu, 2001, 2004, 2005; Ndukwu and Agbagwa, 2006; Agbagwa and Okoli, 2006, 2007; Agbagwa *et. al.,* 2007; Agbagwa, 2007; Ekeke and Agbagwa, 2015, 2016, 2017; Ekeke, *et. al.,* 2017). Measurements can be achieved using a meter ruler or microscopically on a calibrated stage. Characters that cannot be measured or counted are *qualitative characters*. These include flower colour, leaf arrangement and leaf surface. Hairiness of leaf surfaces of plants can be a quantitative character if one decides to measure the length of the hairs

using a microscope, or qualitative if the extent and type of pubescence are described. However, both quantitative and qualitative characters are used for describing, identifying and naming plants. While morphology is the main source of characters in early classification schemes, thousands of previously unknown taxonomic characters are currently available from different disciplines and sources (Figure 1). As a result, the affinities between plant groups have been redefined over the last few decades as more and more taxonomic information is accumulated from various sources. By leveraging data from various disciplines and sources, each plant or animal can be assigned several hundreds to thousands of characters that can form the basis for which it can be properly classified, identified and named; of course, by reference to an existing classification. In this regard, a few points are worth noting:

i. With thousands of characters, a numerical method of assembling, computing, analyzing and interpreting data becomes necessary. This led to the emergence of the era of Numerical taxonomy.

ii. Taxonomists do not use all the characters in the classification of a taxon (i.e., species). Doing so will be burdensome. Instead, characters are carefully selected to achieve the best possible classification scheme. Characters chosen are those that are consistent and do not exhibit wide variations and high intrinsic genetic variability, the so called "good" characters. The "bad" characters, which are normally excluded from the classification system, are highly variable and inconsistent.
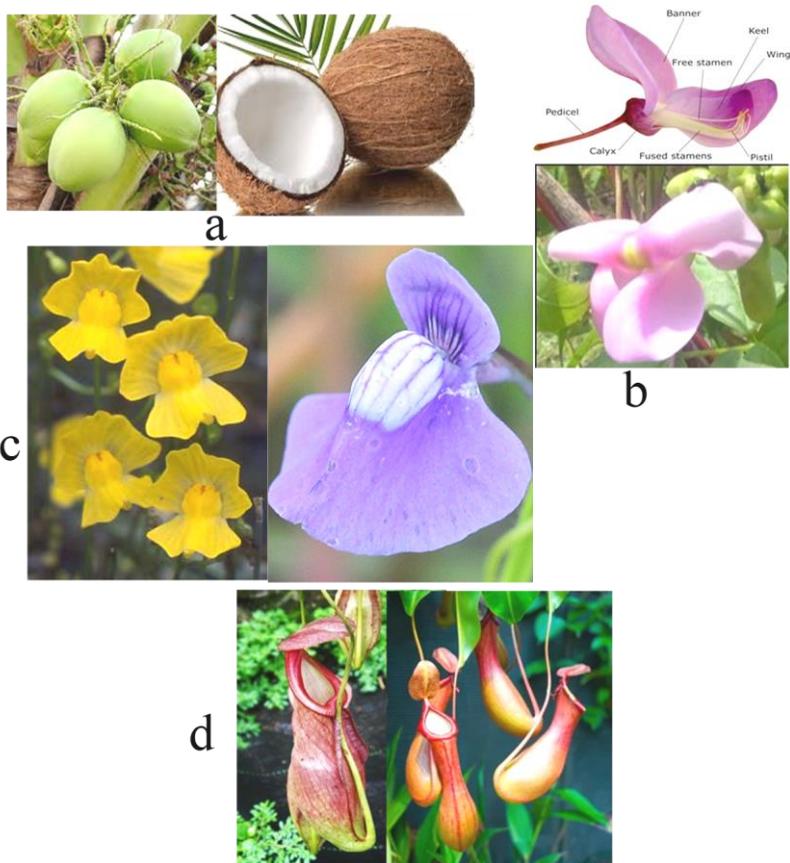
Plate 8: a - characteristic fruit of *Cocos nucifera*. b – characteristic corolla in Papilionoidea. c – bladder and pitcher characteristic to the insectivorous taxa *Utricularia gibba* and *Nepenthes mirabilis*

4.3. Taxonomic Hierarchy

Mr. Vice Chancellor and distinguished audience, characters are veritable tools used for the classification, identification and naming of taxa. Each taxon (i.e., animal, microorganism, plant) is related to another taxon based on certain common characters such as overall morphology, phylogeny or phenetic relationships. This chain of relationships leads us to the

concept of Hierarchy in Taxonomy. A taxonomic hierarchy first recognizes and assembles organisms into groups based on certain characters and on how they resemble each other. These groups are then assembled into larger and more inclusive groups. This process is repeated until all the organisms have been assembled into a single, large and most inclusive group. These groups (i.e., taxonomic groups or taxa) are arranged in order of their successive inclusiveness. In other words, the least inclusive taxonomic group would be at the bottom, while the most inclusive would be at the top (Singh, 2010). The taxonomic hierarchy discussed here resembles what we know as a family tree.

The groups formed and arranged are next assigned to various categories with a fixed sequence of arrangement or taxonomic hierarchy. The most inclusive group is assigned to the highest category, generally a kingdom, and the least inclusive to the lowest category, usually a species. The names are assigned to the taxonomic groups in such a way that the name gives an indication of the category to which it is assigned. For example, Ros**ales**, Myrt**ales**, and Malv**ales** all belong to the order category, and Ros**aceae**, Myrt**aceae** and Malv**aceae** fall under the family category. Once all the groups have been assigned categories and named accordingly, the process of classification is complete in which the taxonomic structure of the largest most inclusive group has been achieved. Because of the hierarchical arrangement of categories to which the groups are assigned, the classification achieved is known as **hierarchical classification**.

The origin of the hierarchical system of classification can be traced to Carl von Linné (1707-1778), the father of modern classification or "taxonomy". He is better known as *Carolus Linnaeus*, the Latin name that he adopted. Linnaeus introduced

the hierarchy from broadest (i.e., largest) to most specific (i.e., smallest), which today with some amendments, consists of a kingdom, phylum (for the animals) or division (for the plants), class, order, family, genus and species. The hierarchical system has two basic formats of presentation, namely, **box-in-box** and a **dendrogram** with the former resembling a pedigree/family tree chart. These formats are illustrated in Figure 2a and b

Kingdom
Division
Class
Order
Family
Genus
Species

In current classification systems, intermediate levels are usually identified by prefixes such as sub- and super- (e.g., subphylum, subclass and superclass, superorder). Furthermore, levels or ranks after species (e.g., subspecies and varieties) are a common occurrence.

A major feature of the hierarchical system of classification is the continuous decrease in the number or variety of organisms as one descends the hierarchy. As such, kingdom has the highest variety of organisms, while species has the least with one organism. Organisms in a kingdom have certain important features in common, but also show many differences. By contrast, organisms in a genus are very similar. The species is the smallest unit of classification and individuals within a species are identical.

The taxonomic hierarchy of the common fruit tree *Mangifera indica* L. is presented below as an example.

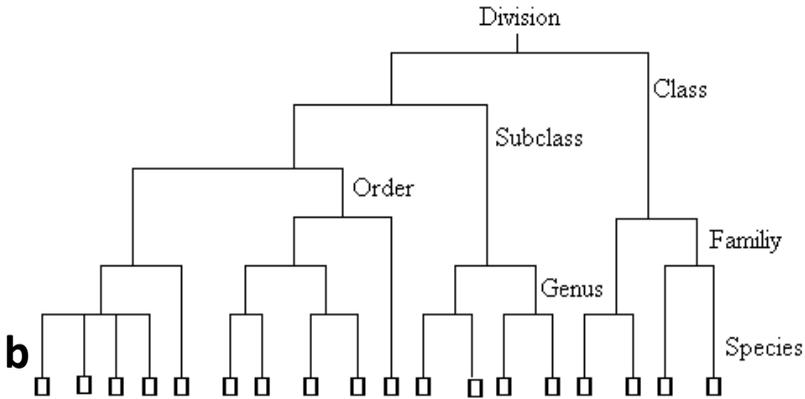| Kingdom | Plantae |
Division	Spermatophyta (Seed Plants)
Class	Angiospermae
Order	Sapindales
Family	Anacardiaceae
Genus	*Mangifera*
Species	*indica*
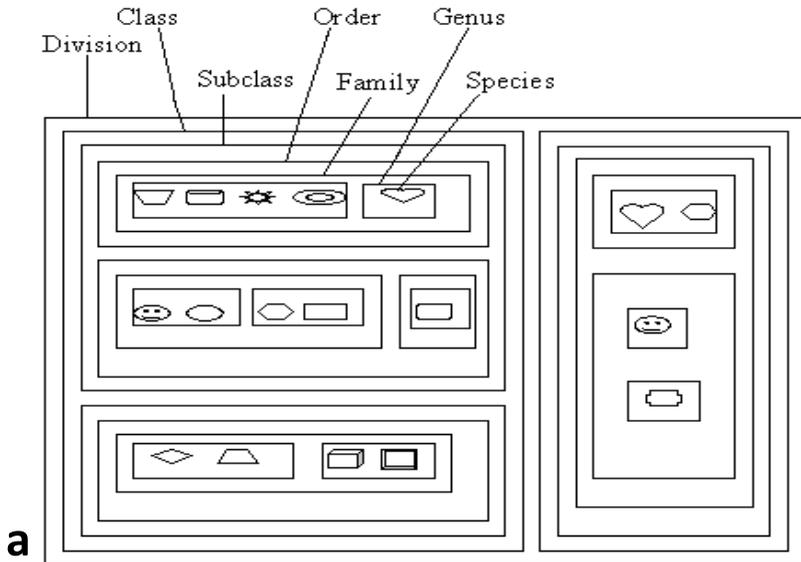
Figure 2: Basic format of presentation of the Hierarchical System of Classification a – box-in-box format; b – dendrogram format. Adapted from Singh (2010)

4.4. Classifying and Naming Organisms

The binomial (two-name) system is a scientific naming system introduced by Linnaeus in 1758. In this system, each species is given a genus and species name, which is usually derived from Latin or Greek. For example, the scientific name for humans is *Homo sapiens*, the honeybee is *Apis mellifera* and mango is *Mangifera indica*. Genus and species names are always italicized or underlined. The genus or generic name is a noun, which typically names some aspect of the organism, such as *Coffea*. The species or specific name is usually an adjective that describes the genus. In the case of coffee, the species is *arabica*, indicating that the plant was thought to originate in Arabia. The scientific name of coffee, *Coffea arabica,* refers to only one plant and cannot be confused with any other. Scientific names of plants and other organisms are often followed by a letter or letters, which stand for the scientist who named the organism. The coffee plant's complete scientific name is *Coffea arabica* L., with L. standing for Linnaeus.

The genus and species names often tell something about the organism. They can describe the appearance of the organism, reflect the common name of the organism, indicate a chemical present in the organism, tell how the organism tastes or smells, or describe how the organism grows. The genus or species name can honor someone such as a renowned biologist, a person in power or a prominent person in history. The name can also reflect the country where the species originated from.

Genus and species names may sometimes seem unnecessarily complicated and even difficult to remember or pronounce. Nonetheless, the use of scientific names is worthwhile for several reasons. The most important reason is that scientific names are used worldwide due to the confusion created by common names. For example, calabash is a common name applied to *Lageneria siceraria* (Cucurbitaceae) and *Crescentia cujete* (Bigoniaceae). These two plants are not related but share the same common name because of their fruits. Such confusion is eliminated by the binomial system of naming organisms. Once organisms are named, grouping or classifying them can help provide an understanding of how they are related. Table 4 contain selected binominal names for organisms.

Table 4. Examples of Common Plants, Animals and Microorganisms with their Scientific and Common Names (Agbagwa and Nzeakor, 2013)

	Scientific name	Common name	Family
	Plants		
1	*Mangifera indica* L.	Mango	Anacardiaceae
2	*Oryza sativa* L.	Rice	Poaceae
3	*Zea mays* L.	Maize	Poaceae
4	*Saccharum officinarum* L.	Sugar cane	Poaceae
5	*Cocos nucifera* L.	Coconut	Arecaceae
6	*Elaeis guineensis* Jacq.	Oil palm	Arecaceae
7	*Solanum melongena* L.	Garden egg	Solanaceae
8	*Lycopersicum esculentum* Mill	Tomato	Solanaceae
9	*Nicotiana tobacum* L.	Tobacco	Solanaceae
10	*Arachis hypogea* L.	Groundnut	Fabaceae
11	*Citrus sinensis* (L.) Osbeck.	Sweet orange	Rutaceae
12	*Musa paradisiaca* L.	Plantain	Musaceae
	Animals		
13	*Homo sapiens* L. 1758	Man	Hominidae
14	*Equus caballus* L.1758	Horse	Equidae
15	*Bos taurus* L. 1758	Cattle	Bovidae
16	*Macaca mulatta* Zimmermann, 1780	Rhesus monkey	Cercopithecidae
17	*Sus domesticus* Erxleben, 1777	Domestic pig	Suidae
18	*Felis catus* L. 1758	Domestic cat	Felidae
19	*Canis familiaris* L. 1758	Domestic dog	Canidae
20	*Ovis aries* L. 1758	Sheep	Bovidae
21	*Rattus rattus* L. 1758	House rat	Muridae
22	*Gallus domesticus* L. 1758	Chicken	Phasianidae
	Microorganisms		
23	*Phytophthora infestans* (Mont.) de Bary	Potato blight fungus	Peronosporaceae
24	*Ustilago nuda* (C.N. Jensen) Rostr.	Smut fungus	Ustilaginaceae
25	*Aspergillus fumigatus* Fresenius	Lung-disease fungus	Trichocomaceae
26	*Aspergillus flavus* Link.	Aflatoxin fungus	Trichocomaceae
27	*Clostridium tetani* Flügge	Tetanus bacteria	Clostridiaceae
28	*Mycobacterium tuberculosis* Zopf.	Tuberculosis bacteria	Mycobacteriaceae

4.5. Predictive Classification System

The search for a predictive classification system and the history of classification and taxonomy occurred in seven distinct phases. This is summarized based on the work of Stace (1989)

- **Ancient Taxonomies and Classification Schemes**

Within the Ancient Classification phase, the sequence of the history of Plant Taxonomy after the era of Folk Taxonomy is as follows:

i.   **Theophrastus** (370–285 BC) - is referred to as the father of Botany. He was the first to develop a permanent and logical classification system. He classified about 480 plants into trees, shrubs, subshrubs and herbs based on their gross morphology (habit).

ii. Dioscorides (1st Century AD) – was a Greek physician in the Roman army. He was interested in the medicinal properties of plants. He described the useful properties of about 600 taxa.

- **The Herbalists**

Botany was synonymous with herbalism (*the study of plants regarding their value to man, particularly as foods and medicines*) during this phase (the Middle Ages to the 16th Century) and was practiced for herbal and therapeutic purposes. The Herbalists leveraged the invention of printing during this period and documented most plants they collected, including some illustrations. Expectedly, many myths and superstitions were attached to the efficacies of plants in healing ailments – plants or plant parts that resembled parts of the human body were thought to have been created by the '*Almighty*' for providing cures to diseases of those parts (so-called doctrine of signatures). This is the same to date in some parts of Africa, particularly where herbalism is almost inseparable from the 'native doctor' practice of consulting the gods. The Herbalists marked an important stage of development in medicine and pharmacognosy. Representatives of this period are herbals of **Otto Brunfels** (1489–1534), **Jerome Bock** (1498–1554) and **Leonart Fuchs** (1501–1566).

- **The Early Taxonomists**

This group of taxonomists switched from the traditional doctrines of the ancient taxonomist and herbalists. They developed systems of classification some of which are still in use today. Some of these early taxonomists and their accomplishments are highlighted below.

i. **Andrea Caesalpino** (1519–1603) – was an Italian scientist and recognized as the first plant taxonomist. He classified about 1500 species mainly on the basis of their growth habits, fruit and seed forms, and some floral and vegetative characters.

ii. **Gaspard Bauhin** (1560–1624) - was a Swedish botanist described about 6000 plant species. Through his work, plants were listed with their synonyms for the first time. He distinguished between *genera* and *species* as major taxonomic categories, giving rise to the *binary system* of nomenclature.

iii. **Joseph P. de Tournefort** (1656–1708) – Frenchman described about 9,000 species that were classified into 698 genera and 22 classes, and promoted Bauhin's rank of genus. This was later adopted by Linnaeus and is in use today.

- **Phase 4. Linnaeus and his Apostles**

Carl Linne also known as Carolus Linnaeus (1707–1778) is a Swedish biologist who is regarded as the founder of modern plant and animal taxonomy. The system of nomenclature that we use today is to a great extent his. His major works on plants were *Genera Plantarum* (1737) and *Species Plantarum* (1753). Linnaeus proposed a Sexual System of classification in which flowering plants were divided into 24 classes. His work covered about 7700 species in 1105 genera. His *Species Plantarum* (1753) was the first to give plants a Latin binomial name. This publication is still used today as the starting point

for the nomenclature of all green plants. Linnaeus had many correspondents and students who were called his "apostles"

- **Post Linnaean Natural Systems Phase**

The Linnaean Sexual System was an artificial system of classification. Although useful, the system was gradually replaced with a classification systems based on several characters that depicted more of the natural affinities of plants. The work of the individuals listed below and others not mentioned laid the foundation of modern plant families.

i. M. Adanson (1727–1806) - documented 58 plant families.

ii. Antoine-Laurent de Jussieu (1748–1836) – divided plants into three groups: Acotyledons (cryptogams plus a few misunderstood monocotyledons), Monocotyledones (monocotyledons) and Dicotyledones (dicotyledons and gymnosperms).

iii. J. de Lamarck (1744–1829) best known for Lamarckism, a theory of evolution, which postulates that characters acquired during an organism's lifetime become inherited.

iv. A. P. de Candolle (1778–1841) was a Swiss botanist. Who introduced the word *taxonomy*. He divided plants into two major groups: Cellulares and Vasculares, which are more commonly known today as non-vascular and vascular plants, respectively.

v. A. de Candolle (1806–1893) – made two outstanding publications that covered all species of dicotyledons and accounted for over 58000 species in 161 families. Gymnosperms were included in these publications, but monocotyledons and cryptogams were not. de Candolle also published a great number of family and genus monographs.

vi. **G. Bentham** (1800–1884) and **J. D. Hooker** (1817–1911) were both associated with the Royal Botanic Gardens, Kew. They described 200 families and 7569 genera in

meticulous detail, and subdivided many of these families and genera into subgenera and/or sections.

- **Phylogenetic Systems Phase**
  The phylogenetic systems phase represents an era of classification based on diverging and converging pathways of plant evolution.

Contributors to this era who based their classification systems on evolutionary pathways include:

i.   W. Eichler (1839–1887) - in his classification scheme, he retained the Cryptogamae (i.e., Thallophyta, Bryophyta and Pteridophyta) and Phanerogamae (Gymnospermae and Angiospermae) as the two major groups of plants.

ii. Charles E. Bessey (1845-1915) was the first American to make a major contribution to plant classification. He separated the pteridophytes and gymnosperms (like the algae) into a number of divisions, and the dicotyledons were subdivided commencing with the Magnoliaceae-Ranunculaceae assemblage

Phylogeneticists illustrated and still illustrate their opinions by constructing charts or 'family trees', which show the lineage of existing families. These are mostly drawn as dendrograms. Dendrograms that are supposed to represent phylogenies are called *phylogenetic trees* (Fig. 3a, b and c)**,** *cladograms* or *phenograms*.

It is worthy to note that it is almost impossible to reconstruct with certainty past evolutionary pathways because the data we use come from studies of modern organisms and fossils. We do not even know everything about modern organisms, and the available fossil record includes only a few of the organisms that lived in the different geological timescales. Therefore, the data that scientists use to make phylogenetic trees will always

be incomplete. We will never know enough about the ancestors of all modern organisms to accurately reconstruct the tree of life. This is a challenge.

- **Modern Phenetic Methods (Taxometrics)** - **Numerical Taxonomy**
Mr. Vice Chancellor and distinguished audience, the challenges with the phylogenetic systems increased advocacy for the Phenetic Classification during the 1950s and 1960s. Some of those who advocated for the phenetic classification system are Heywood (1974) and Raven (1976). A **phenetic system** is simply based on the overall similarity (i.e., overall characters) of the organism being classified. This entails gathering massive pools of data from all available lines of taxonomic evidence e.g., morphology, anatomy, cytology, DNA phytochemistry, etc., that cannot be manipulated manually to produce classification. Fortunately, this school of thought coincided with independent efforts from other researchers including Sneath (1957, 1972) and Michener and Sokal (1957) who introduced the methods and concepts of numerical taxonomy or taxometrics, i.e., the computer aided taxonomy.

Numerical taxonomy is a classification system in biological systematics, which deals with the grouping by numerical methods of taxonomic units based on their character states. It aims to create a taxonomy using numerical algorithms such as cluster analysis rather than the subjective evaluation of their properties (Stace 1989). Numerical taxonomic methods simply help in the management of the enormous data that arise from phonetic approaches. This eventually produces an entirely phonetic classification with maximum predictivity.
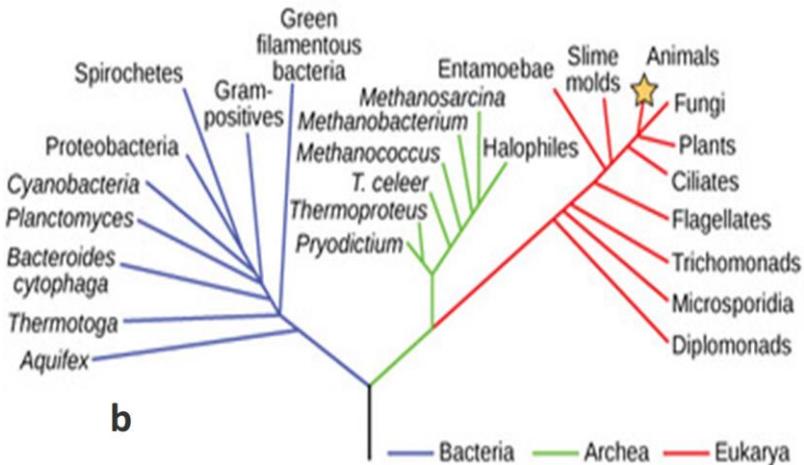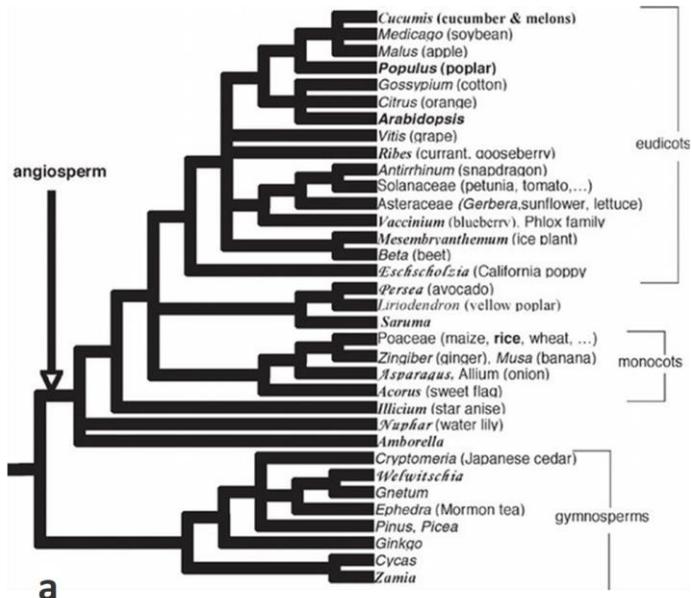
Fig. 3a: Phylogenetic tree of flowering plants and their gymnosperm relatives – Altman *et. al.,* (2006). Fig. 3b: Rooted phylogenetic tree showing the relationship of the three domains of life (Bacteria, Archaea, and Eukarya) – an attempt to identify when various species diverged from a common ancestor – Sumner (2019)
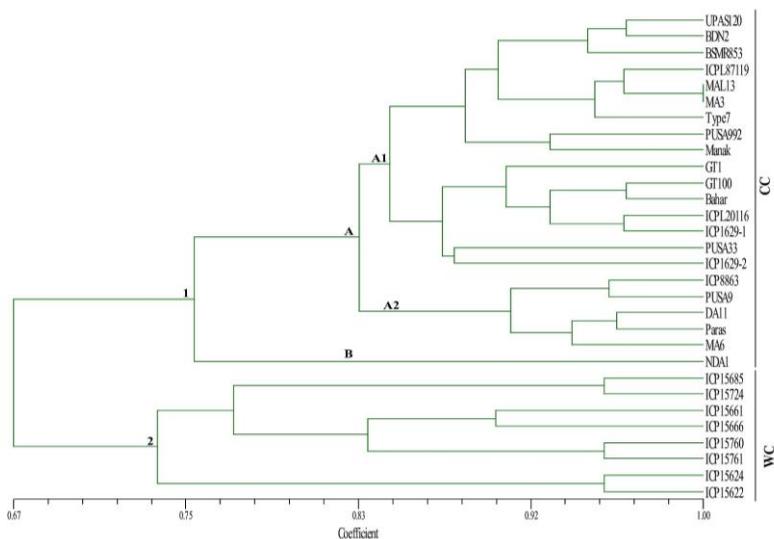
Fig 3c. Dendrogram produced by Jaccard's coefficient and the unweighted pair group method with arithmetic average (UPGMA) clustering method establishing phylogeny between cultivated and wild *Cajanus* species based on *Vigna* SSR primers – Agbagwa *et.al.,* (2015)

Mr. Vice Chancellor and distinguished audience, from the very low predictivity associated with Folk Taxonomy, Ancient Classification Systems, the Herbalists, the Early Taxonomists, the Linnaean Sexual System, and the challenges of the early phylogenetic classifications, we now have a highly predictive phenetic system of classification that includes modern phylogenetic methods. Results of phenetic classifications are illustrated in similar ways as the phylogenetic classifications with modifications based on the focus of the classification.

Having arrived at a phenetic classification Mr. Vice Chancellor, outstanding taxonomic complexity emanates from

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two things: (i) the name given to the plant and (ii) descriptive terminology of the plant, which taxonomists are supposed to know. For example, the plant named *Dioscorea cayenensis* subsp. *rotundata* is described as follows:

*"**Leaves alternate proximally, opposite and ultimately decussate distally, 6–16 × 4–13 cm; petiole ca. as long as blade, winged, base clasping, basal lobes stipulate, growing as extensions of wings, less than 1 mm wide; blade 5–7-veined, ovate, glabrous, base typically sagittate, margins entire, apex acute to acuminate. Staminate inflorescences axillary, 1–2 per axil, paniculate, fasciculate; panicles bearing flowers singly, bracteolate, in a zigzag pattern along rachis, internodes less than 2 mm; rachis to 25 cm, secondary axes 1–3(–6), fasciculate, less than 3 cm, each subtended by deltate-ovate bracteole shorter than 1 mm. Pistillate inflorescences solitary, 4–8(–20)-flowered, 6–35 cm, internodes ca. 1 cm."**** This whole "technical jargon" simply refers to white yam. The complexity in terminology is such that you may use a Flora for one whole day without locating the plant you are searching for.

Jaw-breaking binary names as *Vigna unguiculata* (cowpea beans), *Lycopersicum esculentum* (tomato), *Trichosanthes cucumerina* (snake tomato), *Irvingia gabonensis* (ogbono), *Saccharum officinarum* (sugar cane) and *Triplochiton scleroxylon* (obeche), although part of the complexities, contribute to the uniqueness of the taxonomist.

5.0. The Process of Plant Identification
Mr Vice Chancellor and distinguished audience, each person in this auditorium has one thing or the other to do with plants daily. From the chewing stick, as you wake up in the morning (for those of us who still chew sticks) to your breakfast, as you

walk to your office or business place, to your church premises, to the local shrine in your village and most importantly in your research, you encounter and work with plants. From the biological (Microbiology, Animal and Environmental Biology) and related sciences (Biochemistry, Chemistry) to Agriculture, Pharmacy and Pharmacognosy, researchers work with plants and plant materials. At the World Bank Africa Centre of Excellence in Oilfield Chemicals Research and elsewhere, scientists and engineers and their students are frantically searching for *plant-based* in-country oilfield chemicals for the oil and gas industry to limit importations and recalcitrant chemical pollution. You certainly want to know the plants around you (their names and uses). You want to know the plants you are working with. You want to have a preliminary idea if the plant contains an active ingredient of interest to you. You need expert services in plant identification. Please, ***consult a Taxonomist***.

Identification has already been defined as the naming of an organism by reference to an already existing classification. It is the determination of an organism as being identical with or similar to another organism or group of organisms (Okoli, 1992). This implies that there should always be a classification system that is already existing with which we can compare an unknown animal or plant. This further suggests that anyone wishing to identify a plant, must have some knowledge of plants particularly their external morphology such as leaf characteristics, inflorescence structure and fruit shape. This basic knowledge aids in comparing the unknown plant with existing information. Plant identification is carried out following one or more of the methods outlined below:

i.   Comparison with already identified plants kept in a botanical garden (e.g., Royal Botanic Gardens Kew), and herbarium for preserved plants (e.g., The Herbarium at

Kew Gardens and the University of Port Harcourt Herbarium).

ii. Comparison with good illustrations, drawings and photographs from authentic published sources such as West African Trees (Gledhill, 1972), and A Handbook of West African Weeds (Akobundu, *et.al.* 1998; Ogazie, *et.al.,* 2019).

iii. Descriptions in manuals, Floras (e.g., different volumes of the Flora of West Tropical Africa by Hutchinson and Dalziel 1954–1972), monographs, research reports and diagnostic keys including traditional and computer-based keys.

It is important to note that the services of a curator or practicing taxonomist is required in using these methods.

Mr. Vice Chancellor and distinguished audience, I have listed the different methods that are used in the identification of plants. However, with technological advances, there are methods that rely on image recognition algorithms that a non-taxonomist can use. One such method is described below:

iv. Automated Image Recognition (Automatic Plant Identification App) System – Within the last ten years, there has been tremendous effort to identify species using image recognition technology. Such efforts have benefitted the identification of pests, disease causing organisms and plants. The rise in the use of computer-based image recognition has been aided greatly by the continuous advancement in artificial intelligence and machine learning. Specifically for plants, several automated image recognition applications (apps) for identification suitable for use on mobile phones or tablet computers exists. These apps include PlantNet., Plant. Id, PlantSnap., PictureThis., iPlant, Flora Incognita, Google Lens and Seek. These apps were developed mostly to

recognize leaf, fruit and flower morphology of plants. These apps are easy to use. You simply position the camera of your smartphone or tablet on the plant part, and by image recognition, the name of the plant is given including species, genus or family level information. The amount of information provided depends on the precision of the app. A recent comparative study on ten of these apps (Jones, 2020) applauded the efforts at easing the burden of plant identification. With regard to the accuracy of the apps, Jones (2020) noted that "There were large differences in performance with the best apps identifying >50% of samples tested to genus or better. Although the accuracy is good for some of the top-rated apps, for any quantitative biodiversity study or for ecological surveys, there remains a need for validation by experts or against conventional Floras. Nevertheless, the better-performing apps should be of great value to beginners and amateurs and may usefully stimulate interest in plant identification and nature." Furthermore, Jones (2020) stated "For beginners and amateurs, such apps have great potential for providing shortcuts to the often technical or tedious keys in most botanical floras, at least suggesting the family or genus. *A potential disadvantage, however, is that their ease of use may actually inhibit the development of botanical skills. With all apps at present, any suggested id (name) always needs validation against conventional keys (whether on paper or a smartphone), or at least against a database of reliable images. More rigorous botanical studies such as those on biodiversity critically depend on accurate plant identification; automatic apps potentially have a role here but can only replace botanists if errors can be eliminated, or uncertain identifications flagged.*"

v.   Finally on plant identification, the easiest method for the *layman* is to ask a curator or taxonomist.

6.0. Molecular Diversity

Mr. Vice Chancellor and distinguished audience, I began a worthwhile journey in the "solar system" Plant Molecular Biology in 2005 upon my assumption of duty as Lecturer 1 in the Department of Plant Science & Biotechnology of this great, University. Maybe because I trained under a distinguished Professor of Genetics, Professor Bosa' E. Okoli, and genetics in our clime was almost seen as biotechnology, I was drafted to teach biotechnology courses (Bioinformatics, Genomics, Molecular Biology and Environmental Biotechnology). These courses were not originally in the Botany programme I trained under but were introduced a few years earlier concomitant with the change from Botany to Plant Science & Biotechnology. The concepts and applications of these courses are modern to date and, in fact, are still evolving. With the challenge of having to teach courses that I had little or no knowledge of their basic concepts, principles and applications but determined to distinguish myself, I plunged into the new areas with total zeal and dedication coupled with denial of comfort and pleasure. Leveraging different international fellowships from 2009 to 2015, I embarked on intensive life-changing overseas academic research training in molecular systematics, molecular biology and genomics.

With a broad-based background in Biosystematics and Taxonomy, my approach and focus on Molecular Biology and its applied discipline of Genomics is to understand the molecular diversity and variation in plants and thus unravel the origin and evolutionary relationships amongst plant species, genera, families, amongst others, which is the whole essence of **phylogenetics**. I search for genes controlling important

economic/agronomic traits in wild species and deploy them to improve their cultivated/crop relatives. My main interest is in wild and cultivated crop legumes.

Mr. Vice Chancellor and distinguish audience, having further informed you of my background and training, I would like to move on to discussing the topics of molecular biology and genomics from the angle of molecular diversity.

6.1. Molecular Biology

Molecular biology deals with the structure and function of proteins and nucleic acids (i.e., Deoxyribonucleic Acid – DNA and Ribonucleic Acid – RNA), which are essential to life. Topics covered in molecular biology include, but are not limited to, the processes of replication, transcription, translation and cell function. Nucleic acids are the most important macromolecules for the continuity of life. They carry the genetic blueprint of a cell and instructions for cell function. DNA in particular bears the hereditary information that is passed on from parents to children, providing instructions on how and when to make the many proteins needed to build and maintain functioning cells, tissues and organisms.

Molecular biology is a continuously emerging and growing field with numerous techniques being developed to study biological molecules, their interactions and molecular processes. For instance, Polymerase Chain Reaction (PCR) is a molecular biology technique for enzymatically replicating and amplifying small quantities of DNA without using a living organism. Developed in 1983 by Kary Mullis, an American biochemist, the technique revolutionized molecular biology studies.

6.2. Genomics

The complete genetic makeup of an organism is known as its *genome*. The genomes of almost all living creatures, both plants and animals, consist of DNA, the chemical chain that includes the genes that code for different proteins and the regulatory sequences that turn those genes on and off. The specific protein that is produced by any given gene is determined by the sequence in which four nucleic acid building blocks, adenine (A), thymine (T), cytosine (C) and guanine (G), are laid out along DNA's twisted, double-helix structure. The study of genomes, called *genomics* is a branch of *molecular biology* that involves mapping, sequencing, and analyzing genomes to determine the structure and function of genes. Genes make up the DNA sequence and are the seat of hereditary materials. Therefore, they carry economically important traits. Plant genomics searches the entire genome of plants, identifies the genes controlling important economic and agronomic traits, determines their location on the chromosome, and manipulates genes for crop improvement for the betterment of mankind.

The subgroups of genomics are:

Structural Genomics
* Deals with the study of the structure of the entire genome of an organism.
* Attempts to identify all the genes in the genome and to determine their locations on the chromosome.
* Determines the size of the genome of a species in megabases (Mb) and also the number of genes present in the entire genome of a species.

Structural genomics involves:
* High resolution genetic and physical maps
* Gene Sequencing

Functional Genomics
- Deals with the study of the function of all genes found in the entire genome of a living organism.
- The goal of functional genomics is to determine how the individual components of a biological system work together to produce a particular phenotype. Functional genomics focuses on the dynamic expression of gene products in a specific context; for example, at a specific developmental stage or during a disease.

There are several specific functional genomics approaches depending on what we are focused on:
- DNA level (genomics and epigenomics)
- RNA level (transcripomics)
- Protein level (proteomics)
- Metabolite level (metabolomics)

Comparative Genomics
- The study of the relationship of genome structure and function across different biological species or strains.
- Uses the understanding of gene organization, expression and evolutionary differences.
- Makes extensive use of molecular markers and molecular marker systems.

Comparative Genomics
i. Helps in identifying DNA sequences that have been "conserved" or preserved in many different organisms over millions of years. This is an important step toward understanding the genome itself.
ii. Helps us to further understand what genes relate to various biological systems, which in turn may translate into innovative approaches for treating human diseases and improving human health.

iii. Provides a powerful tool for studying evolution. By taking advantage of, and analyzing, the evolutionary relationships between species, and the corresponding differences in their DNA, scientists can better understand how the appearance, behavior and biology of living things have changed over time.

iv. With advancements in DNA sequencing technology, comparative genomics is finding wider applications in agriculture, biotechnology, and plant and animal sciences as a tool to unravel the smallest differences among animal and plant species.

In a bid to understand the underlying evolutionary reasons for fruit diversity in twenty-three morphotypes of *Lagenaria siceraria,* Awala and Agbagwa (2020) deployed structural, functional, and comparative genomic techniques and sequenced the chloroplast genome of the species. The chloroplast genome map of the species is a circular double stranded DNA molecule of 157,145 base pairs (bp) (Figure 4). The sequence alignment of the twenty-three *L. siceraria* landraces shows great variation in the arrangement of the nucleotide bases. Howver, all the sequences belong to *L. siceraria* with percentages ranging from 95% to 100% for query cover sequences, and 98% to 100% for identity sequences with an E-value of 0.00. The total nucleotide sequence rearrangement of bases serve as basis of variation between the morphotypes and appear to be a significant part of the evolution of the genome, which has a greater effect on the evolution of the phenotype than sequence alteration by base substitution. A similar study by Chukwu and Agbagwa (2021) revealed clear phylogenetic relationships between cultivated *Sorghum* cultivars and their wide relatives (Figure 5).
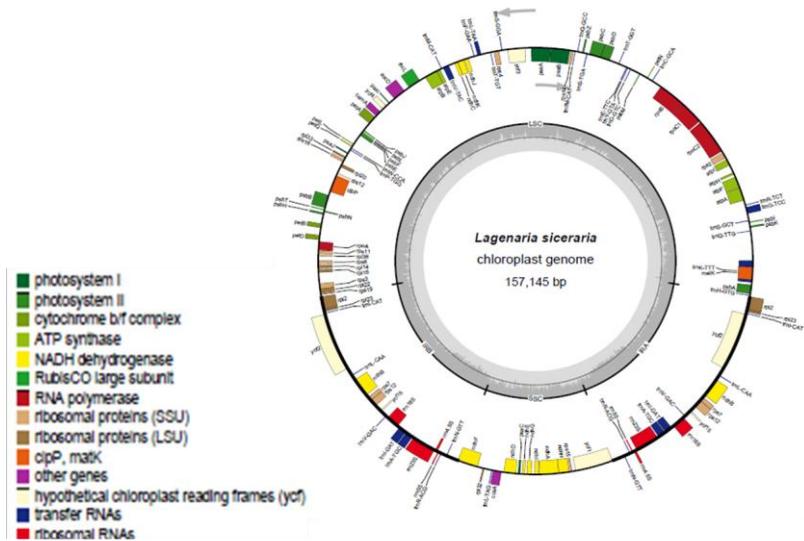
Fig. 4: Chloroplast genome map of *Lagenaria siceraria* (Awala and Agbagwa, 2020)

Fig. 5: Chloroplast genome map of *Sorghum* (Chukwu and Agbagwa, 2021)

6.3. **DNA Mutation/Variation: The Basis for Molecular Diversity and Molecular Systematics Studies**

Mr. Vice Chancellor and distinguished audience, **molecular diversity** depends on heritable DNA. It occurs within one individual, between individuals of the same species, between related species, within and between families and ecosystems, and throughout evolution. **Genetic diversity** is the variation in the genetic composition among individuals of a population, a species, an assemblage, or a community. Diversity on a genetic level reflects the similarities and differences in the genes (i.e., segments of DNA on chromosomes) of individuals. These diversities will naturally manifest phenotypically (Plate 9). In this context, *genetic diversity* connotes *molecular diversity* and shall be treated as such.

The three genomes of plants include nuclear DNA, mitochondrial DNA (mtDNA), and chloroplast DNA (cpDNA) genomes (Plate 10). These genomes have been explored and studied extensively. A major outcome of these studies is the determination of complete DNA sequences for the organellar and/or nuclear genomes of several plant species. So far, the genome of more than 50 plants have been fully sequenced with their DNA sequences in the public domain. The number of plant genomes being sequenced is continuously increasing. As expected, the basic organization of these sequenced genomes are fundamentally different since they evolved differently. However, according to Weising, *et.al.* (2005), sequence data collected from recent studies revealed an extensive and ongoing horizontal exchange of DNA between the three different genomes, resulting in a net lateral transfer of genes from the organelles to the nucleus. Various types of repetitive DNA elements, which comprise the largest space of the nuclear genome, are also found in the organelles (i.e., cpDNA and mtDNA genomes) (Weising, *et.al.,* 2005). Heritable

mutations of repetitive DNA elements create DNA polymorphisms in the nuclear and organellar genomes and are major sources of diversity and variation within and between organisms. Detecting these heritable mutations, which invariably are agents of molecular diversity, can provide a good estimation of genetic diversity, and the information obtained can be used to measure the relationships between organisms (Hoshino *et al*., 2012). This has been applied severally (Agbagwa, *et.al.,* (2014, 2015, 2018), Datta, *et.al.,* (2013), Patil, *et.al.,* (2014, 2015a,b), Awala, *et.al.*, (2019).
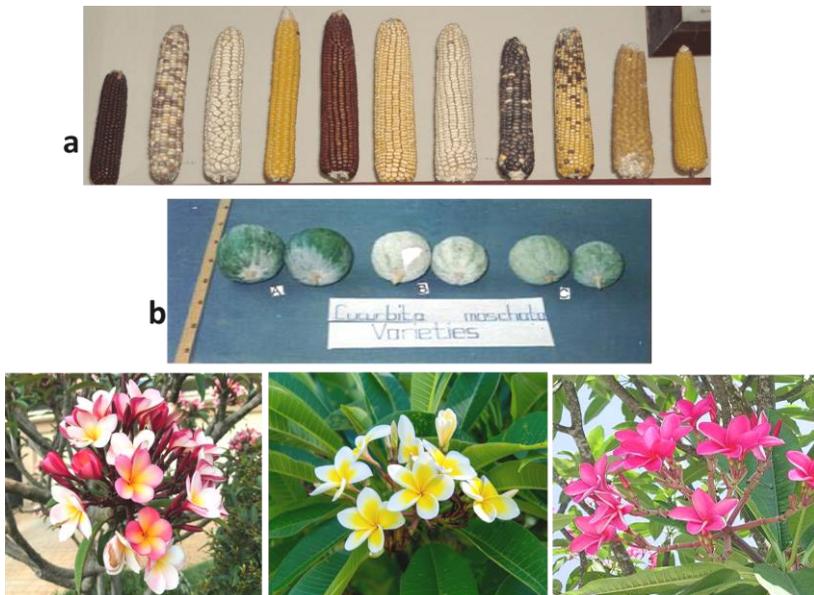

Plate 9: Phenotypic manifestation of genetic diversity in selected plant species. a) Fruits of *Zea mays* (maize); b) Fruits of *Cucurbita moschata* (pumpkin); c) *Plumeria rubra* (frangipani)
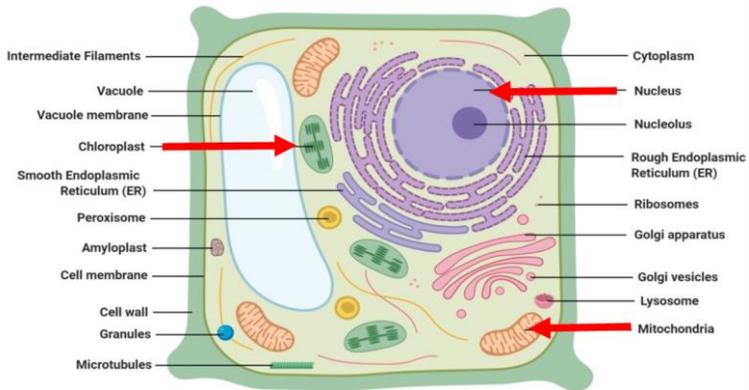
Plate 10: Plant Cell – red arrows show the location of the three genomes – nucleus, chloroplast and mitochondria

6.3.1. DNA Sequence Mutations

A mutation is a permanent alteration to a DNA sequence and the original source of genetic variation. It is the occurrence of heritable changes in the genotype of an organism that was not inherited from its ancestors. It is the ultimate source of variation in species and replenishes the supply of genetic variability. Simply put, heritable mutations as a source of variation are an agent of diversity and speciation.

Several types of genomic DNA mutations exist. Following Weising, *et.al.* (2005), these types of mutations are discussed below.

a. *Base substitution* is the simplest and most frequent type of DNA mutation. It involves the substitution of one nucleotide residue in the DNA sequence by another (Figure 6 a, b and c). According to Graur and Li (2000), base substitutions arise mainly from mispairing during DNA replication, and is the molecular basis of single-nucleotide polymorphism (SNP) markers. *Transition* and *transversion* are two types of base substitutions. These different forms of base substitution

depend on the type of bases being substituted. In *transition*, exchange involves nucleotides carrying the same type of bases. In other words, a purine (adenine - A) replaces a purine (guanine - G) or a pyrimidine (cytosine - C) replaces a pyrimidine (thymine - T). In *transversion*, nucleotides carrying different type of bases are exchanged (i.e., purine replaces or exchanges position with a pyrimidine or vice versa). Due to the basic chemical structure of the concerned nitrogenous bases (Figure 6h), transitions as a form of point mutations, are more common in nature than transversions.

A CGTAGGCTAATTAATTGCTGGCATTACGT

B CGTGGGCTAATTAATTGCTGGCATTACGT

C CGTAGGCTAATTAATTGCTGGGATTACGT

CTGGCA

D CGTAGGCTAATTAATTG-TTACGT

E CGTAGGCTAATTAATTGCTGGCATAAAGGCTTACGT

F CGTAGGCTAATTAATTGCTGGCA TGCTGGCATTACGT

G CGTAATCGGATTAATTGCTGGCATTACGT

Figure 6: Types of mutations commonly encountered in DNA. a - **Wildtype sequence**. b - **transition**: A to G exchange at the position highlighted in red; c- **transversion**: C G exchange at the position highlighted red; d - **deletion** of the sequence CTGGCA; e - **insertion** of the sequence AAAGGC; f - **duplication** of the sequence TGCTGGCA; g - **Inversion** of the sequence AGGCTAA

A mutation due to a base substitution within the protein-coding region can lead to three different outcomes: missense, nonsense and silent mutations. In **missense mutations**, the altered codon leads to the insertion of an incorrect amino acid into a protein molecule during translation. In **nonsense mutations**, the altered codon prematurely terminates the

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synthesis of a protein molecule. In **silent mutations**, the altered codon codes for the same amino acid as the unaltered codon.

Purine   &   Pyramidine

Adenine - A

Cytosine - C

Guanine - G

Thymine - T

Figure 6h: DNA double helix and structure of the complementary nitrogenous bases

b. *Insertions and Deletions* are collectively called **indels** and refers to the gain (**insertion**) or loss (**deletion**) of a piece of DNA segment at a particular site (Figure 6d and e). As expected, an insertion changes the DNA sequence by adding one or more nucleotides to the gene, while a deletion changes the DNA sequence by removing at least one nucleotide in a gene. If these processes happen without lethality, variation is expected particularly when the events occur in genes controlling traits. Mechanisms that trigger indels are: (i) activities of transposable elements, (ii) slippage of the DNA polymerase during replication and (iii) unequal crossing over between sister chromatids or between two homologous chromosomes. It is noteworthy that chromosomes carry the DNA, which bear the genes. Thus, chromosomal aberrations ultimately alter DNA sequence arrangements.

Insertion or deletion of one or more nucleotides during replication can also lead to another type of mutation known as a **frameshift mutation**. The outcome of a frameshift mutation is the complete alteration of the amino acid sequence of a protein. This alteration occurs during translation because ribosomes read the mRNA strand in codons or groups of three nucleotides. These groups are called the **reading frame**. Thus, if the number of bases removed from or inserted into a segment of DNA is not the exact multiple of three, the reading frame transcribed to the mRNA will be completely changed (Figure 6i).
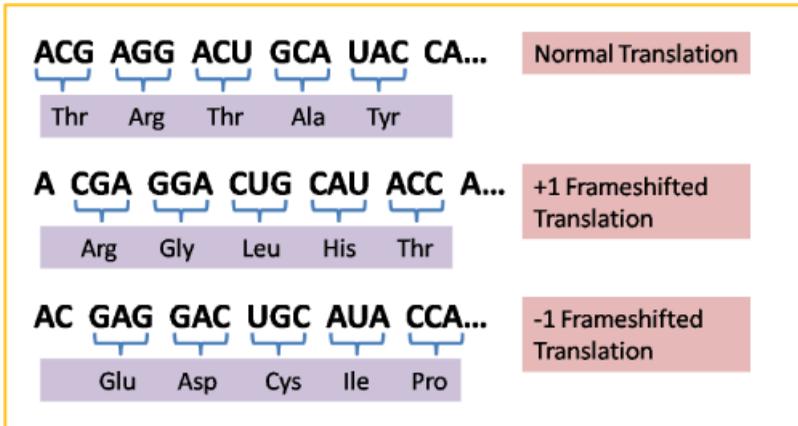
Figure 6i: Illustrating a frameshift mutation

c. *Duplication* is the doubling of the DNA sequence along a segment (Figure 6f). It results from: (i) the slippage of the DNA polymerase during replication and (ii) unequal crossing over between sister chromatids or between two homologous chromosomes. Duplications are common in both the cpDNA and nuclear genomes. Repeated duplications lead to tandem repeats (i.e., microsatellites and minisatellites), which are common in nuclear genomes (Weising, *et.al.,* 2005). Microsatellites and minisatellites as molecular markers have provided great insight into diversity and evolutionary trends in several crop plants (Datta *et.al.,* 2013; Agbagwa *et.al.,* 2015; Agbagwa, *et.al.,* 2021). DNA sequence duplication is an important mechanism by which evolution and speciation occur.

d. *Inversions* arise when a segment of DNA is excised and reinserted in the opposite direction (Figure 6g). Large inversions occur at low frequency in cpDNA and are reliable markers at deep taxonomic levels (Graham and Olmstead, 2000).

The rate of occurrence of the mutations described above can be different depending on the biology of the organism, the genome under consideration (nuclear, chloroplast, or mitochondria) and the type of mutation. As already stated, these mutations are agents of molecular diversity, evolution and speciation events in organisms (Plate 9). They create *DNA polymorphisms* that are detected as **molecular markers**, which when analyzed, provide a good estimate of genetic and of course, molecular diversity.

Mr. Vice Chancellor and distinguished audience, identifying organisms based on **molecular data** relies on the fact that the mutations highlighted above alter the genomes of organisms. These alterations, which manifest as molecular markers, are detected using different **molecular marker techniques**. Molecular diversity leverages molecular marker techniques to understand diversity and variation in organisms, establish relationships and evolutionary trends, and confirm the identity of each organism.

6.4. What is a Marker?

A marker is a heritable characteristic associated with and useful for *identification* and *characterization* of a specific *genotype* (Rastogi and Pathak, 2009). A marker can also refer to any attribute or property of a species showing heritable variation. This is the same as a character. These characters may originate from morphological, physiological, anatomical or biochemical properties of the species. Broadly speaking, there are four types of markers, namely, morphological markers, cytological markers, biochemical markers and DNA (molecular) markers.

- Morphological markers are related to shape, size, color and surface of various plant parts. The classical experiments of

Gregor Mendel (1822–1884) popularized the use of morphological markers in plant breeding. While performing experimental crosses on garden peas, Mendel utilized shape and color of seeds and seed coats, shape and color of pods, the position of pods (i.e., axial or terminal) and overall plant height (tall or dwarf) as heritable markers. Characters that are related to variations in shape, size, color and surface of various plant parts are still called morphological markers in the field of plant breeding. Such markers refer to available *gene loci* that have obvious impacts on the morphology of a plant. They are used for crop improvement projects in a similar manner as Mendel did.

- Cytological markers are markers related to variations in chromosome number, chromosome morphology and chromosome behavior. These markers fall within the scope of cytogenetics.
- Biochemical markers are related to variations in proteins and amino acids and are therefore derived from the study of products of gene expression (i.e., proteins).

6.4.1. Molecular Markers or DNA Based Markers

Molecular markers are identifiable DNA sequences, found at specific locations of the genome and associated with the inheritance of a trait or linked gene. They are thought of as signs along the DNA trail that pinpoint the location of desirable genetic traits or indicate specific genetic differences (Semagn, et. al. 2006) In fact, molecular markers are used to 'flag' the position of a particular gene or the inheritance of a particular characteristic.

In conventional breeding experiments involving genetic crosses, characteristics of interest are usually linked with the molecular markers. Individuals in which molecular markers

are present can therefore be selected since the markers indicate desirable traits. The molecular marker approach to plant and animal breeding, which is also known as marker-assisted or molecular breeding, has supported the rapid development of improved crops and livestock with enhanced vigor and productivity. Molecular marker-based breeding of plants circumvents the need for several planting seasons with crosses and field trials associated with conventional breeding. It therefore reduces the laborious process of screening, identification, selection and transfer of desirable traits to new crop cultivars.

Molecular markers provide relevant information on genome organization. As such, several practical applications can be attributed to the use of molecular markers. These include identification of varieties through DNA fingerprinting and the development of genetic maps, which facilitate selection of economic traits such as disease resistance without rigorous screening and cloning of genes. Molecular markers are also widely used in evolutionary and phylogenetic studies. Furthermore, they are used for marker-assisted breeding, understanding and conserving genetic resources, and genotype verification. The DNA fingerprints of any species verify and confer uniqueness to that species. It is noteworthy that the sequence of DNA is different in every individual. Thus, a specific sequence of DNA can be utilized as a tool to screen variations within a given population. With molecular markers, proper phylogenies are established and expressed as phylogenetic trees. It is important to note that the use of molecular markers to define phylogenies is the crux of Molecular Systematics.

Two broad groups of molecular markers are recognized. These are **hybridization**-based and **Polymerase Chain Reaction**

(PCR) – based molecular markers. Restriction fragment length polymorphism (RFLP) is an example of hybridization – based molecular marker. RFLPs have their origin in the DNA rearrangements that occur due to evolutionary processes, point mutations within the restriction enzyme recognition site sequences, insertions or deletions within the fragments, and unequal crossing over. The PCR – based markers are of two types based on the primers used for amplification. They are either (i) arbitrary or semi-arbitrary primed PCR markers or (ii) site-targeted PCR markers

- i) Arbitrary or semi-arbitrary primed PCR techniques are those that do not require prior sequence information e.g., Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Sequenced Related Amplified Polymorphism (SRAP), Inter-Simple Sequence Repeat (ISSR).
- ii) Site-targeted PCR techniques are developed from known DNA sequences e.g., Expressed Sequence Tags (EST), Cleaved Amplified Polymorphic Sequence (CAPS), Simple Sequence Repeats (SSR), Sequence Characterized Amplified Regions (SCAR), Short Tandem Repeats (STR).

The PCR-based markers are the popular markers in the present-day molecular diversity studies. With these markers, a region/segment of DNA complementary to a particular marker, is amplified several times before the DNA can be analyzed and studied sufficiently.

6.5. Brief on Polymerase Chain Reaction
Polymerase chain reaction (PCR), which was invented by Kary Mullis in 1983, is a molecular biology technique for enzymatically replicating (amplifying) small quantities of DNA without using a living organism. By applying this technique, exponential amplification of a particular region of

DNA is achieved. The amplified DNA region or segment, which is up to 10kb, is usually the region the researcher has interest in. For example, it might be a gene whose function a researcher wants to understand, a genetic marker that flags a trait of interest in a crop or used by forensic scientists to match crime scene DNA with suspects. Typically, the goal of PCR is to make enough of the target DNA region so that it can be analyzed, studied sufficiently, and applied in line with the researcher's interest. For instance, DNA amplified by PCR may be visualized by gel electrophoresis, sent for sequencing, or cloned into a plasmid for further experiments, etc. PCR is used in many areas including agriculture, biology and related areas including medicine and forensic science.

The key ingredients of a PCR reaction are *Taq* polymerase, primers, double-stranded DNA, and nucleotides (DNA building blocks). The ingredients are assembled in a tube, the PCR tube, along with cofactors needed by the enzyme, and are put through repeated cycles of heating and cooling that allow DNA to be synthesized.

Concise steps for PCR include:
i.   Extraction and purification of double-stranded DNA from plant/animal samples.
     DNA (nuclear, mitochondrial and/or chloroplast) extraction from the plant material to be studied is the first step for all molecular-based studies. For molecular marker studies, DNA can be extracted from fresh, lyophilized, preserved or dried samples. However, fresh materials are preferable for good quality DNA yield and less use of purification reagents. Different protocols (e.g., Agbagwa, et. al. 2012) and kits exist for use.

ii. Denaturing of double-stranded DNA at high temperature (92-95 ºC) to form single strands (templates).
iii. Annealing (binding) of short single strands of DNA (known as primers) to the single stranded complementary templates at ends flanking the target sequences. Annealing temperature range is commonly 55 – 60°C.
iv. Extension – This signifies the synthesis of the DNA by a thermostable DNA polymerase (*Taq* polymerase). It is done at 72 ºC, the optimal working temperature for the DNA polymerase.

The processes of denaturation, annealing and elongation constitute a single cycle (Figure 7a) and is performed in a machine called thermocycler (PCR machine). This cycle is repeated 25 - 35 times in a typical PCR reaction, which generally takes 2 - 4 hours, depending on the length of the DNA region being amplified. If the reaction is successful, the target region can go from just one or a few copies exponentially (Figure 7b) to millions.

Advantages of PCR techniques include:
i. It is a relatively simple technique to understand and to use, and it produces results rapidly. It is not laborious like the hybridization-based techniques
ii. It requires a small amount of DNA to produce million copies of same DNA.
iii. It is a highly sensitive technique with the potential to produce millions to billions of copies of a specific product for sequencing, cloning, and analysis.
iv. Radioisotopes are not used as is the case with hybridization-based techniques. This makes the technique relatively safe
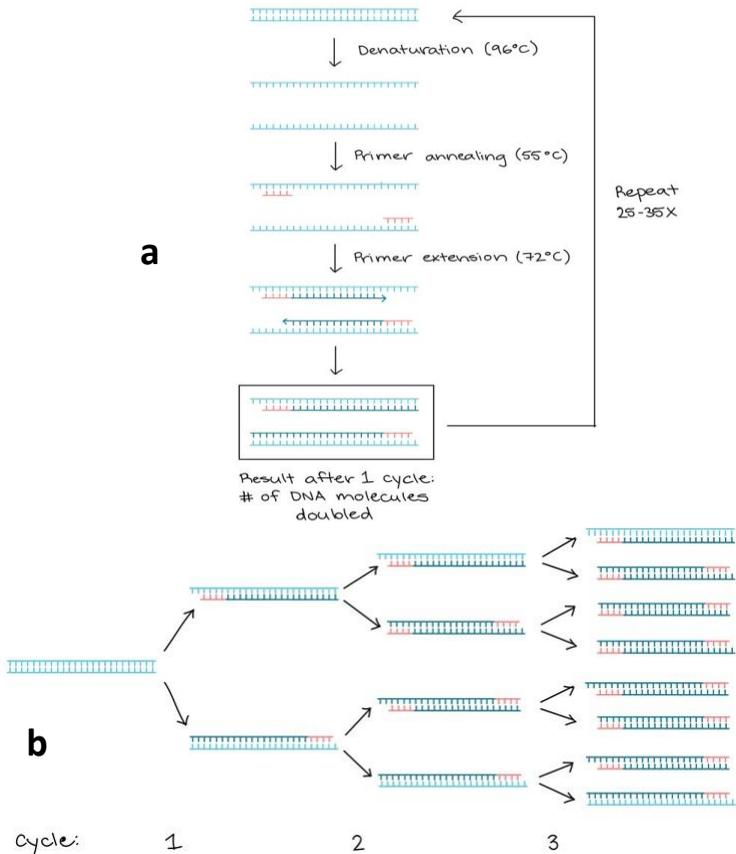v. DNA sequences from preserved tissues can be amplified, sequenced and analyzed.

Figure 7a: Polymerase Chain Reaction Cycle – denaturation, annealing and extension; Figure 7b: depicting Exponential DNA amplification (khanacademy.org/science/ap-biology/gene-expression-and-regulation/biotechnology/a/polymerase-chain-reaction-pcr)

6.6. DNA Barcoding and Molecular Systematics

A DNA barcode is a small (short) section of DNA that has enough variation to make it possible to distinguish between closely related species by analyzing variability within this region (Chase, 2006). DNA barcoding itself is a molecular technique for identifying species of organisms using a short

DNA sequence from a standard well-defined position in the genome. It leverages data generated from DNA sequences of organisms that are deposited in DNA databases such as those found at the National Centre for Biotechnology Information (NCBI) GenBank and Barcode of Life Data systems (BOLD). Being a short sequence relative to the entire genome, DNA barcodes can be obtained quickly and cheaply (Singh, 2010). The DNA barcoding approach is facilitated by the Consortium for the Barcode of Life (CBOL), an international collaboration of natural history museums, herbaria, biological repositories and biodiversity inventory sites. Research within the CBOL is conducted by academic and commercial experts in genomics, taxonomy, electronics and computer science. The mission of CBOL is to rapidly accelerate compiling of DNA barcodes of known and newly discovered plant and animal species, establish a public library of sequences linked to named specimens, and promote the development of portable devices for DNA barcoding.

If you allow me to return to the supermarket analogy from earlier, each product, no matter how closely related it is to other products, has a unique barcode that helps in its identification. This is the case with organisms (Plate 11). In practical terms, the piece of DNA that serves as a barcode has several base positions that differ among closely related species. Thus, a DNA barcode will allow unambiguous species identification based on sufficient sequence variation between closely related species. Amongst the criteria for selecting appropriate regions that can serve as DNA barcodes, universality, robustness and discrimination, stand out. Based on these criteria, the animal barcode of choice is the mitochondrial gene cytochrome c oxidase I (COI). For plants, the Plant Working Group (PWG) of the Consortium for the Barcode of Life (CBOL Plant Working Group et al., 2009)

analyzed several chloroplast genomic regions across the plant kingdom. The group came up with standard plant DNA barcode combinations that increase the level of identification accuracy through incorporating both maturase K (*matK*), which offers high resolution and less universality, and ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (*rbcL*), which also offers high universality, but less species resolution (Balachandran *et al*., 2015).
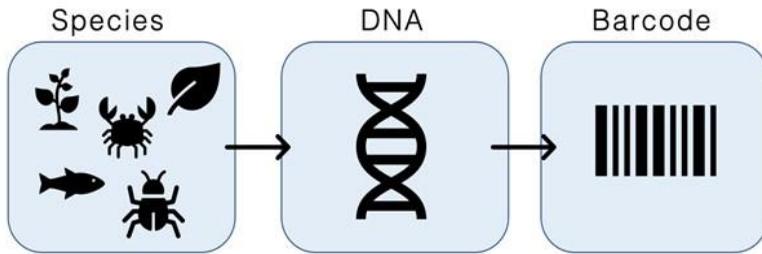

Plate 11: DNA Barcoding Scheme (Wikimedia.org.)

Apart from *matK* and *rbcl,* other standard regions of DNA recommended for plant barcoding studies include nuclear DNA (e.g., *ITS*) and chloroplast DNA (e.g., *trnL-F, psbA, trnH,* and *psbK*) (Janzen et al., 2009; Vijayan and Tsou, 2010; Hollingsworth et al., 2011). DNA barcoding has three main steps: DNA extraction, PCR amplification using the barcode sequence as a marker, and DNA sequencing and analysis.

DNA barcoding provides insight into species-level taxonomy. It contributes to the taxonomic process of defining and delimiting species. DNA barcoding supports the process of identifying unknown specimens to known species, which is key to biodiversity conservation. Plants preserved in the herbarium for prolonged periods lose most of their unique

morphological characters and become difficult to identify. DNA barcoding eliminates such challenges because DNA can be extracted from preserved herbarium specimens regardless of their age. DNA barcode markers are used in the authentication of animal and other wild-collected commercial products sold in markets around the world (Nicole *et al*., 2012). Traditional medicines, teas, and herbal supplements make up an important and large component of the global commercial market in biodiversity. Forensic investigators use DNA barcoding to monitor illegal trading of these products including the trafficking of endangered species (Kress, 2017).

7. Treasure Houses of Taxonomic Information - The Herbarium, Botanical Garden, Taxonomic Literature and DNA Data Bases

Mr. Vice Chancellor and distinguished audience, for completeness, I will briefly discuss some of the treasure houses of taxonomic information. Collectively, these treasure houses provide immense support in teaching and research for the taxonomist and even non-taxonomist.

7.1. The Herbarium

A herbarium consists of preserved plant specimens, each with a label bearing documentary information. Herbaria are repositories for vascular plants, bryophytes, lichens, algae and fungi. Specimens are used as references for comparison and identification with unknown samples, documenting species distribution and variation within species, and identifying times of fruiting and flowering. A herbarium allows for easy retrieval, access and archival storage of specimens. The specimens may be whole plants or plant parts, which are usually dried and mounted on a sheet of paper. Specimens can also be stored in boxes or kept in alcohol or other preservatives. Specimens in each herbarium are collected over

time primarily through research-directed field collections by the curator, herbarium staff and students. It is also a common practice for one herbarium to receive gifts and exchange specimens with other herbaria. Multiple samples of individual species collected from different habitats are typically preserved so that variation among individuals can be documented and related to ecological or evolutionary factors. Herbarium specimens provide materials for research on variation at the DNA level, genome structure and gene expression. Therefore, a herbarium is a critical resource for research studies on biodiversity, ecology and evolution, and a foundational resource for taxonomy. To underscore the importance of herbarium in biodiversity and taxonomic studies, the American Society of Plant Taxonomists (2004) stated that, **"**specimens provide the foundation of nomenclature, the basis for identification, the common reference for communication, and the vouchers for floras, as well as for evolutionary and genomic studies. Molecular and morphological characters that allow us to reconstruct the history of life can be obtained from herbarium specimens. All fields of biological science from the level of molecular biology to ecosystem science are dependent on collections, not just for application of names, but as the basis for referencing all aspects of biodiversity". Examples of herbaria include the New York Botanical Garden (NY) (Bronx, New York, USA), Komarov Botanical Institute (LE) (St. Petersburg, Russia), Royal Botanic Gardens (K) (Kew, England, UK), Missouri Botanical Garden (MO) (St. Louis, Missouri, USA) and Forestry Herbarium Ibadan (FHI). The University of Port Harcourt herbarium is not yet indexed.

7.2. Botanical Gardens
Botanical garden or botanic garden is a garden dedicated to the collection, cultivation, preservation and display of a wide range of plants labelled with their botanical names. They may

contain specialist plant collections, herb gardens and plants from particular parts of the world. Botanical gardens may contain greenhouses, and shade houses with special plant collections such as tropical, temperate or exotic plants as seen in the Royal Botanic Gardens, Kew (Plate 12). Botanical gardens are often run by universities or other scientific research organizations. They often have associated herbaria and research programmes in plant taxonomy or some other aspect of botanical science. The number of botanical gardens in the world is estimated to be about 2500 (Golding *et al*., 2010). It is estimated that 6 million accessions of living plants encompassing about 80,000 taxa of vascular plants are maintained in botanical gardens (Jackson, 2001; O'Donnell and Sharrock, 2017), Therefore, botanical gardens play a central role in the *ex situ* conservation and exploration of global plant biodiversity (Mounce *et al*., 2017), and have a significant role in the preservation of plant species that are important for the well-being of humans (Waylen, 2006; Dunn, 2017). Botanical gardens are likely to become increasingly important as climate change becomes more severe (Donaldson, 2009; Primack and Miller-Rushing, 2009; Ren and Duan, 2017). The range of scientific activities conducted by botanical gardens often includes conservation, propagation, horticulture, seed science, taxonomy, genetics, biotechnology, education, restoration ecology and public education (Maunder *et al*., 2001; Donaldson, 2009; Chen and Sun, 2018). Plant diversity is currently declining at an unprecedented rate, resulting in corresponding decreases in ecosystem services. Currently, about a third of the world's vascular plant species face extinction due to a variety of anthropogenic activities such as over-harvesting, over-exploitation through destructive agricultural and forestry practices, urbanization, environmental pollution, land-use changes, exotic invasive species, and global climate change (Pitman and Jørgensen, 2002; Ren and Duan,

2017). Therefore, there is an increased need to develop integrative conservation approaches for plants, particularly those wild species that are in danger of extinction (Li and Pritchard, 2009).
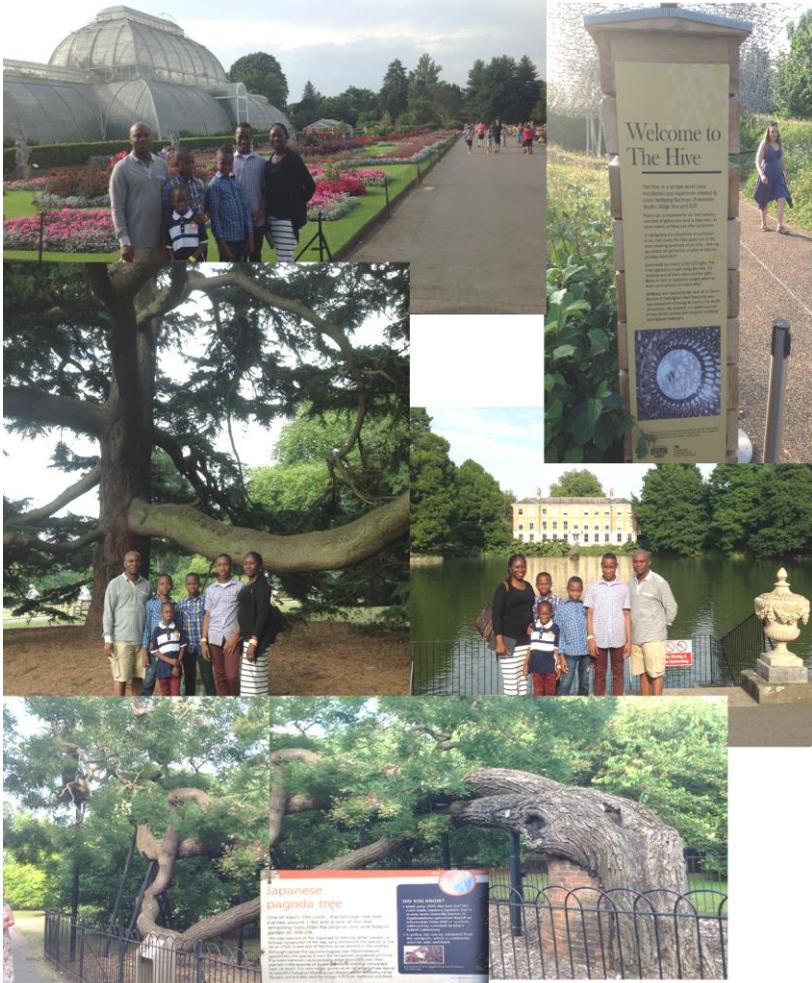
Plate 12: showing different scenes at the Royal Botanic Herbarium Garden, Kew, an ecotourism centre and major source of income to the government. The heritage tree *Styphnolobium japonicum* (Japanese pagoda tree) was planted about 1760 approximately 256 old years in 2016

Services offered at a botanical garden include tours, educational displays, art exhibits, book rooms, open-air

theatrical and musical performances, and other forms of entertainment (Plate 11). Examples of botanical gardens are the Aburi Botanical Garden and Bunso Arboretum in Ghana, and the Limbe botanical Garden in Cameroon.

7.3. Taxonomic Literature (Flora, and Monograph and Revision)

Taxonomy is a descriptive science, and the outcome of the description of each taxon is well documented. Data or descriptive information with which each taxon is described is usually large making taxonomic literature (literature pertaining to the description of every classified and identified plant species) voluminous. However, this voluminous descriptive information is extremely relevant in solving identification problem of an unknown plant. Different types of taxonomic literatures are in existence. These include Floras, Monographs and Revisions, Periodicals, Taxonomic Dictionaries and Glossaries. Floras, Monographs and Revisions are presented briefly.

7.4. Floras

A **Flora** (with uppercase letter F) is a book. It contains systematic arrangement of the species of a given area or a particular region, usually restricted to a major segment of the plant kingdom (e.g., angiosperms), with keys and descriptions and often illustrations. A researcher or student consults a Flora to determine the names and characteristics of the plants of the area covered by the it. Normally, a Flora covers a region or subregion in a continent, country, a section of a country, a state, or even a city. In each area, the Flora is in fact the taxonomist's Bible.

Each Flora has its uniqueness in the way plants are arranged following any of the existing classification systems (e.g.,

Engler, Bessey, Hutchinson, etc.). Each plant in the Flora will be followed by the complete scientific name, author citation, reference to source of original publication, synonymy, and geographic distribution within the area in question. No Flora accounts or contains all known species on earth. Examples of Flora are Flora of West Tropical Africa (Hutchinson and Dalziel, 1954 - 1972), Flora of Nigeria: Grasses (Stanfield, 1970), Flora of Nigeria: Sedges (Lowe and Stanfield, 1974).

7.6. Monographs and Revisions

A **Monograph** is a treatise including all significant information from different taxonomic lines of evidence covering a group such as family or genus. A taxonomic monograph is a comprehensive treatise representing an analysis and synthesis of existing taxonomic knowledge of that taxon, plus the results of original taxonomic research. The usual subject of a taxonomic monograph is the genus or the family. All elements of the treatise are accounted for by dichotomous keys, full synonyms, complete descriptions, precise designations of types, together with notes as to where the types are deposited, citations of specimens examined, distributional ranges (supplemented by maps of the same), notes on habitats, and discussions of taxonomic and nomenclatorial considerations as may be appropriate.

A taxonomic **Revision** differs from a Monograph primarily in degree of scope and completeness. Often it accounts for only a section of a genus or for the elements as restricted to a continent or smaller geographical area. Many revisions make no attempt to review all previous work on the taxon or to take cognizance of the interrelated sciences of cytotaxonomy, genetics, ecology, etc. A revision may be based only on herbarium studies, whereas monograph should cover the

morphology, anatomy, cytology, genetics, and ecology, etc. (https://www.biologydiscussion.com)

7.7. DNA Databases

A database is a vast collection of data pertaining to a specific topic, e.g., nucleotide sequence, protein sequence, etc., in an electronic environment (Singh, 2006). According to Lesk (2008), a database is an organized collection of information, in a computer-readable form. A DNA database, for example, collects and stores DNA sequences of organisms for easy retrieval and comparison. Some DNA databases provide a resource for people to enter their DNA sequence. The DNA database is then searched for sequences most closely related to the entered sequence. Other databases are publicly searchable, but it is not possible to input your own results. DNA databases are at the heart of molecular systematics. Without DNA databases, it becomes difficult to identify new species based on variations in nucleotide sequences. Examples of DNA databases are GenBank (National Center for Biotechnology Information - NCBI), EMBL (European Molecular Biology Laboratory), DNA Data Bank of Japan - DDBJ (GenomeNet), SWISS-PROT (NCBI and EBI -European Bioinformatics Institute), etc.

8.0. Contributions to Knowledge

Mr. Vice Chancellor and distinguished audience, I shall once again draw from the fountain of botanical and encyclopedic knowledge of Onofeghara (1986) with slight modifications. Taxonomy, my field of profession, is like a "galaxy". The different lines of taxonomic evidence (Figure 1) that supply or generate taxonomic data are "solar systems". So far in my academic journey, I have traversed over 90% of these "solar systems" leveraging them to generate data for plant classification and purposeful cutting-edge research and

teaching. I could thus perhaps be the figurative "jack of all trades and master of them all". I shall now attempt to highlight some of the modest contributions we have made.

8.1. Biosystematics and Taxonomy

Two incidents during my undergraduate training defined my journey into Biosystematics and Taxonomy. The first was in the course BOT 305.2 (Plant Taxonomy). The lead course lecturer then, Dr B. E. Okoli, gave an assignment that each student should prepare a mini herbarium of fifty plants as part of the assessment for the course. Instead of fifty plants, I collected one hundred plants and our department's curator as at that time, Mr J. Opayemi, identified them for me. I dried and mounted all one hundred plants in a hard-cover notebook and submitted it for the course lecturer's grading. Being that I collected those plants, which included several weeds – grasses and sedges by myself, the names the curator gave each of them stuck to my brain. The second incident was in the course BOT 408.2 (Weed Science), which I took a year later. The second course lecturer then, Dr B.C. Ndukwu (Prof. B.C. Ndukwu of blessed memory), shocked the entire class on the examination day by bringing twenty plants mostly weedy grasses and sedges, into the examination hall for identification. While most of my colleagues were intimidated by sighting and realising that the plants were to be identified right there and then in the examination hall, I was smiling, having collected and identified most of the plants the previous year. Expectedly, I brilliantly identified 18 of the 20 specimens, as Dr. Ndukwu later told me after the results of the course were released. He had tracked me with my matriculation number. These two incidents and the fact that I come from a typical African village, inspired me to focus my botanical studies on taxonomy and biodiversity.

The task of a taxonomist is to use different lines of evidence to differentiate plants at the species, genus and family levels.

With morphology, micro-morphology and systematic anatomy, we have identified variations, which enabled us to classify or improve earlier classifications of different plant species (*Cucurbita* species - Agbagwa and Ndukwu, 2001, 2004a Plate 13, Ekeke, *et.al.,* 2017; *Gnetum* species – Agbagwa and Ndukwu, 2005 Plate 14; *Emilia* species – Ndukwu and Agbagwa, 2006; *Abrus* species – Agbagwa and Okoli, 2006, 2007, Plate 15; Agbagwa, 2007; Agbagwa, *et.al.,* 2007; *Jatropha* species – Nwokocha *et.al.,* 2012; *Combretum* species – Ekeke *et.a.,* 2013; Ekeke and Agbagwa, 2017; *Terminalia* species – Ekeke and Agbagwa, 2015; *Caladium* species – Ekeke and Agbagwa, 2016). We have also identified species that were completely unknown to science (Agbagwa and Ndukwu, 2005; Agbagwa and Okoli, 2006; Agbagwa, 2007). Our published research results have helped and are still helping many students, researchers, farmers, biodiversity consultants, and plant lovers in the identification and collection of plants in the wild with little or no support from curators (Agbagwa and Ndukwu, 2004a & b; Ekeke, *et.al.,* 2019; Ogazie, *et.al.,* 2018 & 2019). We resolved the identification crisis amongst three species of the genus *Cucurbita* in Nigeria using morphological and anatomical approaches. We have unraveled the great and hidden potentials of several species and proposed conservation strategies for them (Agbagwa and Ndukwu, 2004b and 2005; Agbagwa, 2014; Ebong, *et.al.,* 2005). Our work on *Benincasa hispida*, the wax gourd (Ekeke, *et.al.,* 2017, Plate 16), is the first report of the occurrence of this vegetable cucurbit in south-south and south-east of Nigeria, and a major addition to the vegetable pool of the area. It is noteworthy that scientists and all other science-allied specialists, engineers and environmental consultants, and other individuals with no

taxonomic skill, continue to seek our professional assistance and support in providing precise identification of the plants they intend to experiment on or use.

Chromosomes are the carriers of genetic information. Therefore, chromosome number, structure and behaviour are indispensable in plant evolution and speciation and play unique roles in taxonomy. Leveraging cytological and cytogenetic methods in taxonomy, Agbagwa and Okoli (2005) confirmed that *Abrus canescens* and *A, precatorius*, which are diploid medicinal plants, have 22 chromosomes. They also reported for the first time that *A. pulchellus* is a tetraploid with

Plate 13: Members of the genus *Cucurbita* are important vegetable group. Fruits and leaves are eaten. Agbagwa and Ndukwu 2004 a & b.

Plate 14: *Gnetum africanum* - okazi

2n = 44. The first ever karyotype of *Abrus precatorius* and *A. pulchellus* (Agbagwa, 2011) revealed metacentric, submetacentric and acrocentric chromosomes in both species (Plate 15). The ideogram (Plate 15) confirms that *A. pulchellus* has double the chromosomes of *A. precatorius.* Agbagwa (2014) observed meiotic irregularities (i.e., multivalent configurations at diakinesis, lagging chromosomes and non-disjunction at anaphase) in the polyploid *A. pulchellus* (Plate 15), which was implicated with low fruit and seed set in the species in comparison with its diploid progenitors. Along the same line, Ekeke, *et.al.* (2013) established the mitotic chromosome number of ten species of the genus *Combretum*

and worked out a basic chromosome number of x = 13 for the genus. *Combretum* is a promising floricultural genus (Plate 17). These findings on *Abrus* and *Combretum* provide a rich resource for the genetic modification and improvement of plants for herbal medicine practitioners, farmers and floriculturists.
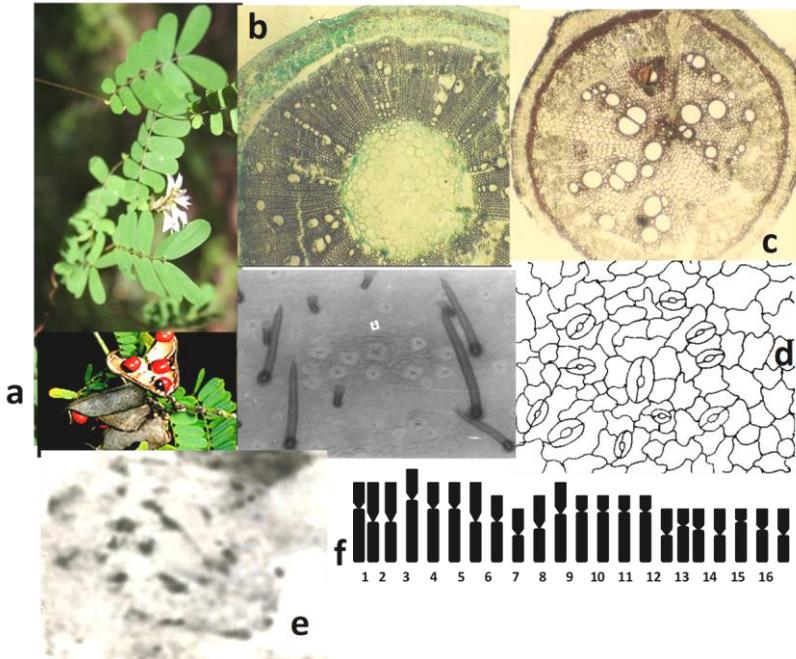

Plate 15: Studies on *Abrus*, a medicinal genus. a – leafy twig of *A. precatorius* showing flower and characteristic seed.; b & c – stem and root anatomy of *A. precatorius;* d – stomata-in-group in fruits of *A. pulchellus;* e - lagging meiotic chromosomes, and f - ideogram of *A. pulcheluus* respectively.

Breeding Systems and **Reproductive Biology** deal with the variety of ways plants mate within and between each other to reproduce their kinds. Dispersal of pollen to the stigma by different plant species is not haphazard but controlled. According to Richards (1990), plants have an even more diverse array of methods by which breeding systems manipulate and control the genetic structure of populations, and patterns of evolution, than animals have. That breeding systems manipulate and control the genetic structure of populations, and patterns of evolution, make it an important tool in taxonomy. Deforestation is a major driver of biodiversity loss, which include the loss of pollinator resources and pollinators. We have pursued breeding system and reproductive biology studies from different angles and several studies are still ongoing. Some of our efforts include Agbagwa *et.al.* (2007) on *Cucurbita,* Agbagwa and Obute (2007) on *Abrus*, Ekeke and Agbagwa (2015, Plate 16) on *Combretum,* Ekeke *et.al.* (2018) on *Cucumis sativus* (Plate 18), Agbagwa and Ekeke (2021) on *Trichosanthes cucumerina* (Plate 19)*,* Agbagwa and Odoya (2021) on *Irvingia*, and Agbagwa, *et.al.* (2021) on myrmecophyte interactions and coevolution with ants. These studies further show the precarious state of south-east and south-south areas of Nigeria due to deforestation and loss of biodiversity; they are equally tremendous contributions in our understanding of plant breeding systems and reproductive biology/ecology, plant-insect relationships and the role of this relationship in speciation. With a dearth of information in this area, our studies shall continue to serve as a baseline and provide reference materials to students and researchers who wish to conduct similar studies. Regarding the genus *Cucurbita* where the three common species (*C. moschata*, *C. maxima* and *C. pepo*) are good vegetables, we have continuously advocated for the acceleration of breeding efforts for these species to be used alongside *Telfairia*

occidentalis (also known as ugu and popularly called pumpkin). Recently, we have commenced eating and sharing with our willing neighbors, healthy ripe fruits of *Trichosanthes cucumerina*, harvested from our own gardens. The fruits of *T. cucumerina* are more than palatable in soup and stew. We are already breeding species of *Combretum* for release to floriculture gardens. Our studies on *Cucumis sativus* (cucumber) was necessitated by the sudden rise in cucumber farming as a means of income and supporting livelihood across Niger Delta. The study revealed that bees are the most effective pollinators, that plants pollinated by bees have better fruits than the hand-pollinated ones. Unfortunately, bees and other pollinators are facing challenging times from deforestation, which has drastically reduced their resources thereby threatening their existence. The recent continuous air pollution from hydrocarbon burning is even worsening the situation for pollinators and other visitors to the plant. Though we recommend bee farming close to cucumber farms to alleviate the problem, this is an entirely different vocation/business that requires its own expertise and skills, which the cucumber farmer may not have and want to have. Even if this is achieved i.e., bee farming around cucumber farms, the government at the state and federal levels must deal decisively with continuous air pollution arising from hydrocarbon burning without which, pollinator decline will continue.
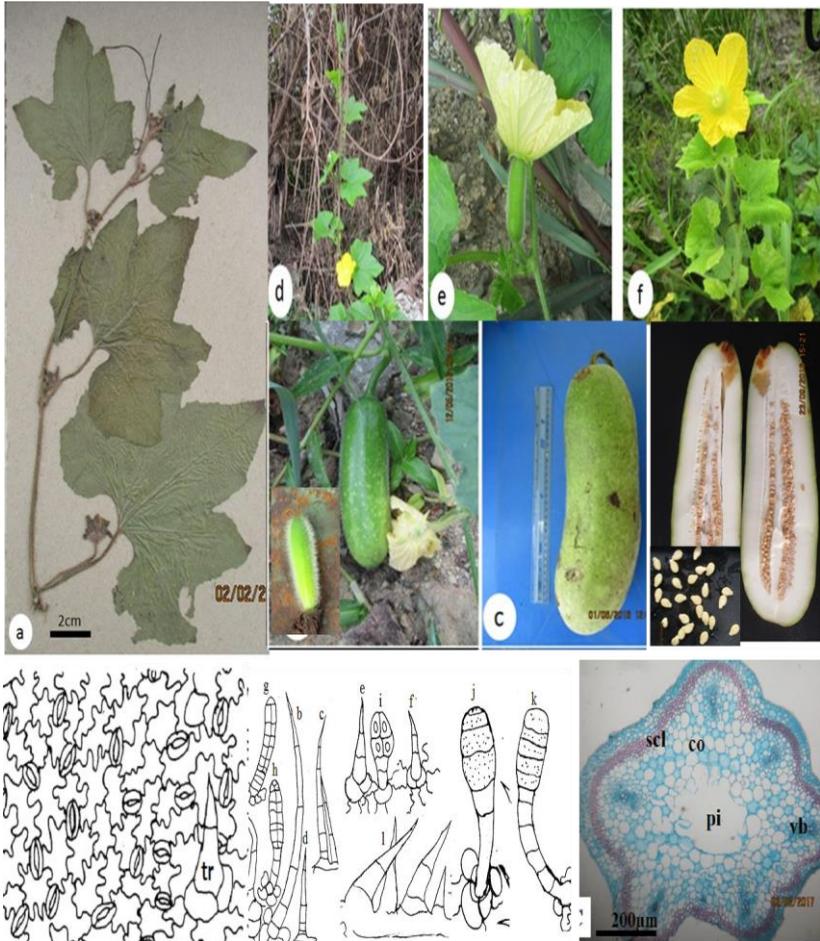
Plate 16: *Benincasa hispida* (wax gourd), a new record to the Flora of Southern Nigeria – Ekeke *et.al.,* 2017

Plate 17: *Combretum* – a genus with promising ornamental species and candidates for floriculture
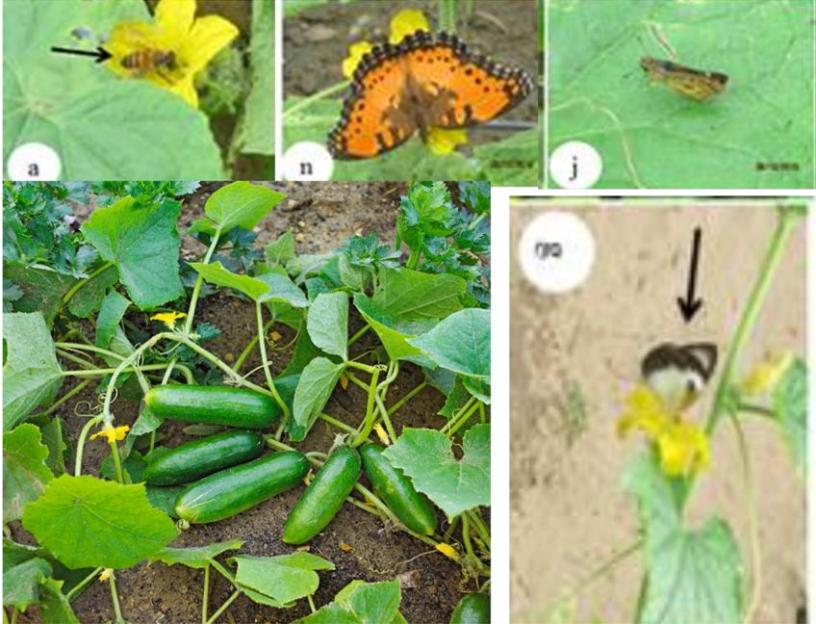
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Plate 18: Aspects of the breeding biology of *Cucumis sativus* – cucumber– Ekeke *et.al.,* 2018

Plate 19: *Trichosanthes cucumerina* – neglected but nutritious and palatable in soup and stew – Ekeke and Agbagwa, 2021

Phytochemistry- According to Egbuna *et.al.* (2018), "Phytochemistry is the study of the chemicals produced by plants, particularly the secondary metabolites, which are synthesized as a measure for self-defense against insects, pests, pathogens, herbivores, UV exposure and environmental hazards. Phytochemistry takes into account the structural compositions of these metabolites, the biosynthetic pathways, functions, mechanisms of actions in the living systems and their medicinal, industrial, and commercial applications. The proper understanding of phytochemicals is essential for drug discovery and for the development of novel therapeutic agents against major diseases. The fact that related plant species produce similar phytochemicals makes phytochemistry a major taxonomic line of evidence called **chemotaxonomy**. We have carried out phytochemical screening and localization of ergastic substances in several species including *Jatropha* species in the Niger Delta (Nwokocha, *et.al.*, 2011), *Combretum* species (Ekeke and Agbagwa, 2014), *Benincasa hispida* (Ekeke *et.al.* 2019), *Sorghum* species (Chukwu and Agbagwa, 2020) and Agbagwa (2021) on *Dinnettia tripetala* (Plate 6bii). In *Combretum* species, we were able to establish the presence of ergastic substances in the species, and their distribution and exact location within the plant tissues. According to Ndukwu (2012), results from such studies ensures that "we can act with precision towards phytochemical extraction of the substances when needed".

8.2. Biotechnology

Broadly speaking, biotechnology involves the use of living systems, dead or alive or their derivatives, to generate goods and services for human use. Two main features of biotechnology are: (i) utilization of biological entities (e.g., microorganisms, and cells of higher organisms either living or dead), their components or constituents (e.g., enzymes), in

such a way that (ii) *some* products or services are generated. These products or services should, obviously enhance human welfare. We have achieved these goals of biotechnology through several of our research activities, which are enhancing human welfare. Tangible products of our research efforts include enhancement of germination, growth and flowering of *Celosia argentea* using extracts of *Senna alata* (Agbagwa, *et.al.,* 2002, 2003; Agbagwa, 2014; Plate 20), production, screening and evaluation of biocatalysts from plant sources for trans-etherification stage of biodiesel production (Chukwu, *et.al.,* 2012) and microorganism-mediated production of bioethanol from the rhizome of the grass, *Imperata cylindrica* (Stanley, *et.al.*, 2019). We have also reported on factors affecting stakeholder's preference for cowpea (*Vigna unguiculata*) grains (Odogwu, et.al, 2021) and identified lignin modifying enzymes from two mushrooms, *Pleurotus ostreatus* and *Lentinus squarrosulus*, for mycoremediation (Chuku, *et.al.,*2021). Mycoremediation is an economical, eco-friendly and effective strategy to combat the problem of soil and water pollution. The results obtained so far with mycoremediation using lignin modifying enzymes from the aforementioned mushrooms have expanded our search for more species with such capacities. Our work with mycoremediation has provided an eco-friendly solution to the various malignant oil impacted sites in the Niger Delta. The encouraging results from this work spurred us to commence an intensive study on mushrooms of the Niger Delta. This we did by securing a 2020 Tertiary Education Trust Fund (TETFund) Institution Based Research (IBR) grant. Mushroom cultivation and husbandry have tremendous potentials to support Sustainable Development Goals (SDG 1, No Poverty; SDG 2, Zero Hunger; and SDG 3, Good Health and Well-being. We are therefore combining our search for eco-friendly species with reconnecting the people of the subregion to the possibilities

and immense advantages of mushrooms. Preliminary collections (Plate 21) show prosperous future with this group of organisms.

We are also happy to report that the use of crude extracts of *Senna alata* for the enhancement of vegetative growth of horticultural crops have produced tremendous results that benefit human affairs. Vegetables grown with *Senna alata* leaf extracts recorded earliness in flowering, large and healthy leaves. Extraction and application of the extracts have been simplified to enable local farmers extract and apply the extracts, which contain phytohormones, with minimal assistance.

Plate 20: a - *Senna alata*, source of phytohormones for improvement of *b – Celosia argentea*

Plate 21: Repositioning mushrooms in the Niger Delta for food and nutritional security, and extracellular enzymes for mycoremediation: A taxonomic approach. Ongoing 2020 TETFund IBR Project – Agbagwa, Chuku and Ikechi-Nwogu
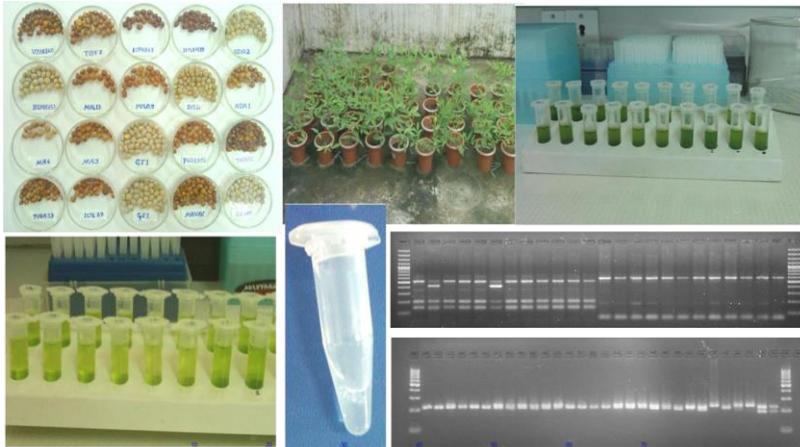
Genomics and Molecular Diversity. DNA extraction is *sine qua non* to molecular-based studies. Plant DNA extraction kits are expensive and can only work on a limited number of samples. Europe, America and some parts of Asia have uninterrupted power supply and heavy research funding. In such places, researchers use DNA extraction protocols that require the use of liquid nitrogen to preserve the plant and enhance grinding or lyophilization, and state-of-the-art instrumentation. Expensive DNA extraction procedures impede biotechnological advancement in Africa and Asia. We considered these challenges and by modifying existing protocols, Agbagwa *et.al.* (2012) developed a new protocol for DNA extraction from plants. This protocol, which was developed using legume plants, is applicable to other plant species with slight modifications. The protocol can result in DNA yields ranging from 328 to 4776 ng/μL, which is quite high. The protocol also yields DNA with high purity as judged from the 260 to 280 nm absorbance ratio of 45 trial samples of cultivated and wild *Cajanus* species with ratios ranging from 1.66 to 2.20, and a mean of 1.85. Furthermore, DNA extracted from this protocol has very low levels of protein and polysaccharide contamination. Forty samples can be extracted daily at a cost of US $1.8 to US $2.0 per plant sample. DNA samples resulting from the protocol can be used in all PCR-based downstream reactions (Plate 22). The availability of a cheap and dependable DNA extraction protocol, such as the one we developed, makes molecular biology more accessible to biological and agricultural scientists who are interested in implementing such techniques in their research. Our DNA extraction method has been in use since 2012.

We have made cutting-edge research contributions for human welfare by applying different molecular markers (e.g., RAPD, AFLP, AFLP-RGA, SSR, SRAP, SSAP, EST, CAPS, *rbcl* and

matK) and tools in diversity studies of crop legumes. These include research results documented in Agbagwa, *et.al.,* (2011, 2014, 2015, 2018), Datta, *et.al.,* (2013), Patil, *et.al.,* (2014, 2015 a,b), Roberts *et.al.,* (2018), Awala, *et.al.*, (2019), Chuku, *et.al.*, (2020) and Agbagwa and Tang (2016). A good example of our contribution with these markers is differentiating tuber bearing *Sphenostylis stenocarpa* (African Yam Bean) from non-tuber bearing cultivars using Sequence Related Amplified Polymorphic (SRAP) DNA (Agbagwa and Tang, 2016). This will facilitate molecular breeding of cultivars for grains, tubers or both. Also, we identified cross-transferable microsatellites from *Vigna* that supported molecular diversity studies in wild and cultivated *Cajanus*. The study demonstrated convincingly that microsatellites are transferable across related genera. Therefore, introgression of desirable alleles, diversity and phylogenetic studies and molecular breeding of lesser-known crops can continue to be performed using microsatellites developed for the more highly studied relatives of these crops. The study supports the inclusion of *Vigna* and *Cajanus* into the tribe Phaseoleae on a phylogenetic basis. The use of *Vigna* markers, which are readily available, has increased the number of SSRs available for pigeonpea studies (Agbagwa, *et.al.* 2015). Other contributions of our research efforts to human welfare include identification, selection and use of crop cultivars with desirable traits, identification of disease resistant wild relatives and their use in molecular breeding, cross transfer of genomes and its application to crop improvement, determination of molecular markers of choice in molecular breeding and whole genotype identification.

Plate 22a: Molecular biology laboratory sessions in Beijing China and Kanpur, India

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Plate 22b: DNA extraction process, DNA amplification and sequencing summarized

To continue with these high profile molecular based studies, permit me Mr. Vice Chancellor, to inform you that on behalf the Department of Plant Science and Biotechnology, a colleague, Dr. B.A. Odogwu and I with the support of the department, submitted an equipment research grant proposal to Seeding Labs Instrumental Access, Boston USA in 2019. Our application was successful. As such, molecular biology/biotechnology instruments with an estimated cost of $350, 000 were shipped to the department in June this year. Mr. Vice Chancellor and distinguished audience, I would like to point out that Dr. Odogwu and I have seen a direct relationship between state-of-the-art equipment and cutting-edge research output. We have the expertise and knowledge to replicate the research we performed in America, Asia and other parts of Africa here in the University of Port Harcourt. We do not want our knowledge and expertise to go to waste because of the lack of equipment and funding. Thus, we are motivated to secure state-of-the art laboratory equipment through competitive grants. In this regard, it is worth mentioning that *for the 2019 grant competitions, Seeding Labs received 58 applications from 20 countries across the globe. Fortunately, our application was among the 18 from 10 countries that were successful*. Our success in securing competitive grant funding will bridge the gap between theory and practice in the Department of Plant Science and Biotechnology, sister departments, and will surely attract more funding to the university.

Working with a consortium of Chinese molecular biologists and bioinformaticians in Beijing with funding from the Strategic Priority Research Program of the Chinese Academy of Sciences, National Natural Science Foundation of China, National Basic Research Program of China, and National Excellent Youth Science Foundation of China, we conducted

studies on DNA methylation patterns in the Y chromosome of 72 African and Asian donors (Zhang, *et.al.,* 2016). This study revealed that the African and Asian samples had similar DNA methylation patterns with a remote divergence time in that DNA methylation patterns on the Y chromosome are conserved during human male history. This indicates that the Y chromosome is not as fragile as previously suggested. Our results provide a unique research platform to study epigenetic-related diseases. With the aid of deep-rooted pedigrees and the Y chromosome phylogenetic tree, students and researchers can perform novel family pedigree-associated epigenetic studies for certain diseases.

8.3. Biogeography deals with geographic patterns of species distribution and the processes that lead to these patterns. It is the study of living things in space and time. **Phytogeography** is a branch of biogeography that is concerned with the distribution of plants in space and time. It is concerned with all aspects of plant distribution, from the distribution of individual species ranges, to the factors that govern the composition of entire communities and floras. Organisms and biological communities often vary in a regular fashion along geographic gradients of latitude, elevation, isolation and habitat area. They occupy different ranges based on biogeographical factors. This adds biogeography to the toolkit of taxonomy. By deploying phytogeographic methods, we have established the pattern of evolution, distribution and habitat preferences, and diversity of some plants including *Abrus* species (Agbagwa, 2002), *Combretum* species (Ekeke and Agbagwa, 2017), *Lagenaria siceraria* (Awala, *et.al.,* 2019), and on *Sorghum* species (Chukwu and Agbagwa, 2020). With *Lagenaria siceraria*, we observed that the separation of landraces over time across the ecological zones in Nigeria has resulted in allopatric speciation of the species, which explains

the morphological diversity of the fruits (Awala, *et.al.,* 2019; Plate 23). From these studies, these species can be easily collected by students, researchers and others working on plants since their habitats and distribution have already been determined and published. Adequate biodiversity conservation and planning, and establishment of crops can be easily undertaken.

Plate 23: Fruit diversity in *Lagenaria siceraria*

8.4. Ecology and Environment

Mr. Vice Chancellor and distinguished audience, I used the phrase 'consult a taxonomist" earlier in this lecture. In 1996, that "action phrase" brought good tidings to me and as we normally say in the Pentecostal circle, "my life has not remained the same" since then. From late 1995 to the greater part of 1996, university education in Nigeria was at a standstill. The military junta then had threatened to "import" lecturers from elsewhere to replace the striking academic staff of Nigerian universities. Students and their lecturers were at home and hunger filled the land. By this time, I had completed

all my M.Sc. courses and research work in Biosystematics and Taxonomy. I was just waiting for the external examination. One afternoon, Dr. L.O. Odokuma (now Prof. L.O. Odokuma) came looking for me at my uncle's house at Omoi/Orosi (Psychiatric Hospital) Road, Port Harcourt. His goal was "*to consult a taxonomist*". As a brief background to this story, a multinational oil and gas company experienced a well blowout about two years earlier after an exploratory drilling campaign. The host community alerted the company and responsible government agencies of the sudden death of plants in the vicinity and surroundings (about 750 m^2 area) of the well location. The company was accused of burying dangerous drilling chemicals in the area, which according to the host community, led to the death of the plants. The company mobilized a leading environmental consultancy firm that hired a renowned plant scientist who served as a consultant. The consultant had several years of postdoctoral teaching experience and was thus considered competent to unravel and recommend solutions to the problem. The first season of investigation of the area by the consultancy firm yielded little or no information as to the reasons for the death of forest trees. The investigation was further hindered because the renowned plant scientist/consultant could not identify any plant in the field or link the death of plants in the affected area to any known cause. In the presence of the representatives of the consultancy firm, the consultant kept asking the locals that accompanied the team to the field about the native (i.e., folk) names of the plants. As expected, the consultancy firm was disappointed as they were headed towards losing the contract from the multinational firm. Because of the failure of the multinational firm to come up with valid conclusions regarding the death of the plants within the vicinity of the exploded well, Dr. Odokuma, a member of the consultancy team, asked me to join the investigation in the second season. The best tip Dr.

Odokuma gave me was, "Iyke, you are going to be asked the scientific names of plants right there in the field. Be ready to give a name to all the plants". That was exactly what happened on the day we arrived at the site to commence the investigation. As we pulled into the access road to the well location, questions about the scientific names of the plants began. I confidently identified all the plant species by their names including *Pterocrapus santalinoides, Cleistopholis patens, Musanga cecropoides, Anthocleista vogelii, Piptadeniastrum Africana* and *Myrianthus arboreus*. I was at my best. The ***right consultant has been consulted*** and we were headed towards identifying the problem and solution. Mr. Vice Chancellor and distinguished audience, as we arrived at the site, the God of sound knowledge and wisdom descended on me. The heavens opened and the solution was as evident as the problem. Plants that originally thrived in seasonal freshwater swamps were suddenly subjected to permanent flooding. Given this drastic change in the environment, it is not unreasonable to expect that the plants will eventually die. An obvious solution to the problem was to simply open the dykes by creating culverts (Agbagwa, 2002, 2008; Plate 24). With the problem identified and the correct solution implemented, I was immediately retained by this well-established and prominent environmental consultancy firm.

Plate 24: section of the site showing flooded area with dead trees

Taxonomy, biodiversity and ecology are inseparable. A niche created by some of us to properly identify ourselves and our roles in ecology is called *ecological taxonomy or eco-taxonomy*. The taxonomist undertakes studies for the "the description of the variation of organisms," and "investigates the causes and consequences of such variation". The causes of variation are right there in the environment. This simply means that the taxonomist needs to understand those ecological factors that have contributed to biological diversity. From an eco-taxonomic standpoint, we have conducted extensive research on the biodiversity and environment of the Niger Delta and beyond. We made significant contributions to conservation, sustainable exploitation and use of biodiversity (Osuji, *et.al.,* 2006; Agbagwa and Akpokodje 2010; Agbagwa and Ekeke 2011, and Agbagwa and Ndukwu 2014). We have also conducted studies on the responses of plants after exposure to air and soil pollutants, and soil seed banks

(Udeagbala, *et.al.,* 2017a, b; Obianefo, *et.al.,* 2017a, b). Results from these studies have formed part of the knowledge and resource material for researchers and students.

To develop outstanding human capacity at the postgraduate level (postgraduate diploma, masters and doctorate) for the sustainable management of the environment and natural resources of the Niger Delta in particular and to enhance the technical skills and managerial capacity of the workforce of government organisations, industries and the local community/civil society through specially designed professional short courses in the environment, natural resources and sustainable development, we (Prof. Enuvie, G. Akpokodje, late Prof. B. C. Ndukwu and Dr I. O. Agbagwa) submitted a grant proposal to the John D. and Catherine T. MacArthur Foundation, Chicago, USA for the establishment of the Institute of Natural Resources, Environment and Sustainable Development (INRES). This grant proposal was the only one approved by the MacArthur Foundation in 2011 out of a total of 15 proposals submitted by Nigerian universities. In line with its mission, INRES has produced 139 postgraduates who are from different parts of Africa since 2013 (PGD 20; MSc 109; PhD, 10). Most of the graduates are staff of government agencies and industries and are already impacting directly on the decisions and policies of their establishment that affect the environment and natural resources.

Oil and gas exploration and production is almost the only industry in the Niger Delta. It is not news, therefore, that academics and the likes within this catchment area jostle for placement or side jobs with these multinationals to shore up their monthly earnings. Between 2002 and 2007, we had the opportunity to render services as Environmental

Consultants/Experts to the Health, Safety and Environment department of the Nigerian Agip Oil Company. During this period, we helped in strengthening the environmental compliance and performance of the company with the regulatory bodies (Federal Ministry of Environment, Department of Petroleum Resources, State Ministries of Environment within NAOC's operational areas) by facilitating early commencement and completion of several environmental studies, including Environmental Impact Assessment (EIA), Environmental Evaluation Study (EES), Post Impact Assessment (PIA) and Environmental Audit (EA). We ensured that stakeholder engagement sessions were held to secure stakeholder buy-in (social licence) as part of the overall sustainability plan of each new project. Due to the importance of the mangrove ecosystem where most swamp area operations of NAOC take place and our previous knowledge and involvement in mangrove revegetation projects, we were asked to supervise the company's first mangrove revegetation project. We followed up with the site contractor and brought our knowledge to bear in raising nurseries of mangrove plant species and in the eventual planting of the nurseries. This project supported the restoration of hectares of the mangrove swamp forest previously destroyed by oil and gas exploration and production activities.

Mr. Vice Chancellor and, distinguished audience, in 2007, the Environmental Assessment Department of the Federal Ministry of Environment (FMEnv), Abuja recognised our efforts and contributions in resolving environmental impacts and retained us as one of their EIA report review experts. In our portfolio as expert ecologists, we have reviewed EIA reports ranging from agriculture and transportation to all aspects of energy and industry in the different geopolitical zones of Nigeria. Through meticulous review and professional

judgement on projects, we have supported the FMEnv in making lasting and sustainable decisions on developmental projects and their implementation. Projects whose EIA reports fell below FMEnv's thresholds were disallowed for the sake of humanity until the right things were done. In the same vein, the Agricultural Research Council of Nigeria in their World Bank-assisted West African Agricultural Productivity Programme (WAAPP-Nigeria) retained our services as lead environmental consultants/lecturer to facilitate training and workshops on the Environmental and Social Management Plan, Environmental and Social Safeguard Policies and Implementation of the Environmental and Social Management Plan. These training and workshops, which were held between 2012 and 2014, were for the senior staff cadre of their 26 research institutes across the country. Evaluations after each training/workshop showed that they were invaluable capacity-building programmes that raised the overall consciousness and understanding of participants on the topics covered.

9. Recommendations and Conclusions

Mr Vice Chancellor, administering a university like ours with minimal funding is more than a herculean task. These recommendations, which I request your permission to make, therefore, also apply to the government, concerned alumni and other stakeholders.

1. The University of Port Harcourt is strategically positioned that a standard herbarium is urgently needed in the Department of Plant Science and Biotechnology as a reference point first for the flora of the Niger Delta and then for Nigeria. Therefore, I recommend a phased implementation of the University Botanic Garden (Plate 24) i.e., the area on the right as you enter the University Park from the main University gate on East-West Road, by implementing the following

     i.   providing a see-through mesh fence from the entrance gate point to the makeshift office of the Botanic Garden. A preliminary species inventory revealed that the entire Botanic Garden area houses several treasured species, including wildlife, that require urgent conservation. Continuous encroachment into the forest due to unrestricted access is causing the department to lose control and ownership of the place. The Arboretum and Taxonomy areas are both conservation and practical teaching sites for ecology, plant taxonomy and natural resources management. The entire area should be protected urgently.

    ii.   constructing a herbarium befitting a university of our status.

  iii.   immediately commissioning a holistic biodiversity inventory of the Botanic Garden to identify, describe and document all species, with their photographs, uses and International Union for Conservation of Nature (IUCN) statuses.

  iv.   accelerating the establishment of a Recreational/Nature Park with the capacity to attract revenue from within and outside the university.

2. Urgent rehabilitation of the Plant Science & Biotechnology Majors Lab that got damaged by fire in March this year. This will facilitate the process of putting to full use the equipment that we got through the Seeding Labs Instrumental Access grant.

3. The rainforest of the Niger Delta is a storehouse of nature replete with wild fruits and vegetables, medicinal plants, soft and hardwoods, amongst others. This storehouse, which has solutions to food and several health challenges, remains untapped. Unfortunately, the exact species diversity, their composition, uses and conservation statuses

are not properly documented; therefore, research cannot effectively be conducted on them. With the continuous threat of deforestation, an urgent large-scale inventory and documentation of the Flora of Niger Delta should be spearheaded by the university. With the university in the lead, support can be sought from funders/multinationals.

4. Urgent intervention of the State and Federal Government in handling the artisanal refining operations in the Niger Delta, and complete stoppage of gas flaring from oil and gas exploration and production activities in the region. The impact of decades of continuous gas flaring coupled with the recent addition from artisanal refining operations on biodiversity (microorganisms, plants, animals including pollinators, and humans) is unimaginable. The truth is that the biodiversity in the Niger Delta is at great risk from air pollution as it has never been before, and urgent intervention is needed.

Mr Vice Chancellor, distinguished audience, in conclusion, every organism on earth needs to be classified, identified and named. It is by knowing each organism and comparing it with an already named species that the incredible blessings bestowed on it by the Almighty God can easily be unravelled. Plants are the sources of man's food and medicine, clothing, shelter, aesthetics and cleaning of the environment via carbon sequestration, amongst others. They can also be toxic, wiping off entire families. *Do you know the names of the various species around you and their benefits*? **Ancient** or **modern taxonomy** can help. ***Consult a taxonomist today***.

Thank you for listening.

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Citation

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Prof. Ikechukwu Ozoemenam Agbagwa, the surviving son of Chief Geoffrey and Lolo Comfort Agbagwa (both of blessed memory), was born on Monday, 9ᵗʰAugust 1971. He started his primary education in 1976 at Community School, Emeabiam and completed in 1982 at Development Primary School Umuokpo-Emeabiam, Owerri-West L.G.A, Imo State. His father, a Headmaster Special Class, was the head teacher in both primary schools, while his mother was his first primary school teacher. He attended Archdeacon Dennis Junior Seminary Mbieri, Imo State where he obtained the General Certificate of Education Ordinary Level in 1987. He holds a Bachelor of Science in Botany (1992), Master of Science in Botany (1997) and Doctor of Philosophy in Plant Science & Biotechnology (2002), all from the University of Port Harcourt.

Prof. Agbagwa began his working career in 1995 during his postgraduate programme as Laboratory Demonstrator in the Department of Botany (now Department of Plant Science & Biotechnology), University of Port Harcourt, and part-time

lecturer in the Science Laboratory Technology Programme (SLTP) where he taught Genetics, Microscopy and Histochemical Techniques. He was an environmental consultant/expert to the Health, Safety & Environment Department of the Nigerian Agip Oil Company from 2002 to 2007. He gained full employment through a competitive interview into the Department of Plant Science & Biotechnology, University of Port Harcourt in 2005 as Lecturer 1, and rose to the Senior Lecturer cadre in 2008. He became a Reader in 2012. After a rigorous academic assessment and interview process between 2015 and 2016, Agbagwa was announced *Professor of Plant Taxonomy & Molecular Biology* with effect from October 1, 2015.

Prof. Agbagwa has been involved actively in teaching, research, mentoring and forming academic linkages, and has supervised more than sixty undergraduates, five post-graduate diplomas, fourteen Masters of Science (M.Sc.) and eight doctoral (Ph.D.) in Biosystematics and Taxonomy, Plant Biotechnology, Ecology and Environmental Management. He has been External Examiner at undergraduate and postgraduate levels to 4 universities. Agbagwa has over 120 scientific research publications in local and international journals in form of peer reviewed journal articles, book chapters and technical papers. He has attended uncountable local and international conferences, short courses, trainings, and workshops in Plant Science & Biotechnology, Health, Safety & Environment, Quality Assurance in Higher Education and Higher Education Administration, and Leadership. With the support of the 8th Vice Chancellor, Prof. Agbagwa as Director, Quality Assurance & Quality Control, facilitated trainings and workshops for university administrators (Provost, Deans, Heads of Departments, Directors of Centres and Institutes, and other senior staff) and students for proper alignment with 21st century Higher Education requirements and standards.

Prof. Agbagwa has received several awards and research grants during his academic journey either as a member of research teams or as an individual. He was a member of the WHO/TDR/MIM Africa Research Capability Grant on Phytomedicine/Malaria Research (University of Ibadan/University of Port Harcourt 1999 – 2001) and a Co-Investigator of the MacArthur Foundation Grant (2011 – 2014) for establishment of Institute of Natural Resources, Environment and Sustainable Development at University of Port Harcourt Nigeria. He received the Plant DNA Barcoding grant for training at Molecular Systematics Lab, Department of Botany and Biotechnology, University of Johannesburg, South Africa (2009),DBT-TWAS Postdoctoral Fellowship in Plant Biotechnology/Genomics, which paved way for postdoctoral research at the Biotechnology Unit, Crop Improvement Division, Indian Institute of Pulses Research, Kanpur India (2011 – 2012), UNESCO-TWAS Associateship Fellowship in Plant Biotechnology/Genomics, Beijing Institute of Genomics, Chinese Academy of Sciences (2013 – 2015),and Chinese Academy of Sciences (CAS) President's International Fellowship Initiative (PIFI) for Visiting Professors at the Molecular Agro-Biology Lab., Institute of Genetics & Developmental Biology, Beijing China (2015 - 2016).In 2019, with a colleague Dr. B.A. Odogwu, Prof. Agbagwa won the Seeding Labs Instrumental Access grant for the Department of Plant Science & Biotechnology University of Port Harcourt from Seeding Labs, Dorchester Avenue, Boston Massachusetts, USA. Targeting SDG 2 (Zero Hunger), 3 (Good Health and Well-being) and 15 (Life on Land), Prof. Agbagwa led his research team in the Department of Plant Science & Biotechnology to win four TETFund Institution-Based Research Intervention grants between 2020 and 2021.This is probably the highest by any professor in the

Faculty of Science, and indeed, in the entire university within one year time frame. The TETFund research funds so far released have been deployed to carrying out field and laboratory investigations for the different projects.

Prof. Agbagwa has served the University of Port Harcourt in the following positions: Member, Board of the Institute of Science Laboratory Technology(2010 – 2012), Assistant Director, Regional Center for Biotechnology(2014 to 2016), Member, Implementation Committee and Academic Board, Institute of Natural Resources, Environment& Sustainable Development (2011 to date), Coordinator, Postgraduate Diploma Programme, Dept. of Plant Science & Biotechnology, UNIPORT (2012 to2016), School of Graduate Studies representative for Faculty of Biological Science in Graduate School of Natural, Applied & Medical Sciences, (2013 to2015), Director, Quality Assurance & Quality Control and Focal Officer, SERVICOM (2015 – 2020), Desk/Liaison Officer for Association of African Universities (AAU) Related Matters (2018 – 2020), etc. He has served as Chairman and member of several *ad hoc* Committees of the University Senate.

Prof. Agbagwa was Lead Environmental Consultant to the World Bank - assisted West African Agricultural Productivity Programme (WAAPP-Nigeria) on Environmental & Social Management Plan (ESMP) and Lead Lecturer, Technical Trainings/Workshops on World Bank Environment & Social Safeguard Policies, Implementation of Environmental and Social Management Plan (2012 and 2014). From 2007 till date, he is one of the professionals retained by the Federal Ministry of Environment (FMEnv) Abuja as expert Ecologist on Environmental Impact Assessment (EIA) Review of developmental projects across the country. Additionally, he has been actively involved for more than twenty years in

providing environmental consultancy services and advice to a number of government ministries and agencies, local and multinational companies.

Prof. Agbagwa is a Life Member, International Association for Plant Taxonomy (IAPT) and International Society for Plant Morphologist (ISPM), Member, Botanical Society of Nigeria (BOSON), American Society of Plant Biologist (ASPB),Nigerian Environmental Society (NES),Association for Environmental Impact Assessment of Nigeria (AEIAN), Institute of Safety Professionals of Nigeria (ISPON), International Institute of Risk & Safety Management (IIRSM), UK, Registered Environmental Professional of National Registry of Environmental Professionals(NREP A2175), and National Mirror Committee of the Standard Organisation of Nigeria (SON). He is a member of the Editorial Board of several Journals.

Prof. Agbagwa is a Knight of St. Christopher of the Anglican Communion, the Vice Chairman and *de facto* representative of the laity at the Chapel Management Council, Our Saviour's Chapel (Interdenominational Protestant Chaplaincy), University of Port Harcourt. He is a lay preacher of the Gospel of Jesus Christ. He is married to Dr. Mrs. Obakpororo Ejiroghene Agbagwa, a Reader in Medical Microbiology, Department of Microbiology, University of Port Harcourt. Both of them are Christians and are blessed with four children: Chimaroke, Soromtochukwu, Otitodirichukwu and Ikechukwu.

Thank you.

Professor Owunari A. Georgewill
Vice Chancellor