NIGER DELTA UNIVERSITY

WILBERFORCE ISLAND, BAYELSA STATE.

40th Inaugural Lecture

Title:

Bio-Molecular Revolution and the Invisible Imperatives: Lessons for Democratic Governance and National Cohesion

Professor Ebimieowei Etebu

B.Sc., M.Sc. (RSUST, Nigeria),
PhD (The Univ. of Sheffield, UK), FIPMD
Professor of Agricultural and Molecular Microbiology
Department of Microbiology, Faculty of Science,
Niger Delta University

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DEDICATION

This inaugural lecture is dedicated to my wife Ebimokemenimighan and children, Pere, Tonye, Tari, Debz and Mercy

NIGER DELTA UNIVERSITY
Wilberforce Island, Bayelsa State, Nigeria

Motto
Creativity, Excellence, Service

Vision
To be a centre of excellence defined by well articulated programme that will produce creative and innovative minds

Mission
To strive to maintain an international reputation for high quality scholarship, research and academic excellence for the promotion of thesocio-cultural and economic well-being of mankind

NIGER DELTA UNIVERSITY ANTHEM (THE BRIGHTEST STAR)

Like the brightest star we are, to lead the way
To good education that is all our due,
The dream of our fathers like the seed has grown;
Niger Delta University if here to stay.

Let us build on this noble foundation
And with love, let our dedication increase,
To rise and uphold this noble vision
Ev'ry passing moment let our zeal never decrease.

In all that we do, let us bring to mind
Our duty as staff and students of N.D.U
Ev'rywhere to promote peace towards mankind.
Creativity, Excellence and Service

CHORUS
Rejoice, great people old and new, rejoice
For the good fruit through us is shown;
Be glad in our worthy contribution
To the growth of humanity (x2)

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The Vice-Chancellor
The Deputy Vice-Chancellor (Administration)
The Deputy Vice-Chancellor (Academic)
The Registrar
The University Librarian
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Distinguished Professors and Members of Senate
Other Colleagues and Friends from the Academia
Staff and students of the NDU
My Wife, Children and family members
Brethren of the Redeemed Christian Church of God (RCCG)
Distinguished guests
My Lords, Spiritual and Temporal
Members of the Press
Ladies and Gentlemen

1.0 Introduction

The day of an inaugural lecture is a memorable day in the life of an Academic, as he/she, having obtained the prestigious rank of professor, takes the centre stage to tell the story of his/her academic journey, and presents a synopsis of the principles and applications of that chosen discipline to the academic community and the wider world. I therefore stand before you today with every sense of humility as a professor of Agricultural and Molecular Microbiology to discuss the revolutionary science of bio-molecules and their invisible imperatives. In so doing, I hope to glean from the discourse few lessons that would add value to democratic governance and engender national inclusiveness in our country.

I would like to start the discourse with a brief description of Agricultural and Molecular Microbiology, being relatively new categorizations of specialties in our clime. Microbiology is a branch of Biological science that deals with the study of living entities invisible to the unaided eyes, owing to their minute sizes of less than 100μm (0.1mm). A Microbiologist therefore, is one who specializes in the study of microorganisms which include bacteria, archaea, fungi, viruses, protozoa, algae, nematodes etc. The exclusive study of these different groups of microbes comprises sub-disciplines such as bacteriology (bacteria), mycology (fungi), virology (viruses), algology/phycology (algae), protozoology (protozoa), nematology (nematodes) etc.

Some of these groups of organisms are not exclusively microbes. For example, there are nematodes that are larger than 100μm. To this effect, sub-disciplines or specialized

disciplines of microbiology are not always restricted to a specific group of microbes but more often than not, they are defined by several phenomena and concepts such as application, habitat, function, methods etc. Some specialized disciplines of microbiology, amongst which are Agricultural and Molecular Microbiology are shown below in Table 1.1

Table 1.1: Some Specialized disciplines of Microbiology

S/No.	Sub-Discipline	S/No.	Sub-Discipline
1	Aero-microbiology	10	Microbial ecology
2	**Agricultural Microbiology**	11	Microbial genetics
3	Aquatic Microbiology	12	Microbial physiology
4	Astro-microbiology	13	Microbial systematics
5	Environmental Microbiology	14	Microbial taxonomy
6	Food Microbiology	15	**Molecular Microbiology**
7	Geo-microbiology	16	Pharmaceutical Microbiology
8	Industrial Microbiology	17	Soil Microbiology
9	Medical Microbiology	18	Veterinary Microbiology etc

Agricultural microbiology is a specialized branch of Microbiology that deals with the study of microorganisms associated with, and their effect on agricultural systems and practices. The Agricultural Microbiologist is thus concerned about the processes and outcome of microbial interaction with plants, animals, soil organic nutrient degradation, transformation and fertility. **Molecular Microbiology** on the other hand**,** is the study of microbial life and processes at the molecular level.

An Agricultural and Molecular Microbiologist is therefore a professional who deals with the deployment of Molecular biological approaches in solving agricultural challenges, particularly those associated with microorganisms.

Irrespective of the discipline one specializes in, the fundamental purpose of education is to acquire knowledge and skills both for self development and to solve societal challenges.

Regarding societal challenges, the onerous societal debacle of the Nigerian State from the outset of her amalgamation in 1914 is the lack of trust and cohesion amongst the citizenry, polarized along many divides; particularly ethnicity and religion. Sadly, several events and news that have continually made the headlines till date show we are drifting farther apart as a people, and we would continually experience stunted and retrogressive growth if we do not consciously and dispassionately strive to change the narrative.

I would say it took Americans to fix America. We are all abreast with how respect for the rule of law and the supremacy of the American Constitution steered their democratic ship to safety, sailing through an unprecedentedly turbulent and murky water of politics, only a few months ago. Like America, the English fixed England, the Germans fixed Germany, Chinese fixed China, and only Nigerians will fix Nigeria. It is important we all strive within our sphere of influence to fix the challenges of our immediate and possibly wider societies for our common good.

It is my pleasure therefore to use this auspicious opportunity and forum to discuss some of the fundamental principles and phenomena of Agricultural and Molecular Biology with a view to drawing lessons that would potentially solve or at least ameliorate societal challenges of democratic governance and inclusiveness in Nigeria.

Vice Chancellor sir, I believe you can now feel the beat of my heart in choosing this title for my inaugural lecture. I hope those in government here present and those that would eventually read or hear of this lecture would glean from the inferences and potential solutions I would proffer. As biological beings, we could rely on biological principles of nature to learn and leverage on them to reinvigorate our space of democratic governance and national inclusiveness.

Having given a synopsis of my field of professional specialization, and setting the tone of my lecture, let me get on to the business of the day by introducing the bio-molecules that epitomizes governance in biological systems. In doing so, permit me to state from the outset that the lessons drawn from this discourse and the recommendations I would proffer may not be entirely new, but I am hoping that they would nonetheless stimulate our humanity and sense of nationality to help us chart a new course in the voyage of our democratic governance and national cohesiveness.

1.1 The Basic Unit of Life and its Seat of Governance

Every human society is made up of humans; could be likened to a federation of biological systems such as reproductive system, digestive system, circulatory system etc while every system is made up of organs, organs in turn are made up of tissues, and tissues are aggregates of **CELLS** which are the basic units of living entities.

Being the basic units of life, cells perform life processes through organelles inherent in them. Organelles, sometimes nicknamed 'Cellular organs' are small specialized structures or

vesicles that carry out specific functions in the cell (Fig. 1.1). In addition to being responsible for the internal workings of the cell, these specialized 'cellular organs' determine how host cells relate with other cells and their environment.

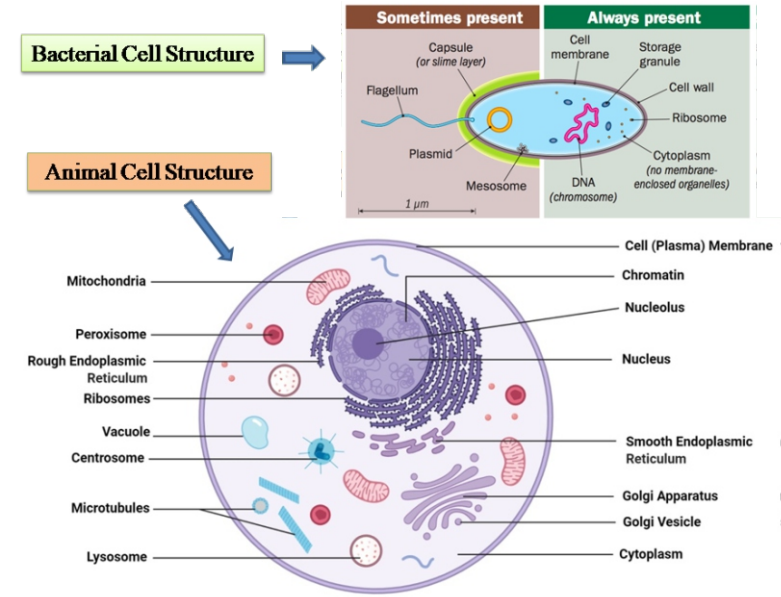

Fig. 1.1: Pictoral representation of a Bacterial and Animal Cell

Fig. 1.1 Pictorial representation of a bacterial and animal cell (Source: Google Images

Prominent among the organelles is the nucleus or nucleoid (as in eukaryotes and prokaryotes respectively). Within the nucleus or nucleoid are biological molecules responsible for the totality of cell function. For this reason, the nucleus is

rightly considered to be the seat of governance of the cell.

Whilst Scientists had always thought of macro bio-molecules as major players of life's process, identifying and unraveling their roles was a herculean task, and when they were finally discovered and fairly understood, it plunged humanity into a revolutionary dilemma I refer herein as **Bio-Molecular Revolution.**

2.0 Bio-Molecular Revolution

The word revolution means different things to different people. For some, it is synonymous with upheaval or revolt but Todd (1998) in his exquisite book Revolutions, 1789 – 1917, posited that no single definition of the term revolution has been acceptable to all and sundry. Notwithstanding, the Webster Collegiate dictionary defines revolution as "a sudden, radical, or complete change". It also defines revolution as "a changeover in use or preference especially in technology". Revolution in this lecture is therefore used to connote drastic means of effecting change(s) in human societies and/or way of life.

Right from the beginning of time, man has continually sought for answers regarding himself and his environment. The quest to unravel the seeming mystery of life and its diversities of expression progressed steadily over time and eventually led to the birth of a revolutionary interdisciplinary field of study called **Molecular Biology.**

The phrase 'Molecular Biology' was first used by Warren Weaver of the Rockefeller Foundation, USA in 1938 while attempting to explain life form a physical and chemical

viewpoint. Unlike several other fields and disciplines of study that could be traced to an individual's findings or position in history, molecular biology is an aggregation of many intertwined strands of knowledge.

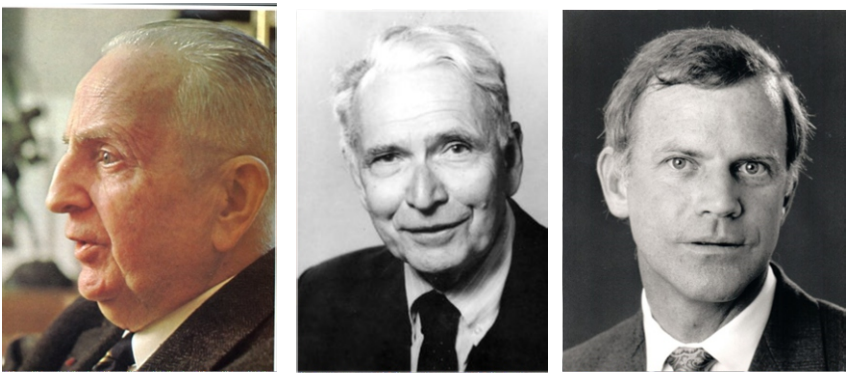

Fig. 2.1: Some contributors to Bio-molecular Revolution (Adapted from Google Images)

Molecular Biology revolves fundamentally on the molecular basis of life and it's processes; bordering on proteins, DNA and RNA. The discovery of these macro bio-molecules, and the subsequent understanding of their structures, functions and interrelationships have revolutionized virtually every facet of human endeavor. Awed by the power and potentials Molecular Biology, Erwin Chargaff attested to the building up of an impending Bio-molecular revolution as far back as the 1950s. In making this position eloquently clear he reportedly claimed that Molecular Biology **"was running riot and doing things that can never be justified"** (Newton, 2016).

It has been over 60 years Erwin Chargaff took this far reaching position to assert the potential power of Molecular Biology. Can we really say that Molecular biology has indeed run riot? This is a rhetorical question I would like everyone to answer for themselves as we look into the applications and potentials of Molecular Biology.

2.1 Applications and potentials of Molecular Biology

The principles of Molecular Biology have been deployed in a wide range of discipline and human endeavours. These include but not limited to:

- Understanding life processes
- Deciphering evolutionary relationships among living things
- Identification, taxonomy and classification of living things
- Diagnosis, forecast and management of plants, animals and human diseases
- Environmental pollution monitoring and control
- Forensics and crime detection and control
- Adjudication of judicial impasse
- Environmental and public health epidemiological studies
- Livestock and Plant breeding
- Agricultural biotechnology and Food processing
- Pharmaceuticals and drug discovery – Vaccines and Immunizations
- Ecological conservation and management
- Paternity test
- Toxicology

- Archaeology and paleontology etc

(Etebu and Pondei, 2013: Etebu and Osborn, 2009, Chang and Chan, 1993; Singh *et. al.,* 2019; Etebu and Tungbulu 2015; Etebu, 2019; McCartney, 2010; Phillips, 2008)

Molecular Biology is like a ferocious revolutionary tsunami sweeping across the globe and human societies (whether for good or evil is a matter of individual perception and leaning). One thing is certain, there is hardly any human or individual that has not been directly or indirectly impacted by Molecular biological approaches. Some of the specific ways and impacts of molecular biology are discussed hereunder.

2.1.1 Ancestral identity tracing: Bio-molecular approaches are the bases of several commercial Establishments, especially in developed countries where immigrants in foreign countries resort to tracing their ancestral origin (Debus-Sherrill and Field, 2019).

2.1.2 Forensic and paternity tests: Through Molecular biological approaches, murder and homicide cases have been successfully resolved in the courts of law and culprit(s) served with justice (McCartney, 2010; Phillips, 2008). Quite recently, the Nigerian Social media space has been awash with stories of men fathering children of other men without knowing until "DNA test" unearthed the truth. A very prominent politician popularly called MKO Abiola (of blessed memory) could be said to have heightened the crave for DNA parentage testing among Nigerians as he was believed to have made it a mandatory condition in his will for all his children to qualify as beneficiary after his demise (Ajumobi and Sessou, 2021).

A recent disclosure within our region that dominated the social media is a testament of the way Molecular Biological approaches (alias DNA testing in this instance) have revolutionized the actions and inactions of our society. Secrets perpetuated under the cover of night are been illuminated decades of years afterwards, when brought under the invasive probing lens of Molecular biology.

2.1.3 Production of Pharmaceuticals: Numerous pharmaceuticals that were hitherto scarce owing to production difficulties are now readily available for prescription and administration to those that need them. One of such pharmaceuticals is insulin relevant for the management of diabetic patients. Accessibility to insulin has become quite easy because of its abundant supply. Prior to the advent of Molecular biological approaches (precisely Recombinant DNA Technology, RDT), pharmaceutical companies relied on pancreas of several animals to produce insulin. With the advent of RDT, Bacterial cells such as *Escherichia coli* and fungal cells such as *Saccharomyces cerevisiae* are genetically altered to produce insulin (Allen *et. al.,* 2019; Govender *et. al.,* 2020).

2.1.4 Agricultural boost in food production: Molecular approaches are deployed in variety of ways to increase crop yield to fight hunger and starvation. For example, the term Genetically Modified Organism, otherwise called GMO, is a common scientific phrase in today's information space. Although people have varying and divergent opinions as to the acceptability and consumption of

products of GMOs, millions of hectares of land are cultivated for this group of food and introduced into our food chain (Maghari and Ardekani, 2011). Genetic materials are known to move from one organism to another in nature through a variety of mechanisms. Leveraging on this natural phenomenon, Molecular Biologists are able to genetically modify organisms such that organisms develop certain desired traits that are either lacking, or are in short supply in them.

2.1.5 Animal Cardiovascular disease treatment: A report published in 2012 asserts that pigs with malfunctioning hearts had their heart beats normalized on injection with a genetically engineered virus. Upon injection, a Tbx 18 gene from the virus integrated with the heart muscles of the recipients, to resuscitate the heartbeats of the pigs. Scientists think that this technique would restore the heartbeat of human with similar heart challenges (Kapoor *et. al.,* 2012).

2.1.6 Disease resistant transgenic cows: The diary industry was known to lose about $2 billion and $200 million in USA and Britain respectively owing to mastitis disease affecting the mammary glands of certain cows. The disease is caused by a bacterium *Staphylococcus aureus,* and only 15% of infections are usually successfully treated with antibiotics. To arrest this challenge, a group of Scientists deployed a Bio-molecular approach relying on a related bacterium *Staphylococcus simulans* known for encoding a protein that kills *S. aureus.* They extracted and altered the relevant gene from *Staphylococcus simulans* and introduced same into DNA of the cows; thus modified

their DNA. Following modification of their DNA, the transgenic cows produced the protein that naturally destroys *S. aureus,* causal agent of mastitis disease (Khamsi, 2005).

2.1.7 Attenuation of Live Vaccines: Live vaccines are often preferred than other forms because they confer long lasting immunity. To ensure that they only induce immunity without causing disease, the vaccines are treated to reduce virulence of the disease causing agents. Traditionally, this is achieved through several sub culture regimes of the microbe on growth media, and in animals or egg cell cultures. In some cases, virulence is reduced through deployment of chemical and physical mutagenesis. In recent times, molecular methods are deployed to genetically modify microbes to either reduce their virulence or undesirable effect they would have on the tissues into which the vaccine would be administered (Frey, 2007).

2.1.8 Plant disease Diagnostics and forecast: Molecular techniques have been applied to both detect and quantify plant pathogenicity genes in soil as a measure of inoculum density/potential without recourse to culture. Such results alongside other factors responsible for disease have been relied upon to design disease predictive models of specific plant diseases. Direct quantification of plant pathogenicity genes in soil-DNA that bye-passes the need for culture was first carried out on a suite of pea pathogenicity genes that empower pathogenic variants of *Nectria haematococoa* to cause foot rot disease among pea (*Pisum sativum*) plants (Etebu, 2008; Etebu and Osborn, 2009, 2010, 2011a-d;

2012b).

2.1.9 Human disease diagnostics and control: Molecular approaches are effectively employed in the diagnosis of numerous diseases in humans. Some of these include amongst others, Cholera, anthrax, dysentery, typhoid, schistosomiasis, malaria, ascariasis, hepatitis, cryptosporidiosis, polio etc (Etebu and Pondei, 2013; Chang and Chan, 1993; Guatella *et. al.,* 1989). A good case in point in this regard is the present global fight against COVID-19 pandemic disease caused by the Severe Acute Respiratory Syndrome Corona Virus-2 known by the acronym SARS-COV2. A variant of the Polymerase Chain Reaction (PCR) was the only means of diagnosis of this disease approved by the World Health Organization, prior to the development of immunological assay(s) which in themselves are also within the purview of Molecular Biology (CDC, 2020).

Regarding control of human diseases, bio-molecular approaches is leading this line of medical practice. For the first time in human history, mRNA vaccine is deployed to control the spread of human diseases; COVID-19 to be specific (CDC, 2021). Only a few months ago, Scientists have turned the spate of bio-molecular revolution on female mosquitoes in Florida, USA to curb the malaise of diseases such as malaria, zika, yellow fever, dengue etc (Lanese, 2021)

2.1.10 CRISPR and Gene Editing

One approach of molecular biology that is sweeping across the scientific community and human society is the gene-

editing tool called CRISPR aided by a protein called the Cas protein. CRISPR is the acronym for "Clustered Regularly Interspaced Short Palindromic Repeats". CRISPR often termed "Molecular Scissor" is a natural system in bacteria that evolved to ward off invading viruses by chopping up their DNA. Scientists relying on this natural phenomenon are now able to modify this natural defense system of bacteria and redirect it to easily identify and cut DNA of other organisms; including bacterial sequences it naturally protects.

Leveraging on this seemingly simple natural phenomenon, CRISPR offers a plethora of potentials that could be considered positive or negative, depending on one's leaning and disposition. On the positive side, the technology would potentially solve the problem of global food security, shortage and hunger. The technology has been effectively deployed to correct destructive mutations responsible for adverse medical conditions such as cancer and many other genetic disorders in animal and human cells (Uddin *et. al.,* 2020).

2.1.11 Cell and Gene therapy (CGT)

Cell and gene therapy is an investment sector growing in leaps and bounds in the western world. Reports have it that as much as £20 billion was used to fund experiments relating to cell and gene therapy in the UK.

Relying on Bio-Molecular principles and approaches drugs capable of resolving specific genetic disorders are now in the market. In particular, Zolgensma known to be the world's most expensive drug (£1.79m per dose) is able

to address the genetic basis of muscular dysfunction of the spinal cord in what is termed Spinal Muscular Atrophy (SMA); a leading cause of death of babies in the UK (Nawrat, 2021). Notwithstanding the huge financial investments in the growing sector, there is reportedly a huge dearth of people with relevant skills even in the UK. This being the case with the UK, I wonder what we would say regarding Nigeria.

However, the emergence of COVID-19 has greatly popularized Molecular Biology in most countries of the world, especially third world countries like Nigeria, where only a handful of Specialists in the discipline exists. COVID-19 like an insurgent has placed a demand on nations of the world to appreciate the place of Molecular Biology. I hope this clarion call would translate to redesigning the Nigerian University curriculum to accommodate this indispensable discipline of the day.

2.1.12 Designer Babies

Relying on CRISPR technology, a biophysicist, He Jiankui successfully produced the first genetically engineered human twin babies (Lulu and Nana) intended to be resistant to HIV (Cohen, 2019). The babies were successfully birthed in 2018 (Cyranoski, 2020). Although the Scientist deployed the technology for a 'good cause' he was sentenced to 3years jail for “illegal medical practice”, apparently for jettisoning ethical guidelines on the application of the technology. Scientists are very skeptical regarding uncontrolled deployment of this powerful tool of Bio-molecular science, owing to its potentially dire negative consequences, should it be misapplied or get into

wrong hands or agencies that would deploy same for a destructive purpose. The technology could potentially be used to genetically design humans, such as with super high intelligence and strength, whose capabilities (positive or negative) cannot be fathomed or known (D'Alessio, 2019; Uddin *et. al.,* 2020). For these uncertainties, it is generally agreed amongst Scientists that CRISPR should at best be deployed to edit genes on somatic (body) cells, and never to be used on germ cells (Uddin *et. al.,* 2020).

2.1.13 Stem cell Research and the growing skepticism

Molecular biological principles and phenomena are pivotal to the emergence and development of stem cell research. One of the goals of these researches is to address the acute and persistent shortage in transplantable human organs as well as to having better understanding of human development, disease progression and ageing. However, notwithstanding the enormous potential benefits, there is growing palpable fear regarding experiments involving the growing of human stem cells in non human embryos such as pigs, sheep and monkeys that would lead to hybrids of human and other non humans (Briggs, 2021).

So far, chimeric embryos involving human cells are destroyed early and not allowed to grow into full term. The fears stem from the fact that if the practice is left unchecked, a radical Scientist may throw caution to the wind and allow human hybrids to fully develop. Such a situation would exasperate an already contentious line of Bio-molecular research.

Vice Chancellor sir, having listened to some of the

applications of Bio-molecular science with its vast expanse of potentials, you would agree with me that there is truly an ongoing Bio-molecular revolution. What I am not sure of, is whether or not you would agree with Erwin Chargaff who thought Molecular biology was running agog with procedures of unjustifiable outcomes and potentials. Whatever your take is, Bio-molecular science impacts every human directly or indirectly.

3.0 Structure and functions of principal Bio-molecules

I have so far defined Molecular biology simply as the study of life at the molecular level. A more holistic definition would be "***the study of the structure, function, and inter-relationships between and among macro bio-molecules, particularly proteins and nucleic acids".***

3.1 Protein structure

Structurally, proteins are essentially repeating subunits of amino acids joined successively by peptide bonds.

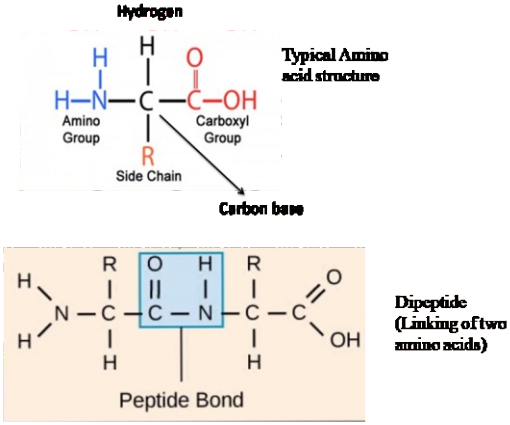

Fig. 3.1: Amino Acid Structure and the formation of Dipeptide (Adapted from Google Images)

There are twenty naturally occurring amino acids encoded by the human genome, and every one of them comprises an amino group, hydrogen, Carboxyl group (acid) and R-side chain (see Fig. 3.1) all attached to a carbon base. Whilst all amino acids possess same amino, hydrogen and carboxyl group, every single one of them possesses a unique R-side chain making it the component that differentiates one amino acid from another (Fig. 3.2). All amino acids except proline, possess a free amino group and a free carboxyl group.

Amino acids are categorized either as polar or non polar (Fig. 3.2)

Fig. 3.2: Structures of naturally occurring amino acids (adapted from Google Images)

Proteins, generally, progressively attain four levels of folding (Reddy, 2020), represented as Primary, Secondary, Tertiary and Quaternary structures (Fig. 3.3)

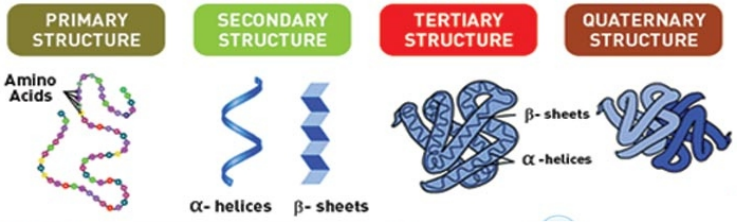

Fig. 3.3: Protein structure at different levels of folding (Adapted from Reddy, 2020)

3.2 Functions of Proteins

Proteins are classified based on different criteria, one of which is function. With respect to function, proteins perform at least seven (7) broad roles in life processes (Fig. 3.4). Accordingly, proteins are classified as structural proteins (eg., Collagen), transport proteins (eg., haemoglobin), defense proteins (eg., Immunoglobullins), hormonal proteins (eg., Insulin, thyrosin), enzymatic proteins (eg., DNA polymerase, amylase, cellulose, cutinase), storage (eg., Ferritin), and Contractile proteins (eg., myosin, actin) as shown in Fig. 3.4 below:

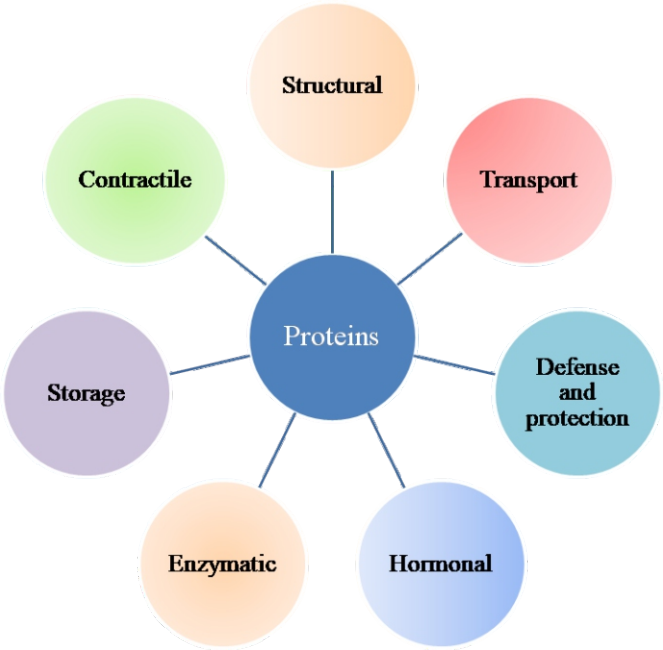

Fig. 3.4: Protein types based on function (Adapted from Google Images)

A collapse in any of the functions shown in Fig. 3.4 would result to the cessation of life for that particular organism. Take enzymatic proteins for example. These set of proteins are responsible for the orderliness of biochemical processes of anabolism and catabolism, required for the sustenance of life of any given cell. Without the function of enzymes, majority of food we eat would be of no value. Food substances play their valuable roles in our body only when they are assimilated and absorbed which are preceded by digestion.

3.3 Structure of Nucleic Acids

Nucleic acids are either Deoxyribonucleic acid (DNA) or Ribonucleic acid (RNA). Both DNA and RNA occur in all living things (except a few viruses that have only either of each type of nucleic acids). Like other macro bio-molecules, nucleic acids are polymers of much smaller bio-molecules called **NUCLEOTIDES** which are joined together by what is known as **Phosphodiester bonds** or **bridges** (Fig. 3.5).

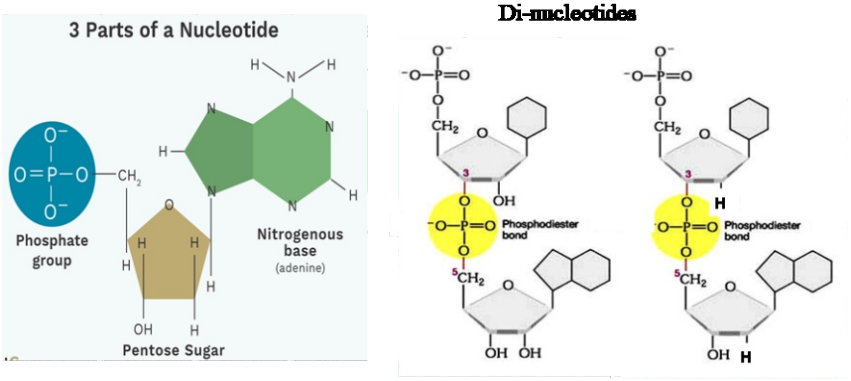

Fig. 3.5: A schematic representation of a Nucleotide and Dinucleotides (Source: Russel, 2010).

Every nucleotide has three (3) components (Fig. 3.5) which are:

- A Ribose/Deoxyribose (Pentose) Sugar
- A Phosphoric acid residue (Phosphate group)
- A Nitrogenous base (Adenine, Cytosine, Guanine and Thymine or Uracil)

The nitrogenous base is what delineates one nucleotide from another. Broadly, speaking, nitrogenous bases as components of nucleotides are either PURINES or PYRIMIDINES.

Structurally, whilst purines consist a double carbon-nitrogen ring with four nitrogen atoms, pyrimidines possess a single carbon-nitrogen ring with two nitrogen atoms as shown in Fig. 3.6 below.

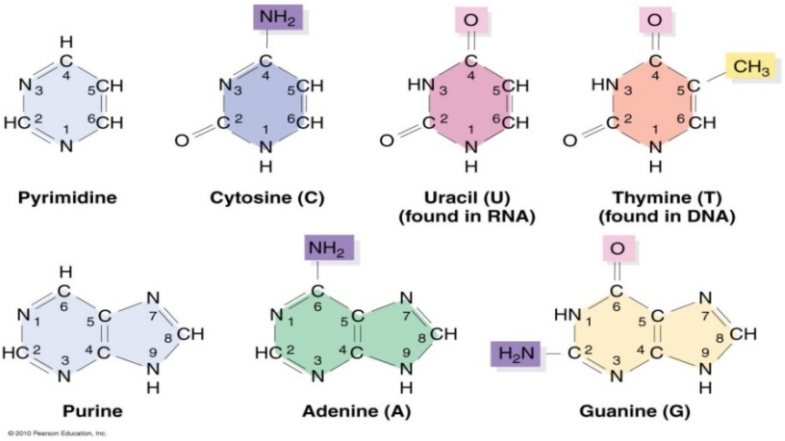

Fig. 3.6: Nitrogenous bases found in Nucleic acids (DNA and RNA) (Adapted from Russell, 2010)

Adenine and Guanine are purines while Cytosine, Thymine and Uracil are pyrimidines (Fig. 3.6). For convenience, the bases and by extension nucleotides are represented by their respective starting letters. Hence Adenine is denoted as A, Guanine as G, Cytosine as C, Thymine as T and Uracil as U. Technically, the different nucleotides with a single phosphate group are Adenosine monophosphate, Guanosine monophosphate, Cytidine monophosphate, Thymidine monophosphate and Uridine monophosphate denoted by the letters A, G, C, T and U, respectively. Whilst Adenine (A), Guanine (G) and Cytosine (C) are found in both DNA and

RNA, Thymine (T) is found only in DNA and Uracil (U) is found only in RNA.

Apart from being different in the sugar moiety and nucleotide sequences, RNA is structurally a single stranded molecule while DNA is a double stranded molecule. Being double stranded, DNA comprises two strands that are both complementary and run anti-parallel to each other (see Fig. 3.7).

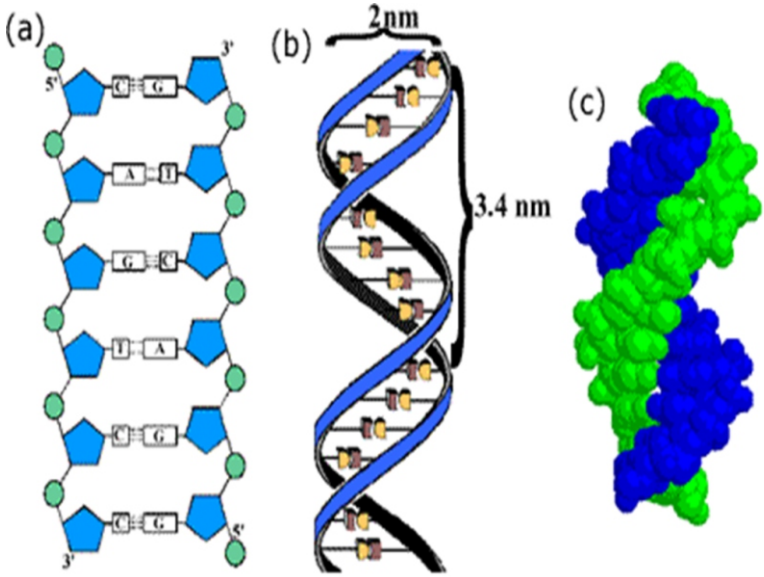

Fig. 3.7: Schematic representation of the complementary, anti-parallel nature of DNA and double helix structure of DNA (Source: Google Images; Pray, 2008a).

You would notice in Fig. 3.7a that while the sugar moieties of the strand on your right seemed to point or face upwards, those on your left seemed to face downwards. This is the anti-parallel nature of DNA.

The two complementary strands of DNA actually are connected by weak hydrogen bonds through the nitrogenous bases of the respective nucleotides on both strands. Specifically, adenine on one strand pairs up with thymine on the opposite strand and vice versa. While adenine (A) pairs up with thymine (T) through double hydrogen bonds, guanine (G) and cytosine (C) are linked through triple hydrogen bonds (Fig. 3.7).

In addition, the two complementary strand of DNA wind around each other, much like a twisted ladder with the nucleotides assuming the similiture of steps within the ladder. This is what is generally referred to as the Double Helix structure of DNA (Fig. 3.7b,c) described by James Watson and Francis Crick in 1953 (Pray 2008a). For this discovery, the duo along with Maurice Wilkins were awarded the Nobel Prize in Medicine in 1962.

Mr. Vice-Chancellor Sir, let me at this juncture draw your attention to one of the revolutionary wonders of DNA. This would blow your mind! So fasten your seat belt.

3.4 Wonders of DNA and Chromosome

Molecular biologist involved in human genomics have variously reported that an average human adult possess tens of trillion of cells. If we take all DNA sequences of all cells of an adult human and stretch them out end to end, it would amount

to about 6.20 x 10^{12} metres (Piovesan *et. al*., 2019). This is equivalent to 6,200,000,000 kilometres or simply 6.20 x 10^{9}km.

Meanwhile reports from National Aeronautics and Space Administration (NASA) show that the distance between the earth and the sun is about 150,000,000 km (https://cneos.jpl.nasa.gov/glossary/au.html). This figure could also be written as 1.50 x 10^{8} km. If we divide 6.20 x 10^{9} km by 1.50 x 10^{8} km, we would arrive at 41.33!

What this means is that, if we are to stretch all the DNA sequences of all nucleated cells in your body and join them end to end, it would cover the distance from earth to the sun by over 41 times! (Piovesan *et. al.,* 2019). Is this not great? This obviously underscores the wonder of the human DNA. One cannot agree less with the Biblical King David who poured encomiums to the Almighty God saying "***Thank you for making me so wonderfully complex! Your workmanship is marvelous….***" (Psalm 139:14 New Living Translation). The King James Version of the same scripture puts it this way "*I will praise Thee; for I am fearfully and wonderfully made: marvelous are thy works…"*

Barring scientific evidence, this is a wonder that beats every stretch of human imagination. Let me jostle you a bit more to explain how DNA is housed in far much smaller vesicles (nuclei) or cells than they are. Let me begin with a microbial example.

The typical size of a bacterial cell ranges between 0.2-5µm (Portillo *et. al.,* 2013) with an average genome size of about 4 million nucleotides (diCenzo and Finan, 2012). *Escherichia*

coli cell in particular is cylindrical with a length of 1-2 μm and 0.5 μm in radius (Riley,. 1999) with a genome of at least 4.66 million nucleotides (Bergthorsson and Ochman, 1995). The distance between two successive nucleotides on a DNA molecule is 0.34nm (ie, 0.00034 μm) (Voet *et. al.,* 2006*).* As such the length of DNA in a typical bacterial cell when stretched end to end would be 0.00034 μm x 4,660,000 which equals 1, 584.40 μm (equivalent to 1.58mm approx.).

What this means is that the length of a bacterial DNA such as *E. coli* is approximately 1,584 μm if joined end to end, and this is conveniently housed in a bacterial cell of just 2 μm long. You work out the ratio to further appreciate the wonder of nature. When you do, you would arrive at 792, meaning a typical bacterial DNA if stretched out is at least 792 times as long as a typical bacterial cell length.

Let us consider the human DNA and the size of the nucleus where DNA resides within the cell. It would interest you to know that a typical human cell is only 10 μm in size whilst the nucleus that majorly houses DNA is 6 μm (Albert *et. al.,* 2002). If all the DNA sequences in a single human cell were to be joined end to end, it will amount to about 2m (equivalent to 2,000,000 μm), and this relatively massive DNA of 2 million μm is contained in a 6 μm sized nucleus. How is this possible you would probably want to ask? The answer lies with the structural configuration of DNA. Putting it more succinctly, DNA is stored as part of thread-like structures called **Chromosomes** majorly in the nuclei of cells.

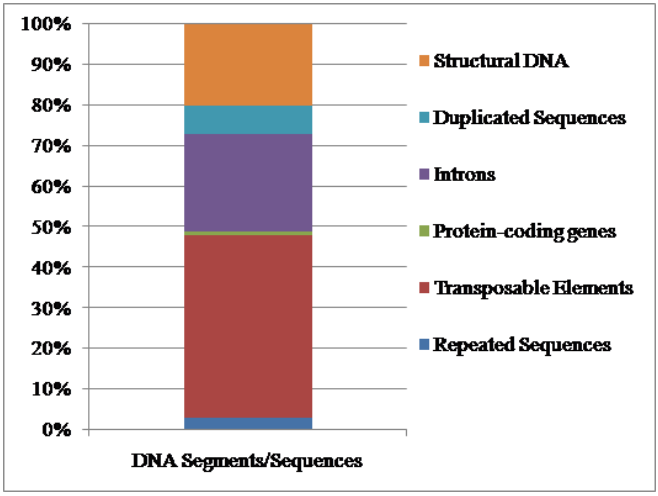

Fig. 3.8: Schematic representation of DNA segments of the Human Genome (Adapted from Google Images)

3.6 Functions of Nucleic Acid

- Storage of genetic information
- Transfers genetic information from cell to cell, and from generation to generation
- Transcription and translation of genetic information into phenotypic traits
- Involved in mutation
- Replication
- etc

4.0 The Central Dogma of Molecular Biology

Vice Chancellor sir, you would easily enumerate a number of differences between any two human individuals if asked to do so. Further still, you would enumerate numerous differences between siblings of the same parents if you are given the task to do so. As a matter of fact, there are differences even between different organs, tissues and even cells of any given individual organism. These obvious and visible facts validate the uniqueness of our individuality.

We have often heard that we owe our individual uniqueness to our DNA, a fact which Scientists have often leveraged upon in the development of diverse DNA/Genetic diagnostic procedures. The question one may ask is how does DNA account for the visible phenotypic manifestation of any given living organism? Answering this question among others is the crux of Molecular Biology which has been christened "Central Dogma of Molecular Biology" postulated in 1957 by Francis Crick and published in 1958 (Crick, 1958).

Whilst proteins drive life's processes and determine the unique individuality of all persons, nucleic acids, particularly Deoxyribonucleic acid often simply code-named DNA, encodes protein via Ribonucleic acid or simply RNA. This is succinctly captured in the concise illustration shown in Fig.4.1 below. I will try to keep this as simple as possible because this is a public lecture with my audience traversing different disciplines of study and career.

Let us take a close look at Fig. 4.1 together. Firstly, you would notice a simplified network of relationships among three Bio-

molecules – DNA, RNA and PROTEIN. The central dogma is particularly hinged on the unidirectional flow of information from DNA leading to the formation of protein. Information flows from DNA to RNA and then to protein. Information does not flow from protein to RNA or DNA, NEVER!!! (Crick, 1958).

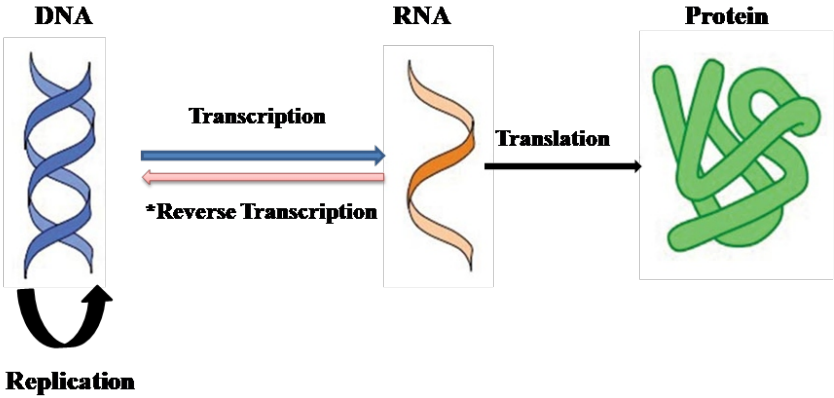

Fig. 4.1: A schematic representation of the essence of Molecular Biology (Adapted from www.coursehero.com)

You would also notice that there is an arrow pointing from RNA to DNA with an asterisks, meaning it is not a common route of information flow but it nonetheless occurs in nature in certain organisms. Specifically, this process is common to a group of viruses called RNA viruses, amongst them are Retroviruses. These viruses, unlike other biological agents possess RNA as their genetic material. They rely on their RNA to produce DNA as an intermediary molecule in their replication cycle. To produce DNA from RNA, retroviruses rely on an enzyme called Reverse transcriptase. Once

produced, this viral complementary DNA (usually designated cDNA) integrates itself into the host's genome where it is replicated, transcribed and translated into viral proteins (Poltronieri *et. al.,* 2015). With this group of viruses, genetic information that would culminate in the synthesis of their proteins emanates and flows from RNA first into DNA. This is the basis for Reverse transcription and the enzyme at the centre of the biochemical process is Reverse Transcriptase. It would interest you to note that this is the basis for the Molecular diagnosis for COVID-19 test.

There is yet another unique flow of information captured in the Fig. 4.1. This is from DNA to DNA. DNA is the only molecule that utilizes information inherent in itself for its synthesis. Those in the biological sciences such as medicine, agriculture, botany, zoology, biotechnology, microbiology, environmental biology, biodiversity etc are conversant with or would have heard of the famous Polymerase Chain Reaction (PCR). PCR is hinged on this flow of information from DNA to DNA.

4.1 Information Flow from DNA to DNA

This is simply DNA replication. DNA replication begins with the unwinding of the double helix at a site called the origin of replication (Albert, 2003). Relying on each of the two strands of DNA serving as templates, two separate complementary strands of DNA are synthesized with the help of specific enzymes and RNA primers (Fig. 4.2).

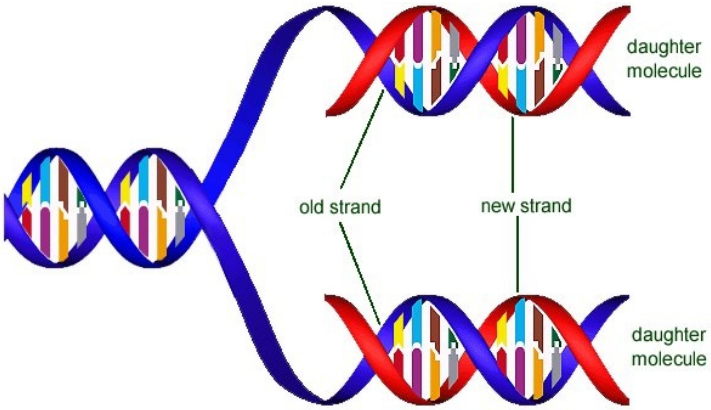

Fig. 4.2: *In vivo* DNA replication (Google Images)

One of the parental strands functions as template for the synthesis of what is called the leading strand while the other does the same for what is called the lagging strand, though in a slightly different way (Albert, 2003).

4.1.1 DNA Replication and the Emergence of Mutants and Polymorphs

The process of DNA replication is often laced with errors; nucleotide bases may be wrongly deleted or added into the DNA strand. In what may be construed as an anticipation, cells have inbuilt corrective measures which detect and amends errors that occur during DNA replication process. Inherent DNA repair mechanism serves to maintain the stability and fidelity of DNA (Smith, 2019).

Notwithstanding the inherent cellular corrective mechanisms a few errors that occur during DNA replication are undetected

and are therefore not corrected. Undetected and/or uncorrected replication errors sometimes results to a permanent change in the DNA sequence which amounts to Mutation (Pray, 2008b), and the resultant cell termed a Mutant.

The repeated division of a mutant cell could lead to accumulation of cells with defective DNA sequences, and this sometimes results to conditions that could be lethal. An example of medical conditions that arise from lethal mutations is cancer (Pray, 2008b).

Non-lethal mutations in a population of a given organism sometimes results to a genetic condition or trait that presents itself in different forms; a phenomenon termed Polymorphism. Polymorphism is the bedrock for genetic variation that engenders biodiversity and adaptation of a given species of organism to its ever changing environment, and it is one of the phenomena that have been hugely exploited in Molecular Biology (Etebu, 2019).

It would be worthwhile at this juncture to briefly explain how this natural process of DNA replication has been developed to take place under artificial conditions in test tubes; a procedure conventionally referred to as Polymerase Chain Reaction (PCR).

4.1.2 Polymerase Chain Reaction (PCR)

Polymerase chain reaction is essentially an artificial simulation of a natural phenomenon. It is the test-tube version or equivalent of DNA replication in nature invented by a Chemist, Kary Banks Mullis (1944-2019); for which he was

awarded a Nobel Prize in 1993. PCR was developed to resolve the slow pace of DNA replication in natural biological systems. Prior to the emergence PCR technology, the process of replicating DNA for detailed studies and/or further applications was abysmally slow and labourious (Etebu, 2013b; 2016).

PCR as a technique relies on DNA polymerase enzyme to exponentially amplify target DNA sequences *in vitro* (Saiki *et. al.,* 1988). The technique is very robust in application; able to detect and amplify specific DNA fragments from complex DNA samples, even if such sequences are rare or belong to microorganisms that are not yet cultured on synthetic media. PCR plays a very strategic role in most molecular biological methods and approaches, and has impacted the entire world of scientific research.

Over a billion copies of a target DNA sequence could be replicated from a single sequence through PCR in just two hours, depending on the cycling regimes (Etebu, 2013b). Applications of PCR-related approaches have not only enhanced the speed and efficiency of Nucleic acid amplifications but they have also enhanced sensitivity and specificity of etiologic diagnoses (Guatella *et al.,* 1989).

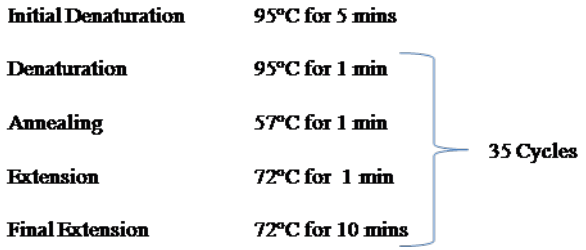

Fig. 4.3: A typical PCR cycling regime (Source: Etebu, 2008)

4.2 Flow of information from DNA to RNA

This is a process in which instructions are transcribed from genes within a DNA sequence to RNA, specifically Messenger RNA (mRNA) via genetic coded languages termed CODONS. A Codon is a triplet of bases on mRNA that encodes an amino acid. There are 64 sets of codes collectively referred to as the **Genetic Code** as shown in Table 4. 1. Whilst 61 of the Codons encode a specific amino acid each, the remaining three (UAA, UAG and UGA) do not specify any known amino acid; instead they bring about a termination of the protein synthesis process.

Table 4.1: The Genetic Code

UUU Phe	UCU Ser	UAU Tyr	UGU Cys
UUC Phe	UCC Ser	UAC Tyr	UGC Cys
UUA Leu	UCA Ser	UAA Stop	UGA Stop
UUG Leu	UCG Ser	UAG Stop	UGG Trp
CUU Leu	CCU Pro	CAU His	CGU Arg
CUC Leu	CCC Pro	CAC His	CGC Arg
CUA Leu	CCA Pro	CAA Gln	CGA Arg
CUG Leu	CCG Pro	CAG Gln	CGG Arg
AUU Ile	ACU Thr	AAU Asn	AGU Ser
AUC Ile	ACC Thr	AAC Asn	AGC Ser
AUA Ile	ACA Thr	AAA Lys	AGA Arg
AUG Met	ACG Thr	AAG Lys	AGG Arg
GUU Val	GCU Ala	GAU Asp	GGU Gly
GUC Val	GCC Ala	GAC Asp	GGC Gly
GUA Val	GCA Ala	GAA Glu	GGA Gly
GUG Val	GCG Ala	GAG Glu	GGG Gly

The process of transcription is similar to that of DNA replication but catalyzed by the enzyme RNA polymerase. Transcription occurs in the nucleus, and the process involves one strand of DNA (Sense or Template Strand) which serves as a template for the synthesis of a complementary strand of RNA called mRNA or pre-mRNA (if the latter requires processing before translation).

Similar to mRNA synthesis, DNA also serves as template for the synthesis of other types of RNA that are required in protein synthesis. Two of such are Transfer RNA (tRNA) and Ribosomal RNA (rRNA). These two molecules are also transcribed from their own specific genes (regions) in the DNA of the cell and they differ both in structure and function from mRNA

4.3 Flow of information from RNA to Protein

This entails translation of genetic message contained in mRNA to protein, as symbolized in Fig. 4.5 below

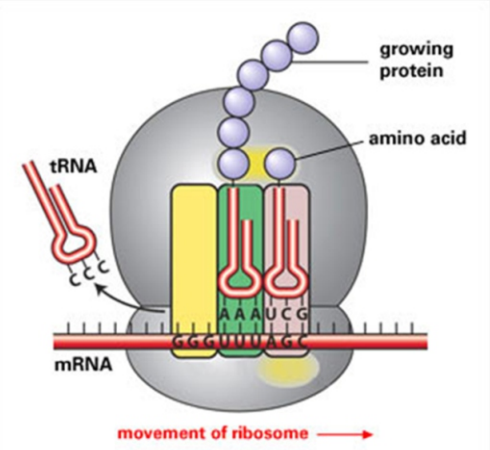

Fig. 4.4: Protein synthesis (Translational process) (Source: Google Images)

Whilst Ribosomes serve as the factories of the cell where proteins are synthesized, the tRNA often called the Dictionary of the language of life translates nucleotide sequence of mRNA into amino acid sequence of protein (polypeptide).

5.0 Regulation of Gene Expression

As you would have noted from the discourse so far, the day to day administration or running of the cell function are carried out by proteins. This onerous function is, however, made possible by different coding segments of DNA sequences called Genes that encode protein. As with all natural phenomena, life itself would be chaotic and would often assume the path of self-destruction if there are no checks and balances. As a result, good as genes are in the synthesis of proteins, their expressions are closely monitored and regulated.

Let me draw an analogy with a typical University system to expatiate on the need for control and regulation of activities of Units/departments of any given system. The University is saddled with the responsibility of equipping students with knowledge and skills that would engender personal and societal growth and development. As we all know, the entire University Management system which includes all academic and non-academic staff dictate what happens in the University. Whilst the entire University Management system, as defined herein, could be likened to DNA (Chromosomes), the different Course Lecturers could be equated as the 'Genes' residing as part of the Management team. This is because, Course Lecturers, like genes of a DNA molecule in a chromosome are responsible for specific behavioural changes in students they impact upon in course of teaching. University Lecturers

therefore occupy a huge vintage position in national growth and development. As such, no organized or responsible Institution would allow her Course Lecturers to go solo and to or teach whatever they like without any form of regulation and supervision. There are channels of coordination, and checks are put in place to appropriately regulate the actions and inactions of Course Lecturers. Such conscious mechanisms of regulations ensure that the overall aim and objectives of the Institution are not jettisoned by the Lecturers who directly impart knowledge and skills to students. Just as Course Lecturers are regulated at different levels and ways in the discharge of their duties, there are biological mechanisms put in place by cells to regulate the expression of genes and the function of its protein product.

Living things employ diverse mechanisms at different levels to regulate the expression and activity of genes in response to prevailing external and internal factors. Some of the mechanisms employed in regulating gene expression include, chromatin condensation, DNA methylation, transcriptional regulation, alternative splicing of RNA, translational control, post-translational modification and protein degradation. (Darie, 2013: Lackner and Bahler, 2008; Verdier and Thompson, 2008).

5.1 Chromatin Condensation

Chromatin could be described as a mass of genetic material composed of DNA and proteins that condenses to form chromosomes during cell division. The core function of chromatin condensation is to constrict and fit DNA within the cell's nucleus. Apart from this role, chromatin condensation also regulates accessibility of the DNA for transcription and other biological processes.

5.2 DNA methylation

DNA methylation is an epigenetic mechanism that involves the transfer of a methyl group onto nucleotide having cytosine as its nitrogenous base to form 5-methyl-cytosine. When this happens, transcription of DNA to mRNA is stalled. DNA methylation is commonly employed by differentiated cells to regulate tissue specific gene transcription.

5.3 Transcriptional regulation: Emphasis on Bacterial Operon

Transcription is a key step in gene expression, leading to synthesis of messenger RNA. Owing to its strategic importance and phase of protein synthesis, the step is given the rapt attention it deserves and is assiduously regulated by some proteins called transcription factors.

Transcription factors which act either as Activators that turn genes "on" or Repressors that turn genes "off" determine what genes are transcribed at any given time in each cell of an organism. Transcription factors play these roles by binding to specific sites on a DNA sequence, and in the process enable cells to utilize information gathered from different sources to perform logical operations to "decide" on whether or not to express a gene. The processes of regulating expression of genes were first studied with the bacterium *Escherichia coli*, in what is popularly called the *lac* operon, by Jacob and Monod (1961).

Bacterial genes occur as Operons (Fig. 5.1). An Operon is a cluster of functionally-related genes on a DNA sequence controlled by a single Promoter. Thus typically, bacterial Operons comprise gene coding sequences and regulatory

DNA sequences. Regulatory DNA sequences are binding sites for regulatory proteins that either facilitate or stall transcription of the gene sequences of the Operon.

Specifically, Regulatory DNA sequences are either Promoters or Operators. Similarly, regulatory proteins are either Activators or Repressors. Activators generally bind to the Promoter site of the DNA sequence, while repressors bind to the Operator sites. When the latter happens, transcription is stalled.

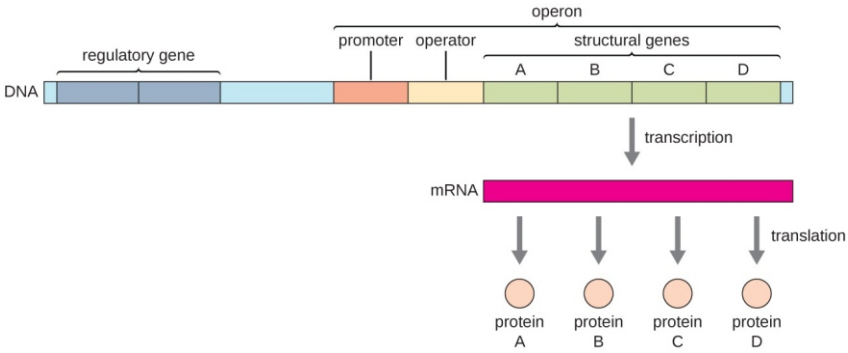

Fig. 5.1: A Schematic representation of a Bacterial Operon (Google Images)

Bacterial Operons are either inducible or repressible. Inducible Operons are usually "off" but are be turned "on" by an inducer. For example, the *lac* operon is an inducible operon that encodes enzymes for metabolism of lactose.

The Operon is turned 'on' to facilitate transcription when lactose is available and in the absence of other preferred sugars. Thus in the absence of lactose, the *lac* repressor binds

the operator to stall transcription while in the presence of lactose, the *lac* repressor would be released from the operator to aid transcription, albeit at a slow rate.

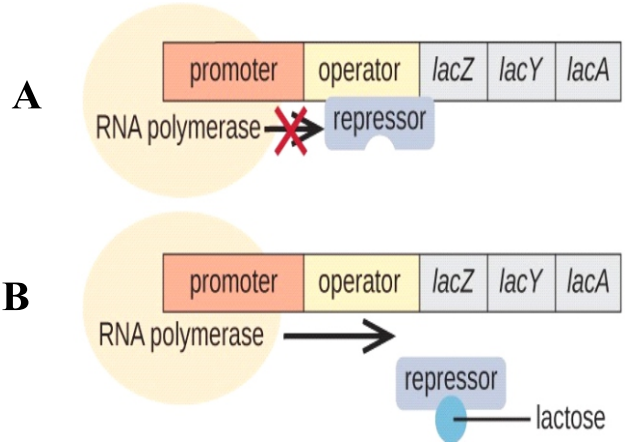

Fig. 5.2: Inducible bacterial Operon (Google Images)

In contrast to inducible Operons, Repressible Operons are by default turned "on" and are continually expressed until a co-repressor is introduced. An example of a repressible Operon is the *trp* Operon. This Operon encodes enzymes that catalyze the synthesis of the amino acid tryptophan. Being repressible, the *trp* Operon is expressed by default until the bacterium encounters high levels of tryptophan in the medium or environment. The presence of tryptophan naturally represses the *trp* Operon to stall its transcription.

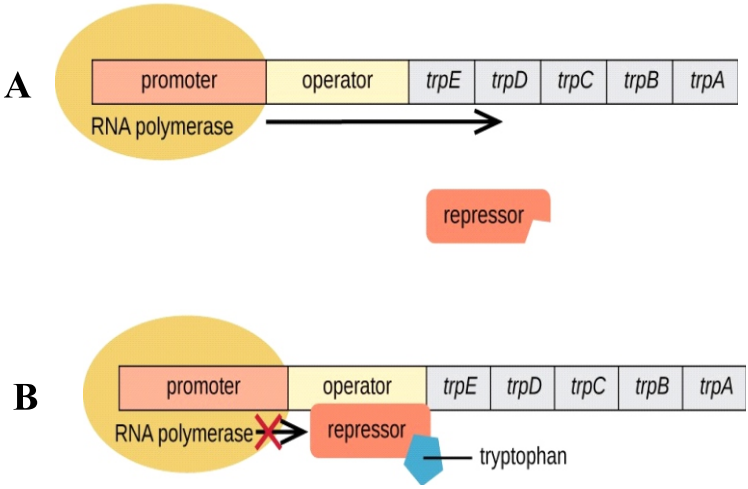

Fig. 5.3: Repressible bacterial Operon (Google Images)

Genes are thus either activated to express a given protein or repressed to stall the expression of the same in response to external and internal stimuli. Since prevailing Environmental factors are very dynamic and never static, protein syntheses are equally dynamic in response to the ever changing conditions of the environment.

5.4 Alternative splicing of RNA

Vice Chancellor sir, you would remember, I did say that eukaryotic DNA comprises both Exons and Introns. Whilst sequences of both regions are transcribed into a primary mRNA transcript, the introns are excised off and the transcript arising from exons are spliced (joined). Thus the mature mRNA transcript of eukaryotes comprises only sequences

transcribed from exons. However, during splicing (joining) one or more specific exons of a gene may be included within or excluded from the final processed messenger RNA (mRNA) (Black, 2003). When this occurs, an Alternative splicing or differential splicing of RNA is said to have taken place. Alternative splicing of a given gene results to formation of different mature RNA transcripts of varying lengths at any given instance. This is a common phenomenal mechanism of gene regulation among eukaryotes and it is responsible for the great diversity of proteins encoded by the human genome (Black, 2003).What this means is that a given gene would not always result to same length and sequence of mature mRNA transcript (Fig. 5.4).

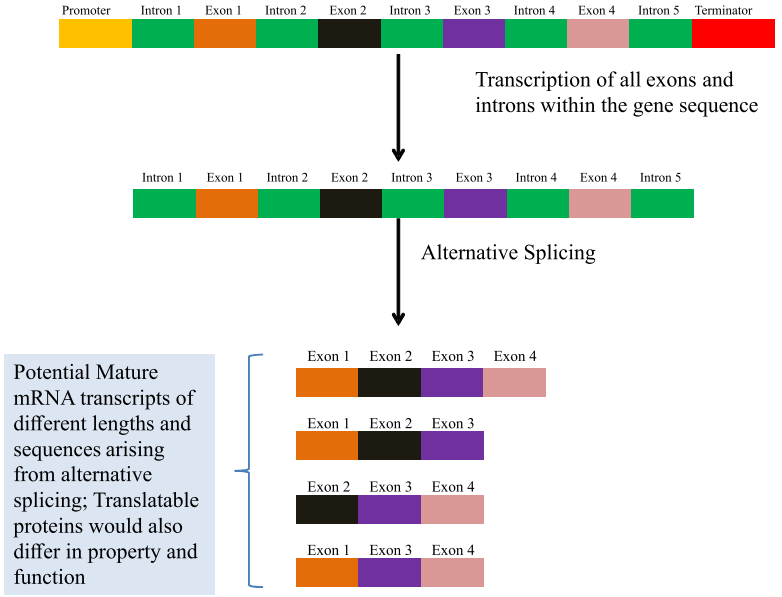

Fig. 5.4: Alternative Splicing of RNA (Source: Etebu, in preparation)

This action therefore gives room for multiple proteins expressible from a given gene sequence of DNA, as it allows a single gene coding for multiple proteins of different lengths and function.

5.5 Translational control

Although conventional studies on gene regulation have often centered on transcriptional control mechanisms, post-transcriptional mechanisms equally play immense role, particularly amongst eukaryotes (Day and Tuite, 1998).

Translation is a very complex process involving loads of essential proteins and RNAs. For example, microorganisms require about 130 genes to encode the entire translation apparatus which includes 50-60 ribosomal proteins, 20 aminoacyl-tRNA synthetases, 10-15 translation factors, and a host of ribosomal (rRNA) and transfer RNAs (tRNAs). Assembling all these components of the cell's translational machinery places a huge energy demand on the cell (Matthews *et. al.,* 2007). So depending on need and other factors, translation could be stalled when specific RNA and protein interact to either degrade the mRNA or prevent the ribosome from accessing the translational start Codon (Day and Tuite, 1998).

5.6 Post-translational modification (PTM)

Post-translational modification (PTM) are key mechanisms to increase diversity of proteins, and hence diversity of living organisms. The total number of genes in a single human being is estimated to be about 20,000 to 25,000 (Linares *et. al.,* 2016). Flowing from this, one would expect the total number of proteins expressible in any human to also be in the

neighborhood of 20,000 to 25,000 if every gene were to express a single protein. This, however, is not the case. The total number of proteins (technically called proteome) in human surpasses one million proteins. The reason for this higher diversity of proteome relative to a person's genome is predicated on the array of regulatory and modification mechanisms that come into play as part of gene expression and protein biosynthesis (See Fig. 5.5).

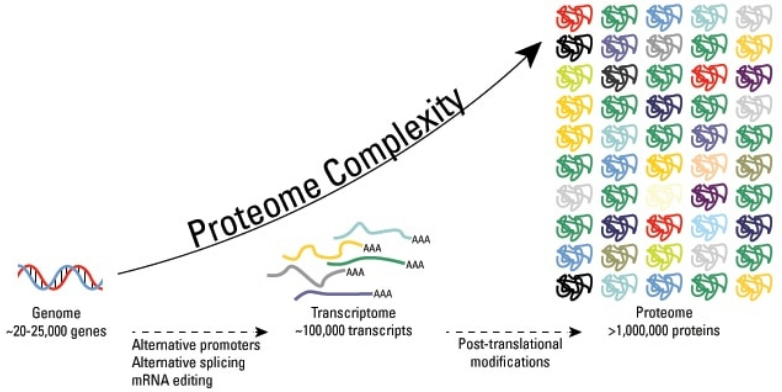

Fig. 5.5: Regulation of gene expression engenders protein diversity (Source: Google Images)

Apart from enhancing greater diversity of proteins expressible from a given DNA sequence, the role of PTMs are better appreciated when we take into cognizance the fact that living cells are often exposed to multiples of environmental and physiological factors from which they receive signals and to which they respond in an integrated fashion (Benayoun and Veita, 2009; Lee and Yaffe, 2016). Depending on the overall decision of the cell, arising from the environmental signals, an already translated protein may be modified or even degraded.

Post translational Modification as a means of gene regulation, occur in three broad ways. These are chemical modification, proteolytic cleavage or protein degradation (Vyas and Mehta, 2011).

5.6.1 Chemical Modification

This entails the modification of expressed protein through covalent addition of small molecules to the amino acid residue or the proteins C-and N- termini. Such small molecules include phosphate, acetyl, ubiquitin, carbohydrate, methyl etc.

5.6.2 Proteolytic Cleavage

Most proteins undergo one form of cleavage or the other after translation. The most common would be the elimination of the initiation amino acid methionine. Some proteins are first produced as inactive precursors of proteins called proproteins. Proproteins are activated following the removal of polypeptides through proteolysis. A good example of this phenomenon is the protein insulin.

5.6.3 Degradation of entire Protein

Cells contain multiple protein degrading systems such as Proteasomes that degrade proteins for different reasons. Proteasomes are proteolytic bio-machines found in Archaea, Actinobacterial species of bacteria and eukaryotes (Lecker *et. al.,* 2006; Humbard and Maupin-Furlow, 2013).

Different kinds of proteins are constantly translated from the DNA library backbone. Some of those proteins come with varying abnormalities due to mutations, biosynthetic errors and other factors (Lecker *et. al.,* 2006). Proteins with

abnormalities need to be eliminated to avoid a negative impact on cell function. To eliminate proteins with deleterious abnormalities, the cell relies on the fault finding capacity of proteasomes that recognize abnormal proteins and rapidly degrades them.

Aside degrading proteins with abnormalities, proteasomes also constantly degrade and re-synthesize proteins (such as regulatory proteins) with no obvious fault or abnormality. They do this as regularly and as often as possible to maintain optimum cell function. The rapid turnover of regulatory proteins allows their levels to change in amounts commensurate to and in response to external stimuli (Cooper and Hausman, 2006).

Thus apart from ensuring protein quality in cells, regulating gene expression guarantees cell stability and integrity of cellular processes (Humbard and Maupin-Furlow, 2013).

6.0 The Invisible Imperatives of Bio-molecular Revolution

The existence of an Invisible community of beings has always been a debatable subject. Whilst some believe in the existence of an invisible world, others consider such beliefs as mere myths particularly with respect to spirit and celestial beings. Religious records are, however, replete with the phenomenon of the invisible. In particular, the Bible says by "faith we know that the visible world was crafted from things that do not appear" (Heb. 11:13). In other words, the world we see was created from the invisible. Consequent upon this, some faith proponents opine that the invisible spiritual world rules and

determines what happens in the physical world. Whilst this claim remains debatable, depending on one's belief system, it would be safe and correct to say that we are all affected and influenced by a community of invisible entities called Microorganisms.

Microbes are amazingly diverse and heterogeneous; literally occurs in every plausible environment. This phenomenon of diversity has further deepened their study through bio-molecular approaches. The importance of microorganisms stems from their roles and activities in any environment they find themselves but they are probably better known and appreciated on two frontal spheres that greatly impacts on human existence and survival. These are:

- Medical Microbiology (Medicine and human health)
- Agricultural Microbiology (Agriculture and food security)

6.1 Microbial diversity: Promoter of Human and Agricultural Soil Health

Vice Chancellor sir, it would interest you to know that every human adult has far more microbial cells residing in and on themselves than their own cells. In particular, every adult human is estimated to possess as much as 10 times more microbes than its cells (Blaser, 2006). The sum total of microbes an individual harbor is collectively referred to as the person's Microbiome, and these play pivotal roles in sustaining man in his environment (Prifti and Zucker, 2013). Whilst the human genome has about 23, 000 genes, the collective number of microbial genes that constitute an

individual's gut microbiome is as much as 3.3 million (Fig. 6.1). Microbes are therefore able to perform a whole lot of different functions not undertaken by our cells. Owing to the indispensable role of microbes to human health, some authors consider the collective genome of our microbiome as "our other genome" or metagenome (Zhao, 2010).

The advent of Molecular Microbiology has opened a wide gate of investigations into the emerging sub discipline of gut microbiology which is increasingly broadening our understanding of microorganisms that inhabit humans, and their polarized roles in human health than was previously known. For instance, gut bacteria are known to protect human carriers by producing anti-inflammatory factors, antioxidants and vitamins whilst in the same breath, some could produce toxins that alter the DNA of their host in ways that result to chronic medical conditions such as cancer, obesity, diabetes etc (Zhao, 2010).

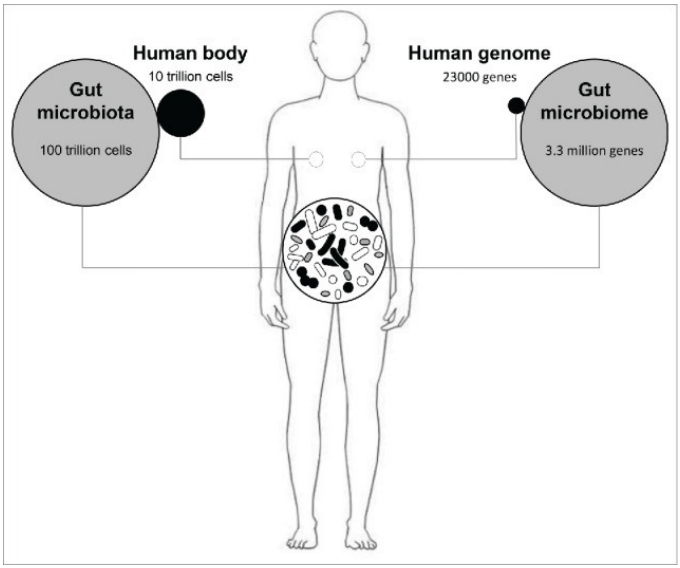

Fig. 6.1: Comparison between human and microbiota cell and gene numbers (Source: Linares *et. al.*, 2016)

Similar to human health, microbes play very important roles that sustain soil health. Soil health is defined in several ways, but from an agricultural viewpoint, it is defined as the capacity of soil to suppress plant pathogens and facilitate crop yield and productivity. Interestingly, the capacity of a soil to suppress plant disease is significantly influenced by a soil's microbial diversity (Abawi and Widmer, 2003; Garbeva *et. al.,* 2004; Etebu and Osborn, 2012a; Etebu, 2015). Soil's microbial diversity engenders resilience to ecological and environmental disturbances.

One of the ways to measure Biodiversity is Simpson's diversity index (SDI) which ranges from 0 to 1 and is represented by the formula

$$SDI = 1 - \frac{\Sigma n(n-1)}{N(N-1)}$$

Where SDI = Simpson's diversity index, n= number of the individual species, and N= total number of all species.

The phenomenon of diversity is very pertinent and important to this discourse because just as microbial diversity engenders resilience in agricultural soils, nations with diverse ethnic nationalities and resources would naturally be expected to be resilient in the face of adversities and challenges, if the citizenry fully understands and applies the natural principles of microbial diversity. Although Nigeria is made up of numerous ethnic nationalities, considered to be diverse, the definition and tools of diversity is grossly wrongly applied. Hence, what should naturally be a blessing to us has become our undoing, unfortunately.

To be in tandem with the natural concept of microbial diversity that breeds resilience to external environmental aggression, Nigeria may have to consider the proposals and suggestions I have proffered hereunder as lesson 10 under section 7 that deals with democratic governance and national cohesion.

6.2 Microbes as Imperatives of Molecular Biology

Microbes which constitute the biotic component of the invisible world are strategic and imperative in fostering our understanding of life process at the molecular level. Thus the discovery and development of Molecular biology is largely fueled by the study and application of members of this

invisible community of Microorganisms. Below are some of the ways microbes and microbiology enhanced the birth and development of Molecular Biology.

6.2.1 Discovery of life cells

The understanding of life metabolic process could be said to have begun with the discovery of the basic unit of life, the CELL. Following the invention of the microscope, Anton van Leeuwenhoek observed living cells of microorganisms in 1674 (Bhattacharjee, 2015). Although, Robert Hooke was the first to observe cells with the use of microscope in 1665 (Wolpert, 1995), he observed dead cells of plant origin. Thus the first living cell observed by anybody was a microbial cell, bacterium to be specific.

6.2.2 Debunking theory of Spontaneous Generation of Life

The first attempt to explain the origin of life from a scientific view point is well documented in the famous theory of spontaneous generation which held sway for the time of the ancient Romans, through the Middles Ages, and until the mid-nineteenth century. It took the efforts of several Scientists including, Francesco Redi, Lazzaro Spallanzani and Louis Pasteur, to disprove the theory of spontaneous generation of life. Their separate but similar experiments were conducted within a period of over two hundred years but it was the work of Louis Pasteur in 1859, which was also the last of the three experiments that finally laid the erroneous theory of spontaneous biogenesis to rest. It is imperative to know that

the authenticity of their conclusive experiments stemmed from the observed activities of microbes (Bhattacharjee, 2015). ***But for microbes, we would probably still believe life originates spontaneously.***

6.2.3 Proof of DNA as the Genetic material

Whilst the structure of DNA was discovered in 1869 and its component units identified in 1919, the true identity of the genetic material which is central to Molecular Biology remained a burning issue until 1928 when Frederick Griffith propounded the principle of transformation among variants of the bacterium *Streptococcus pneumonia* (Bhattacharjee, 2015)

Avery, MacLeod and McCarty who sought to substantiate the proof of the principle of transformation and to show that DNA was truly the genetic material in 1944 also relied on microorganisms as test organisms. Several years later, precisely 1956, Alfred Hersey and Martha Chase conducted another experiment using Microorganisms (Virus and bacteria) that lay to rest any conceivable objection of DNA as the genetic material.

6.2.4 Deciphering the Genetic Code

An important finding that proved the intermediary role of RNA in the synthesis of protein from information embedded in the DNA was the discovery of the genetic code by Marshall Nierenberg and Heinrich Matthaei (Matthaei *et al.,* 1961). These Scientists interpreted the language of the genetic code

whilst working with the bacterium *Eschrichia coli* in the 1960s. In particular, relying on this bacterium, they defined the 1st code or Codon UUU that encodes the amino acid phenylalanine, and subsequently spelt the Codons for all the other amino acids (Bhattacharjee, 2015). Breaking the genetic code was a huge step in the development of Molecular biology, as it relates to the relationship among DNA, RNA and Proteins.

6.2.5 Discovery, Isolation and use of DNA Polymerase enzyme in PCR

One approach that has given molecular biology a giant leap to stardom and recognition is the Polymerase Chain Reaction (PCR). PCR relies on an enzyme called DNA polymerase to facilitate the *in vitro* replication of target DNA Sequence. Interestingly, DNA polymerase was first discovered and isolated from a bacterium *Escherichia coli* in 1957 by Arthur Kornberg who had begun studying the mechanisms of DNA replication in the mid-1950s (Lehman *et. al.,* 1958) with attendant hiccups. However, PCR developed in astronomical proportion following the discovery and isolation of a thermos-stable DNA polymerase enzyme (*Taq* polymerase) in 1976 from another microorganism, *Thermus aquaticus* (Chien *et. al.,* 1976). The successful isolation and use of this microbial enzyme provided the platform for the conceptualization and development of automated thermocyler-based process for DNA amplification.

Several other Polymerase enzymes have been identified and isolated from several different bacteria over the years. Some of such polymerase are *Tth* polymerase isolated from *Thermus thermophiles, Tfl* polymerase isolated from *Thermus flavus, Tli*

polymerase isolated from *Thermus litoralis, Tpe* polymerase isolated from *Thermococcus peptonophilis, Tfu* polymerase isolated from *Thermococcus fumicolans and Pfu* polymerase isolated from *Pyrococcus furious* (Ishino and Ishino, 2014; Bergseid, *et.al.,* 1991). Aside their common uses of exponentially amplifying target DNA during PCR, different thermostable DNA polymerase are used for their varied comparative functional advantages.

6.2.6 Discovery and use of Reverse Transcriptase Enzyme

Similarly, the Reverse transcriptase enzyme is pivotal in performing Reverse Transcriptase PCR (RT-PCR) which is effectively employed in the detection and diagnosis of retroviral diseases and quantification of viral loads (Coffin and Fan, 2016). In addition to detection and quantification of retroviruses, RT-PCR has been extended to also study mRNA in relation to several human disease conditions such as non-Hodgkin's lymphomas, leukemia, and sarcomas (Coffin and Fan, 2016). All these innovative and revolutionary approaches are predicated on the discovery and isolation of Reverse Transcriptase enzyme from microorganisms; retroviruses in particular in the 1970s (Baltimore, 1970).

6.2.7 Discovery and use of Restriction endonuclease enzyme

Several procedures and applications of Molecular biology, particularly in forensic DNA investigations and analyses rely on the use of Restriction Endonuclease Enzyme to obtain

genetic fingerprints of crime suspects or microbes in an environment, in what is described as Restriction Fragment Length Polymorphism (Jeffreys *et. al.,* 1985a, 1985b). Interestingly, Restriction endonuclease enzymes were first discovered in bacteria as far back as the early 1950s (Luria and Human, 1952; Bertani and Weigle, 1953) which further proves the imperative role of microbes and microbiology in the revolution of bio-molecular applications in society.

6.2.8 Vectors in Genetic Engineering

Genetic engineering also known as Recombinant DNA Technology is hinged on the use of Vectors in the formation of Recombinant DNA molecules. Vectors often used in such procedures are viruses or plasmids obtained from bacteria. Thus our understanding of microbes was pivotal to the birth and development of several Molecular biological approaches requiring the use of recombinant DNA molecule.

6.2.9 Bacterial operon – Vanguard to understanding gene regulation

One of the fundamental concepts of the fulcrum of molecular biology is the regulation of gene expression, often simply termed 'gene regulation'. Our knowledge of this concept has been effectively employed in numerous investigative procedures. Like most molecular phenomena and approaches, our knowledge on gene regulatory factors and processes largely emanated from microbial studies, particularly the *lac* operon of *Escherichia coli* (Bhattacharjee, 2015)

6.2.10 Discovery of the CRISPR-Cas gene editing tool

Quite recently, the CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)-Cas (The CRISPR-Cas) system is the new bride courted by Molecular biologists who are into gene editing. CRISPR has shown to be a powerful DNA and RNA manipulation tool with huge and sometimes mind-blowing potentials. Like other molecular approaches, the CRISPR structure was first discovered in the microbe *Escherichia coli* in the late 1980s and early 1990s (Ishino, *et. al.,*1987) and by the year 2000, researchers had found structures similar to CRISPR in 20 different microbes, including *Haloferax mediterranei, Yersinia pestis* and *Mycobacterium tuberculosis* (Mojica *et, al.,* 1993; 2000).

From the foregoing, the genesis and development of Molecular Biology is substantially predicated on our knowledge and interaction with the invisible imperatives of the microbial community.

7.0 Lessons for Democratic Governance and National Cohesion

The word democracy is translated from two Greek words '*demos'*, meaning people, and 'Kratos' meaning power or rule. Connotatively, democracy would mean 'rule by the people' (Konrad-Adenauer-Stiftung, 2011). The people referred herein originally meant the poor or the masses.

The Organization for Security and Co-operation in Europe (OSCE) defines democratic governance as “a system of government where institutions function according to

democratic processes and norms, both internally and in their interaction with other institutions" (OSCE, 2021).

Flowing from these, democratic governance is often described as an act of governance run by a government of the people, by the people and for the people. It is a form of governance where the citizens are either directly involved in formulation of policies through referendum or indirectly through representatives they elect into government (Konrad-Adenauer-Stiftung, 2011). Being representatives of the people, a democratic government is expected to run the affairs of the State for the benefit of all.

National cohesion on the other hand means the presence of sense of togetherness and unity among citizens of a given nation. ***A Nation as defined by Gambari (2008) is the aggregation of people of diverse culture, tribe, religion and other pluralities unified by a common identity.*** It is instructive to note that Gambari is the present Chief of Staff to the president of Nigeria.
I first stumbled on this very important definition of a nation by Gambari in 2018 while preparing to present a paper with the title "The Christian and Nation Building", having being invited to speak in a South-South Senior Friends' Conference of a non-denominational Christian Body (The Student Christian Movement (SCM) on June 23rd 2018.

In course of my preparation on the talk on "The Christian and Nation Building" I came to a personal conclusion that Nigeria is far from being a Nation. In view of this stark reality I decided to look at some of the fundamental principles of nature evidenced in the interrelationship among nucleic acids and

proteins that govern life processes; hoping to rely on same to lend my voice in charting a way to strengthen our shared nationality.

I would therefore like to make some proposals and thoughts I think could be considered by those in positions of Leadership, authority and governance. I wish to reiterate that the proposals herein articulated may not be totally new, but I think they would be germane in driving our democratic ship to our El Dorado.

Three arms of Molecular governance

Like a democratic government the biological cell has three very important macro Bio-molecules that ensure smooth molecular governance. These are:

a. DNA: By its mode of operation and function, this could be said to represent the Legislative arm of the cell, being responsible for the laws (codes) that direct cell function.
b. RNA: By the same token, this would represent the judicial arm of bio-molecular governance of the cell; interprets genetic (molecular) code of the cell. RNAs are like the mediator between the DNA (Legislature) and Protein (Executive).
c. Protein: This represents the Executive arm of the biological cell. They implement the instructional code handed down by the DNA (Legislative arm). Proteins ensure smooth running of biochemical process, and gives the cell its unique physical identity.

Lesson 1: All arms of government must play their different roles in synergy

All three macro bio-molecules (DNA, RNA and Protein) central to Molecular Biology carry out their varied functions and roles in synergy for the overall good of the cell. Similarly, all three arms of government should have mutual respect for one another, and be resolved to act on behalf of the citizenry for the common good of all. They must work in synergy, avoid confrontational and divisive tendencies. They must place our collective and national interest over, and above their personal, ethnic, religious or political interest.

Lesson 2: The quality of our Legislative arm should never be compromised

Just as the cell is as good as the quality of its DNA, a nation is only as good as the quality of its Legislative arm of government, being representatives of the different Units of a nation. The rules guiding the selection and election of members of Local and National Assemblies should be very stringent and uncompromising. Persons with unstable temperament should not be allowed by law to be elected into a legislative office. Legislatures must be people of high emotional intelligence; being able to consider all sides and positions of an issue from an unbiased perspective.

Lesson 3: The Judiciary must uphold the essence of national functionality

Of the three macro bio-molecules under consideration, RNA is the only bio-molecule that occurs exclusively in living things

to advance the performance of a given function. To this effect, RNA (not DNA or Protein) is targeted in a molecular assay aimed at studying microbes that drive ecological processes or function in an environment. RNA is therefore the proof of functionality of a biological system. A functional human society is one whose judicial system is alive to her responsibilities, and discharges same without fear or favour. The wider society (including the other two arms of government) on their part must recognize and respect the rule of Law.

The usefulness of the judiciary is better appreciated in conflict resolution as it relies on the State's Constitution and bye-laws in the dispensation of justice. The judiciary, therefore, is expected to provide direction and guidance in the event of chaos arising from either ignorance or outright disregard to the law. The judiciary, in my opinion going by the natural role of RNA, should also be vanguard of amendment of the law where it is against the natural course of justice.

Lesson 4: Avoidance of 'errors' while enacting laws

DNA replication is often prone to errors but the cell in anticipation, have inbuilt corrective measures where rare error occurrences during DNA replication are detected and repaired. Inherent DNA repair mechanism serves to maintain the stability and fidelity of DNA (Smith, 2019).

Errors should be avoided as much as possible in governance. Those responsible for enacting laws should not knowingly introduce land mines in the form of clauses in our laws which

they intend to exploit to undo the good intentions of the law when and if the implementation of the law no longer serves their personal interest. Laws should therefore be as unambiguous as possible, be in tandem with common sense and natural course of justice.

Although public hearings are held before bills are enacted into laws, the final outcome of the debates solely rests on what the Legislators want and may not necessarily be the general pulse of the people aired during such hearings. I am not sure all sides of debates taken during public hearings are subjected into any form of unbiased, strict analysis before a position is taken. A good case in point is the clamour to rewrite our Constitution. It is generally believed that the Constitution's opening statement "we the people of Nigeria" is a lie. Some proponents say all shades of Nigerians were not consulted in drafting the Constitution. If this is the case, Nigeria must be man enough to face the truth and retrace her step to draft a new Constitution, the people's Constitutions. No Institution can thrive for long on the foundation of falsehood.

Senator Olusola Adeyeye of the 8th Assembly passionately declared on the floor of Senate that our constitution in its present form cannot give us the needed peace, justice and progress because it does not conform to known principles of a federation that the Constitution posits we operate (Adeyeye, 2019)***.***

It is my considered opinion, that the issues of concern different people and Bodies have voiced regarding our Constitution should be looked into dispassionately and be acted upon for the common good of all. Democratic leaders in

government must always be ready to listen to the yearnings of the people made through discussions, protest and criticisms, especially when such criticisms are constructive. Leaders must be willing to sacrifice personal views for the overall yearnings of the people they are elected to govern.

Lesson 5: Government must have internal self regulatory mechanism, and allow same to function

Any Organization or institution that does not have an internal regulatory mechanism to curtail the excesses and underperformance of its members may not attain her set goals, and may be short-lived. Interestingly, all three arms of government are meant to regulate one another.

Our laws, of necessity, must have robust control mechanisms to forestall authoritarianism and dictatorship, particularly by the Executive arm of government that controls the State's security apparatus.

Lesson 6: There is need to imbibe the culture of early and constant monitoring, and feedback mechanisms

Vice Chancellor sir, it is common knowledge that processes are more efficiently managed when regulatory controls are put in place from the outset and implemented than interrupting the process midway after the predefined process had begun (Mathews *et. al.,* 2007). In the same vein, it is a lot easier to curtail a negative trend at its infancy rather than allow it grow into a monster before we seek ways to deal with the resultant logjam.

For example, several reports have shown that banditry and insurgency in the north did not suddenly happen, but the government obviously did not nip it at the bud at the time. I read an interesting caption on Facebook some time ago which read ***"if you defend the bad character of your child when he is young, you would have to employ the services of a lawyer to defend his character when he is old".***

Similarly, it is much easier and more efficient to lay a solid foundation at the start of a building, otherwise the foundation may have to be revisited, and that inevitably results to avoidable cost and wastages.

Regarding avoidable costs and wastages, the numerous abandoned projects that litter Nigeria's landscape is a proof of lack of foresight and adequate planning in governance fueled by inordinate crave of corruption in our society. A Project Audit Commission established by former President Goodluck Ebele Jonathan reportedly identified a total of 11, 886 abandoned projects worth N15 trillion spread across the country between 1962 and 2012 (Budgit Nigeria, 2019). Metabolic processes driven by the trio of DNA, RNA and Proteins are averse to unnecessary cost and wastage. The Nigerian 'nation' should copy such natural phenomena.

In view of the above, government laws and policies need constant monitoring, evaluation and review to reflect present day realities. As with molecular governance of the cell, small chemical molecules that modify genetic instructions already translated into its cognitive protein could be likened to pressure groups, formal and informal Non-Governmental Organizations (NGOs), and other Civil Societies. Constructive and unbiased criticisms from such Organizations

should be given due attention in governance.

I hereby posit that every criticism whether borne out of mischief or hatred should be studied, at least informally, so that government could also distill valuable components of such criticisms, and act accordingly to modify relevant laws and policies.

Lesson 7: Outdated/outlawed Agencies and Units has to be disbanded or dissolved

Laws and policies of government should not only be subjected to review by the government for amendment, Agencies formed on the basis of such laws may as well be disbanded when the laws upon which they were formed become inimical to the unity and common good of the country.

I am of the opinion that Nigeria is bedeviled with numerous laws and policies that were relevant and needful at the time, but have turned sour. One of such policies in my opinion, could be the policy that allows open grazing of cattle in Nigeria. The act is obsolete and reprehensible to the common good of Nigeria; has often provoked clashes and senseless killings of Nigerians. It is gratifying to note, however, that State governments and even some of the practitioners of cattle business have come to see the need for change. The flip side, however, is that Nigeria requires lots of meat to meet her food demand. For this reason, the rearing of Cattles and other Livestock needs to be maintained, albeit in consonance with present day technologies and realities. The laws/policies on open grazing should, as a matter of national interest and urgency, be revised, taking into consideration the positions of herders (Nigerian Herders) and farmers. I think a part of this job which

apparently would abolish the nomadic lifestyle of some Africans may require the input of the Economic Countries of West African States (ECOWAS) and African Union (AU).

Just as the cell constantly monitors the activities of its bio-molecules, especially the executive arm (Protein) and degrades them as the need arises, the Nigerian State must borrow a leaf from degradation of proteins after formation in the cell to disband or reinvigorate Units and Executive Agencies that are non-functional or has outlived their usefulness to societal growth and development.

The outcry of citizens toward disbandment of the security outfit code-named SARS readily come to mind in this regard. Thankfully, the government swiftly disbanded the group and replaced it with a new outfit (SWAT) in view of the important roles it played in some parts of the country as aired by some of those governors. Also worthy of note is that the operations of SWAT would be guided by an apparently reformed mandate and policies to forestall a repeat of some of the gory tales that trailed the activities of the disbanded outfit.

In the same token, Executive Agencies with similar roles be trimmed and collapsed into one to save cost of governance. In line with this thinking, Steve Orosanye Committee was inaugurated by President Goodluck Ebele Jonathan's administration on 18th August, 2011. The committee was to restructure and rationalize federal public establishments and Agencies. In carrying out her duties, the Committee identified several Agencies with duplicated functions (Federal Government of Nigeria, 2014). Prominent among these are security and anti-graft Agencies as observed by other workers

(Eme, 2018; Ikpeze, 2013). Duplication of Agencies with same mandate do not only place avoidable burden on the country's lean resources but it has often resulted to conflicts among various securities and anti-graft Agencies. There would be need to merge such Agencies in Nigeria in line with the synergistic roles bio-molecules play in nature.

Lesson 8: Nigeria needs to practice True Federalism being the trademark of multicellular organisms

Nigeria is like a multi-cellular organism composed of different ethnic nationalities that cannot be fused into one without the constituent Units loosing their identities and individual peculiarities. Multi-cellular organisms such as man are composed of different cell types. Every cell expresses proteins according to need, the peculiarity of their environmental and metabolic factors. So, while all autosomal cells possess same genes, not all proteins are expressed in all cells.
Some cells have certain genes on their DNA permanently switched off, and are therefore not expressed into protein, whilst same genes on the DNA of other cells of the same organism are switched on, and are therefore constantly expressed into protein. Each cell therefore has only a fraction of its genes turned on or expressed at any given time, whilst the rest of the genes are turned off or repressed. This is true federalism, where every cell utilizes its resources to produce proteins it requires, and whose functions are intended to be for the common good of the entire organism.

True Federalism should encompass all aspects including devolution of power and fiscal resources.

Lesson 9: There is need to reduce items on the Exclusive list of the Constitution

Although cells express only a fraction of its genes all through its life time by reason of its type, and function in the overall interest of the organism, certain very few genes called the **"Housekeeping genes"** are expressed by all cells. The proteins encoded by housekeeping genes are regularly required to perform routine functions, and are thus constantly expressed for normal growth, whilst majority of other proteins encoded by the rest of the genes within the genome are required only under certain conditions. The important point to note here is the fact that housekeeping genes account for a very small fraction of the total genes.

Bringing this into perspective, the Central Federal government of Nigeria, I recommend should be involved with very few issues relating to national security and integrity, and foreign policies whilst allowing the federating Units to run their unique style of governance in a wider array of issues such as agriculture, education, policing, culture, trade and investments, elections etc. in view of this, I strongly recommend that the Constitution of the federal republic of Nigeria be amended, if it is not practicable to write an entirely new constitution, such that most of the items which are currently in the Exclusive list be transferred to the Concurrent List; only a few items need to be retained in the Exclusive list under a Federal system of government in line with natural Bio-systems. What remains to be clearly defined here is what constitutes a federating Unit in Nigeria. Would it be Local Government Areas, States or Geo-political Regions?

Lesson 10: Practice the true concept of Soil Microbial Diversity

I had mentioned earlier in this lecture that soil harbors diverse and heterogeneous microbes that play different roles, and in the process influence soil health owing to its microbial diversity. Also, I did say that microbial diversity breeds resilience. Similarly, nations with diverse ethnic nationalities and resources would naturally be expected to be resilient in the face of adversities and challenges if the citizenry fully understands and applies the natural principles of biodiversity. Like soil microbes, the geographical space of Nigeria is occupied by not less than 200 different ethnic nationalities with different capabilities, beliefs and general way of life; being diverse in ethnicity, religion, political views, culture etc. Notwithstanding this vintage position, the tools of diversity are grossly, wrongly applied in Nigeria. Hence, what should naturally be a blessing to us, as a people, has become our undoing, unfortunately.

Mr. Vice Chancellor Sir, eminent guests and colleagues of the academia, diversity in eco-biological parlance is not necessarily the presence of numerous different groups or species in an environment. Microbial or species diversity consists of two components; these are species richness and evenness. Species richness simply means the total number of species while species evenness is the measure of the relative number of the different species within the environment (Fakruddin and Mannan, 2013). So, an environment would be said to have high microbial diversity if such an environment has an appreciably number of different species with each species equally represented, such that no one group of species

significantly, numerically dominates others (Etebu *et. al.,* 2018a-c).

A country that is truly diverse as described herein regarding microbial diversity epitomizes egalitarianism. In the same token, human societies whose practices negate the natural phenomenon of microbial diversity is characterized by inequality amongst the citizenry. Negation of egalitarianism would breed two major groups of players or people in the society – The Oppressors and the Oppressed. Such a society can never know peace. Reason being that, whilst the Oppressors would be busy trying to maintain the status quo the Oppressed would constantly fight for freedom and emancipation. As we say in the Izon languaget ***"Iwiri kpo buna gha, Iwiri kaka igba kpo bunu gha"*** meaning "As the tortoise cannot sleep, the rope used in tying it will also not sleep" Is this not the case with Nigeria and every other country where inequality holds sway?

In defiance to what biodiversity truly means, most people have described diversity as simply a measure of the number of different groups that make up the country without taking into consideration the measure of equality of political power and relevance the federating Units are allowed to wield. For example, the relevance and voting strength of a State in Nigeria is tied to population alone. This should not be the case as it would be against the principles of natural microbial diversity. To fall in line with the natural phenomenon of microbial diversity, Nigeria must seek ways to equalize all federating Units of our 'theoretical Federation'.

By way of contribution, I hereby propose the following factors for consideration in determining the voting strength of different States of the federation.

1. Percentage Population of the State
2. Percentage of non-indigenes resident in the State
3. State's gross domestic product (GDP)
4. Federating Unit/State per capita income
5. Percentage monetary generation from State/federating Unit

I strongly believe that Nigeria would be safer and all peoples and ethnic nationalities would have a better sense of belonging if our laws are revised or a people's Constitution written to allow for equality, equity, fairness and justice for all irrespective of State, region, political affiliation or religious inclination.

8.0 Conclusion

The fundamental characteristic that qualifies a Nation is that people of diverse culture, tribe, religion and other pluralities are unified by a common identity within a geographical space. Herein lies the fundamental challenge that has continually hindered and even threatened to completely obliterate our journey to nationhood; our common identity. The Nigerian State is like a child roaming to find her identity. There is not one formidable event in history where all Nigerians, irrespective of ethnicity, creed, religion or politics have ever converged. The only exception is probably football that seems to unite us when our National team is playing against another nation, but even at that the body overseeing our football sport is often embroiled in politics and shenanigans.

We seem to have stronger ties with our non-Nigerian tribal folks than we have with our non-tribal Nigerians. The man in the far north is constantly indoctrinated by the Elites to consider another Nigerian living at the mouth of the Atlantic Ocean as an enemy or a potential enemy and vice versa. Hardly would members of the Nigerian National Assemblies deliberate on any issue without being misconstrued (whether rightly or wrongly) to be selfish and biased. Only a few months ago, the media were awash with reports of the governors of Bauchi and Benue States (all members of the same political party) speak in harsh, divergent and conflicting tunes regarding the need or otherwise for herders to bear arms. Although, they have since mend fences, at least in public, this is the typical Nigerian debacle that has continually corroded our quest for national identity and cohesion. No Nigerian would honestly say we have fared well in fostering cohesion

and inclusiveness in our national life. There are different shades of clamour and drumbeats, bordering mainly on ethnicity and religious ideologies, from virtually all geographical coordinates of the country. These are indeed very trying times, and those in Leadership positions must rise to the Occasion and place the country on the path of attaining Nationhood.

Nigeria would be rightly called a Nation and come of age when a Nigerian is more at home with a fellow Nigerian of another tribe than he is with a fellow tribes-man of another country. To put this more clearly in another way, the proof that Nigeria has become a nation would be when a Nigerian Fulani becomes more comfortable being with a Nigerian Igbo man than he is with a Fulani from Niger republic. Would this ever be in our contemporary Nigeria? Yes, it would be, when the Elites sheath swords of selfish interest and stop the unnecessary indoctrination of Nigerians to hate themselves along ethnic, tribal and religious lines.

I know that inaugural lectures are usually attended by an audience of individuals with diverse skills and areas of expertise. For this reason, I have tried to simplify the subject of Molecular Biology, particularly regarding expression of genes and their regulations as much as possible but you would agree with me from all that have been said, gene expression and regulation is definitely not a tea party. It is a highly complex phenomenon just as governance is.

Indeed, man is fearfully and wonderfully made of trillions of cells that are intricately connected and dependent on one

another in many ways. Interestingly, man is composed of more microbial cells than human cells that interact in different ways to sustain life's metabolic processes. Any shift or error in human DNA replication and or gene expression that is allowed to persist may lead to disease and eventually death of the individual. In the same vein any human societal system that does not have clear-cut laid down rules or does not operate in equity, fairness and justice to all her confederating components would be bedeviled with strife, anarchy, poverty, lawlessness, pain, disaster and the like. However just as agricultural soils high in microbial diversity are known to be resilient, a country such as Nigeria with people of numerous ethnic nationalities would be resilient to external and internal aggression, grow and develop in diverse ways if the strengths of her people are properly harnessed in line with the biological tenets of microbial and genetic diversities. The first step for us to achieve nationhood would be to identify our commonality - the Nigerian identity, and seek ways to inculcate same into the life and consciousness of the Citizenry.

9.0 My Modest Achievements/Contributions to knowledge

I have over forty (40) journal publications in referred journals and several conference and other publications. As at Monday 3rd May, 2021, my publications have been cited by not less than 535 scholars and Scientists across the world. See the link provided below (https://scholar.google..com/scholar?hl=en&as_sdt=0%2C5&q=Etebu+Ebimieowei&btnG=).

Some of my modest contributions are:

9.1 Potential side effect of Plant Extracts used as local Alcohol (Kaikai) Additives (Etebu, 1989; Asita and Etebu, 1997)

This line of research forms my entrant into the world of scientific research. My romance with research linked to DNA started with my undergraduate research project where I made an attempt to investigate the carcinogenic potentials of several plants locals use as alcohol additives. Cancer as we know results from cells or cell that replicate(s) abnormally. At the heart of cell replication is DNA replication.

During my undergraduate research supervised by no other than Prof. Asita Okorie Asita, I investigated eight (8) plants namely, *Anthostema aubryanum, Anthocleista djalonensis* (Osuo in an Izon dialect), *Astonia boonei* (called indoudou in Kolokuma dialect of the Izon Language) *Azadiractha indica* (Dongoyaro), *Baphia nitida, Bombax buonopenzense* (Silk

Cotton tree), *Fagara* species and *Rothmania melagostigma*. Specifically, I investigated the antimicrobial activities of alcohol (Kaikai) extracts of these plants as a measure of their mutagenic potentials which in turn is a measure of their carcinogenic potential. Three test microorganisms were used namely *Escherichia coli, Staphylococcus aureus* and *Saccharomyces cerevisiae*.

Apart from *Baphia nitida* every other plant extract were observed to be antimicrobial to at least one of the test organisms; *Alstonia boonei* (also called indoudou) having the highest antimicrobial activity (Etebu, 1989).

To confirm their toxicity and/or mutagenicity, the plant extracts were further subjected to *Salmonella*/Mammalian microsome assay in a separate experiment in Japan. In this experiment *Anthocleista djalonensis* (called Osuo in Kolokuma dialect of the Izon language) was found to be most mutagenic while *Alstonia boonei*, *Anthostema aubryanum* and *Bombax buonopenzense* separately showed appreciable mutagenic activity (Asita and Etebu, 1997).

9.2 Induction of reproduction among *Mycosphaerella fijiensis*

This was my Master of Science Research Project work. This work was done to enhance the selection process of plantain and banana hybrids produced through plant breeding; to compare and assess their disease (Black sigatoka) resistance potentials. Prior to my work it was difficult to artificially stimulate *Mycosphaerella fijiensis* to reproduce, particularly sexual reproduction. I was able to stimulate sexual reproduction

between isolates of *M. fijiensis* (Etebu *et al.,* 2003a) and also demonstrated conditions under which they would reproduce asexually (Etebu, 1997; Etebu *et al.,* 2002; 2005). One of my publications on the findings from this work was actually translated into two other languages for increased readership by the Publishers (Etebu *et al.,* 2005).

Whilst pondering on the already published findings of this article in 2007 I realized that a natural phenomenon which I term Etebu's hypothesis had played out. Though written casually in my PhD thesis, I wish to formally state publicly Etebu's hypothesis as thus ***"Every living system requires a measure of stress for optimal productivity".***

9.3 Potential side effect of use of local chewing sticks

This is my first work as an academic. Prior to this work, scientific literature had been awash with the positive use of chewing sticks. However, I had often encountered visible fungal growth on chewing sticks displayed for sale, and that informed my quest to investigate the fungi associated with selected chewing sticks and their potential health hazard. Four fungal genera, *Penicillium, Aspergillilus, Mucor* and *Botryodiplodia* were isolated from chewing sticks processed, packaged and stored in different ways/conditions (Etebu *et al.,* 2003b), and these had been reportedly implicated with various human ailments.

9.4 Molecular detection and quantification of Plant pathogenicity genes in soil: Model for plant disease prediction

This was the basis of my PhD research project. Using pea footrot disease caused by an ascomycetous fungus *Nectria haematococca* (*Fusarium solani* f. sp. *Pisi* anamorph.) I am glad and proud to state that I was the first in human history to develop and deploy molecular approaches that would selectively detect and quantify plant pathogenic variants of a given pathogen in soil without recourse to culture. Prior to my work, pea footrot disease risk assessment had solely been dependent on traditional cultural methods which were unreliable and cumbersome. This feat was achieved because the molecular assays I developed were designed to target specific disease determining genes exclusively associated with pea footrot disease. Gene numbers of up to 100 per gram of soil for three genes namely PDA, PEP3 and PEP5 were observed as a threshold number of inoculum density of the pathogen capable of causing pea footrot disease in soils.

Combining the bio-molecular assays with other standard procedures of assessing physic-chemical factors of soil, I was able to develop a mathematical model (formula) that could be used by farmers and other agro-allied practitioners and policy makers to scientifically assess the potential risk or otherwise of planting peas on any given agricultural soil. The mathematical model (formula) is $\boldsymbol{DI = 1.97 + (3.48 \times Phosphate) + (-0.66 \times C/N)}$ Where DI represents disease index (0-5); phosphate measured in mg g^{-1}soil; N equals total Ammonium Nitrogen (mg g^{-1}soil); C equals Soil Organic Carbon measured as percentage loss of ignition (LOI). This predictive pea

footrot disease model accounts for 42% of pea footrot disease variance.

These laudable findings have been published first in my PhD thesis, and as several research and review papers (Etebu 2008; Etebu and Osborn, 2009, 2010, 2011a-d; 2012a-b; Etebu, 2015)

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9.5 Research works on *Irvingia* fruit wastes

This line of research forms the bulk of works I have embarked upon since I returned from the United Kingdom after my doctoral studies. So far, five postgraduate (1 PhD, 3 M.Sc and 1 PGD), and at least 60 undergraduate who worked on this fruit under my supervision have either graduated or successfully defended their projects while several others working on the same fruit, also under my supervision, are at various stages of their postgraduate research projects.

Fig. 9.1: Bush mango dumped as wastes (Source: Etebu, 2012)

Fig. 9.2: Field trip on *Irvingia* studies
***Prof. Etebu (extreme right) and his PhD student**
(Mrs Tungbulu) holding a jotter in the middle.

Irvingia (Bush mango) is an edible fruit mostly sought after for its rich kernels used as a soup thickening condiment in our local "ogbono" soup) while the fleshy mesocarp is often thrown away as wastes. I felt these wastes could be used in more profiting or beneficial ways than just dumping them in bushes and water bodies. This formed my research interest in these fruit wastes which I have consistently and tenaciously pursued for the past 13 years. My project students are often called "*Irvingia babes* or *guys*" while my students would usually called me the CEO of *Irvingia* or Central Dogma depending on what fascinates them most with my lectures, Agricultural or Molecular Microbiology respectively.

9.5.1 Microbiology of *Irvingia* fruit and wastes

I have studied the microorganisms associated with postharvest wastes of this fruit in different ways. First of these studies was the systematic decay of its fruits under different storage conditions, and the continued presence of phytochemicals (Etebu, 2012, 2013a). Different fungi such as *Aspergillus, Mucor* and *Penicillium* were found to be implicated with Brownish-black rot disease symptoms. This was the first work ever that studied the systematic decay of the fruit with associated phytochemicals. Postharvest fruits of bush mango were found to contain alkaloids, flavonoids, saponins, tannins and glucosides

Fig. 9.3: Postharvest *Irvingia gabonensis* fruits at different stages of decay

Key: Top left: Mature and disease free fruits
Top right: Fruits ripen 3-5 days after harvest
Bottom left: Fruits showing brownish black rot disease covering about 50% of
Fruits' surface
Bottom right: Fruits completely diseased and spoilt 14 days after harvest
(Source: Etebu, 2012)

In a similar work, but relying on molecular techniques bacteria isolated from postharvest *Irvingia* fruits wastes were analyzed and identified. Bacterial 16S partial RRNA gene sequences were observed as being related to *Bacillus, Enterobacter, Oceanobacillus* and *Staphylococcus* (Etebu and Tungbulu, 2015)

An interesting finding of this particular work was that bacteria with partial gene sequences related to the bacteria mentioned above were not isolated from the fruits beyond 3 days in storage. This showed that post harvest fruits wastes of *I. gabonensis* could be used as a substrate for antibiotics production by antibody producing microbes. This line of research is already being looked into by another of my PhD student.

Still on the microbial quality of *Irvingia* fruits and their phytochemical composition, I did a work to compare the two prominent species of the fruit plant in our environs – *Irvingia gabonensis* and *Irvingia wombolu* (Etebu, 2013a). Results of this particular work showed that *I. gabonensis* fruits are generally bigger in size than *I. wombolu* but both plant species had comparable postharvest fruits disease severity. Although, both species had comparable amounts of flavonoids and glycosides, other phytochemicals; alkaloids, tannins and saponins were relatively more abundant in *I. wombolu* fruits than those of *I. gabonensis*.

9.5.2 Disease and Phytochemicals of postharvest *Irvingia* fruit wastes

Phytochemicals assessed in the previous two specific works were primarily qualitative. Working with my first PhD student,

we needed to generate quantitative data on phytochemicals to enable us study the potential relationship existing between the brownish-black rot disease and phytochemicals (Tungbulu *et al.,* 2016).

Table 9. 1: Correlation/Regression matrix of Brownish-black rot disease and phytochemicals

Parameters	Disease	Alkaloids	Tanins	Saponins	Flavonoids
Alkaloids	0.69*				
Tanins	0.73*	0.91**			
Saponins	0.36^{ns}	0.18^{ns}	0.33^{ns}		
Flavonoids	-0.21^{ns}	0.06^{ns}	0.01^{ns}	-0.74*	
Glycosides	-0.74*	-0.83**	-0.94**	-0.45^{ns}	-0.06^{ns}

*Disease here was Brownish-black rot disease of *Irvingia* fruits

(Source: Tungbulu *et al.*, 2016)

We found out that brownish-black rot disease severity increased with increase in some phytochemicals such as tannins and alkaloids while the disease decreased with increase in glycosides. This work thus provided the prerequisite knowledge of when to maximally exploit the different phytochemicals inherent in *Irvingia* fruits wastes

9.5.3 Disease and Proximate content of postharvest *Irvingia* fruit wastes

Fascinated by the statistical relationship between Brownish-black rot disease and phytochemicals, my research team extended the investigation to assess the effect of storage period on disease and proximate content of *Irvingia* fruits, with emphasis on the potential relationship existing between disease and proximate contents (Etebu and Tungbulu, 2016; Etebu and Oku, 2017). Our findings showed that postharvest disease was positively related to carbohydrate whilst being negatively related to protein. Our results further showed that the nutritional value of the fruits decreased as storage period extended. We therefore, recommended that *Irvingia* fruits are best consumed soon after harvest or processed under microbiologically safe conditions to maintain their microbial, proximate and nutritional qualities.

9.5.4 Disease and Vitamin content of postharvest *Irvingia* fruit wastes

In another related work, we studied the effect of postharvest period on specific fruit parameters, emphasizing on the potential relationship between brownish-black rot disease and selected vitamins, Vitamin A, B and C (Etebu *et al.,* 2016). Whilst a longer storage period led to a greater severity of disease, our findings showed that increase in brownish-black rot of *Irvingia* fruits led to a correspondingly lower content of vitamins A (retinol), B1 (thiamin) and C (Ascorbic acid).

It is our considered opinion that *Irvingia* fruits pulp would make significant contributions to the well-being of locals in the

Niger Delta region of Nigeria where *Irvingia* fruits are widely consumed.

9.5.5 Microbial Metagenomics of postharvest *Irvingia* fruit wastes

To have a holistic and proper understanding of the diversity of microorganisms associated with *Irvingia* fruit waste I have deployed molecular approaches, particularly metagenomics (Etebu *et al.,* 2018b,c) to study the community structure and diversity of microorganisms associated with *Irvingia* (bush mango) fruits after harvest.

Findings showed that bacterial diversity ranged from 0.69 to 0.82 depending on how long the fruits have been harvested. Predominant bacterial genera associated with the fruits were found to be *Acetobacter* (27.30%) and *Lactobacillus* (37.25%). The relative abundance of the specific species of these genera of microbes showed that *Irvingia* fruits wastes are potential substrates that could be used in food and pharmaceutical industries.

Similarly, fungal diversity ranged from 0.57 to 0.70 indicating that there is a lot more diversity amongst bacteria associated with the fruits than it is with fungal species.

In metagenomics studies organismal species are often termed Operational Taxonomic Units (OTUs). Now the predominant OTUs observed in this specific works belonged to Saccharomycetales that are known to effectively ferment sugar. As a result, we are of the opinion that postharvest *Irvingia* fruits wastes could be suitable substrate for ethanol production.

9.5.6 Exploring soil fertility potentials of postharvest *Irvingia* fruit wastes

In a bid to explore the potentials of using *Irvingia* fruit wastes to enhance soil fertility and crop production, part of my research team studied the effect of the fruit waste on soil microbial diversity and physic-chemical properties relying on molecular approaches (metagenomics to be precise) and standard analytical procedures (Etebu *et al.,* 2018a).

Findings showed that whilst bacterial species richness and population decreased, *Irvingia* fruit wastes mitigated the effect of soil tillage on soil bacterial diversity. Bacterial OTUs amplified from *Irvingia* wastes treated soil belonged to several bacterial genera in varying proportions. In particular, 25% of the bacterial species were of the genus *Streptococcus,* while *Acinetobacter, Novosphingobium* and *Shewanella* species accounted for 37.50% in equal proportions. These were followed by *Pseudomonas, Pseudonocardia*, *Clostridium, Sulfobacillus, Delftia* and *Nocardioides*; each representing 6.25% of the total bacterial OTUs.
On the contrary, whilst the fruit wastes seem to aid fungal proliferation and fungal species richness, they drastically impacted negatively on their diversity. Fungal OTUs from same soil were mostly *Issatchenkia hanoiensis* which accounted for as much as 81.42% of total fungal species.

We are also of the opinion that *Irvingia* fruit wastes could be beneficial in agriculture owing to the fact that treated soils had significantly higher amounts of some elements such as total nitrogen, total organic carbon, sulphate, phosphate and calcium amongst others.

10.0 Ongoing and future Research works

I am currently working on several research projects, and many more I intend to investigate in the future. Outlined hereunder are some of the ongoing research works and a couple of ideas I hope to interrogate in the future.

1. The potential use of *Irvingia* fruit waste to induce antibiotic production among members of *Actinomycetes* – On going
2. The potential use of postharvest *Irvingia* fruit waste as bio-fertilizer in Agriculture – On going
3. The potential use of postharvest *Irvingia* fruit waste to mitigate the adverse effects of selected herbicides on soil microbial structure and diversity – On going
4. Development of genetically modified microbes to tackle waste management challenges in Bayelsa State – Future plans
5. Finding balance between plant disease, yield (harvest), nutritional quality and human health benefits of fruits consumption – Harnessing Etebu's hypothesis from the view point of Agricultural and Molecular Microbiology – Future
6. Phylogenetic relationship between various ethnic groups in the Niger Delta and Nigeria – Future
7. Initiation of discourse on the application of bio-molecular phenomena in governance and nation building – This lecture marks the beginning
8. I am currently writing a book on the ABC of Molecular Biology and its Application - Near Completion
9. I hope to write a book of the pains of widowhood and the principles of bouncing back

Acknowledgments

For every glory there is a story, and my journey to becoming a Professor of Agricultural and Molecular Microbiology is no exception. My journey to becoming who I am today had had many turns, smooth at some points, spiky and bumpy at several others. There were times when the sun was high and bright with glamour but there were also ample of seasons when the sun did set, but thankfully it always rose again. The greatest of my life experiences were learnt during the season's of sunset. Again I posit that **"Every living system requires a measure of stress for optimal productivity".**

Let me seize this opportunity to first recognize and thank everyone for gracing this inaugural lecture. For your investment and sacrifice of time, money, encouragement etc. be rest assured you all are part of my success story. Specifically, I thank the Vice Chancellor, Prof. Samuel Gowon Edoumiekumo, management staff, the entire community of the Niger Delta University and the wider society of the Academia for this opportunity granted me to give my inaugural lecture.

I thank the Visitor to the Niger Delta University, our Miracle Governor of Bayelsa State, Senator Douye Diri and his able deputy, Senator Lawrence Ewhrudjakpo. I also thank Hon. Gentle Emelah, Commissioner of Education, ESV. Moses Teibowei, Commissioner for Works and Infrastructure, Prof. Ebitimitula Nicholas Etebu, VC Bayelsa Medical University, Prof. Turner Isoun, Pioneer VC Rivers State University of Science and Technology (now Rivers State University), Prof. Steven Odiowei, one time VC of RSUST, Prof. Kobinah Imananagha, Prof. Seiyefa Brisbe, Rear Admiral Yanga (Rtd),

Rear Admiral Tunji Beckley, Barr. Preye Agedah, Dr. Zuoboemi Agadah, Dr (Mrs) Aturu, Dr (Mrs) Ugolo, Dr (Mrs) Queen Josephine Ezonbodor-Torru and the entire members of a Technical Committee with whom I worked assiduously to plan and organize the first Bayelsa State Education Summit. Equally, I thank Prof. (Mrs) Ayebaemi Spiff, Prof. Kingsley D. Alagoa, Prof. Clement Egumu, Pastor Harold, Dr. Franklin Osaisai, Dr. Emmanuel Denenu, Prof. Promise Mebine, Dr (Mrs) Grace Koroye and all members of the Bayelsa State Science and Technology Education Board. Working with you all on that Board has been an impactful experience, and thank you for gracing this lecture.

Vice Chancellor sir, all that I am and would ever be is a function of the myriad of experiences and lesson I have garnered over time from everyone I have crossed path with. For this reason, I wish to thank everyone who has ever had anything to do with me at any level or circumstance. The story of my life would not have been what it is today without you. So I say thank you for the role you played in shaping my life. Whilst it is humanly impossible to remember in very specific terms the various and sometimes polarized roles and influences different people had on me, there are a handful that are indelibly imprinted in the fabric of my being.

First on the list are my parents, Chief and Mrs Yelwa Etebu (all of blessed memory). You would often hear people choose one parent over the other. I had parents who played different but equally important roles in my life. My father, for instance, taught me with his life not to be unduly bothered by negative rumours or comments people make about my person and/or personality. He taught me how to develop tough skin when fate

throws stones at me, and to remain focused on the goal even in the midst of storms. For this, I hardly see anything as impossible when I set my heart to achieve it. My mother, on the other hand taught me self-reliance and contentment, and the virtue of empathy which has played no small role in shaping my relationship with people, particularly those who are not as privileged as I am.

Also worthy of posthumous commendations are two women my maternal grandmother Late Mrs Kainty Okorokoro and my late wife Mrs Oluyemi Stella Temitayo Etebu (Nee Ogundare) of blessed memories. These women played very different invaluable roles in what I am today. In particular, my grandmother taught me how to let go in life to regain what I lost. This is a virtue in very short supply but a very potent weapon of warfare in life's battles, particularly on issues of relationships, trust and accusation.

My late wife, Mrs Oluyemi Stella Temitayo Etebu (Nee Ogundare) was a rare gem. With her, I knew God's kind of love in marriage between two people is possible. I understood in practical terms what it meant for two to be one. We so much understood ourselves that we virtually sometimes communicated effectively in silence. She was a helpmate indeed. She taught me how to believe in people who may not be as privileged as one is. She had parents that were wealthier than mine, had better exposure to education and human connections; yet she opted to marry me amongst other suitors richer than I was at the time. Her death therefore dealt me a huge blow I was not in any way prepared for. My life, sort of literally came to a standstill following her death on 14th November, 2003. I was devastated. I queried the essence of life

and living. I got angry with God, the Church, family and even myself. I asked questions without getting answers, even when I got the answers, they came as riddles. Up till now I still cannot decipher the answers wrapped in riddles but I hope to understand someday. For several years, I looked forward to seeing her rise from the dead for us to live again as husband as wife but that was not to be.

Coming around to accept the stark reality was difficult and sapping until I met my one time student, Ebimokemenimigha Oyobolo whom I married some years ago. At the time she caught my fancy I did not know she was my student whom I had taught genetics back in Rivers State University where she studied Medical Laboratory Science, majoring in Haematology and Blood transfusion. She is the manageress of my dynasty, an epitome of womanhood, simple and deep. She has a way of assuming naivety to expose and humble my sometimes masculine egoistic tendencies. A great woman and wife raised in the quiet town of Toru-Angiama. She is an express manifestation of inner beauty whose words are always wrapped with a candor of grace and simplicity. I like to thank her from the very innermost recess of my being for believing in me, for being able to identify the gold within the rubbles of emotional trauma that exemplified me at the time. From the very depth of my soul, I thank you the 'Beauty of my life', second only to God my Creator.

This section of my inaugural lecture would be incomplete without the mention of my adorable children who had had to share in the pains of my dark moments. The strength of my youth Pere and his bothers Tonye and Tari and the princesses of my dynasty 'debilistic Debby" and 'mercilistic Mercy'. My

prayer is that they would be greater and more impactful than I am or would ever be.

From the Academic platform, a number of people particularly my teachers made an indelible imprint on me. One of such was my primary six classroom teacher, Mr. Chidi Lloyd of Army Children School, Alamala, Abeokuta, Ogun State back then in 1977-1978. On the secondary school front numerous teachers helped to shape up my academic and life pursuit both in Government Secondary School Odi (1978-1983) and Government Secondary School, Borokiri, Port Harcourt (1983-1984). Amongst my teachers in GSS Odi was Mr. Gbenbo (I wish I know where to get him). He was the first teacher who taught me Biology and Chemistry in Class 3 (equivalent to JSS 3 today). He taught me how to use the microscope to identify *Paramecium*, *Euglena*, *Spirogyra* etc. He also demonstrated simple ways of identifying different gases. Mr. James Enarebebe is another teacher I cannot hesitate to mention. Though a graduate of Biology then, he taught me literature in English and exposed me to drama acting in my secondary school days of the early 1980s. Others that played very valuable roles are Messrs December, Moses Teibowei, Ojobowei Teibowei, Late Mr. Digan Bolou, and my principals Late Messrs F. A. Aganaba and A. D. Tulagha.

Also worthy of mention is Mrs. Beatrice Owhonda, Principal of GSS Borokiri, Port Harcourt (1984). She was very instrumental to what I am today. Getting the appropriate grades required for University education was probably the most challenging phase of my academic pursuit. After sitting for my Ordinary Level Certificate Exams in GSS Odi in 1983, I had to re-sit the exams in 1984 because I did not get Credit scores in a

couple of subjects central to my intended course of study. I remember walking into the office of the then principal of GSS Borokiri in Post Harcourt to register for the said exams but did not have enough money. The Principal, Mrs Beatrice Owhonda was about drawing the line to end the list of candidates when I grabbed her hand and pleaded with her to give me a few minutes to raise the needed fees. She looked and saw the desperation in my eyes. I in turn saw the lovingness of motherhood in her response and let go off her hand. Straightaway I dashed off to a street not far away from the school where one of my uncles lived at the time. I narrated my experience with the female principal. Incidentally, his son Collins Etebu (my cousin) was the then Games Prefect, and he also had a convincing story to tell, though not true. He walked briskly across the street with me to the Principal's Office, narrated his well rehearsed story line and quickly added he was the father of the Games Prefect. On hearing that he was the father of the Games Prefect, the principal stopped him from talking further and sent for Collins who came to confirm his claim of fatherhood. That was it. I was allowed to register even when I did not have the complete fees at the time. I read for the O/Level exams like I was preparing for the battle of my life which paid off as I got minimum of credit scores in all subjects required for my intended course of study at the time.

I later got admitted to study Applied Biology in Rivers State University (the Rivers State University of Science and Technology), where I majored in Microbiology option and graduated as the best graduating student of the department. Numerous Lecturers helped mould my academic prowess in the then RSUST. Prominent among these were Prof. Asita Okorie Asita (A Genetic Toxicologist) who was my Seminar

and Project Supervisor; I was fondly called Asita (Jnr.) in those days because of my attachment to and passion for genetics that he taught. That relationship has spanned over 30 years.

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My unalloyed thanks to Prof. Andrew Mark Osborn my PhD Supervisor. Working with Mark was phenomenal. He did not only supervise my work but his laboratory funded part of what I was meant to pay as tuition fees in the University of Sheffield, United Kingdom. I got admission to pursue PhD degree in Microbiology in the University of Essex, Colchester in early 2004. A few months into my programme, two of my Supervisors, Dr. Andy Ball and Andrew Mark Osborn both had new appointments to other Universities, and they both desired I went with them (Andy Ball to Australia and Mark Osborn to Sheffield in the UK). I opted for Mark Osborn for several reasons, particularly because he was a specialist in Molecular Microbiology where my interest was and still is. However, whilst approving my move to University of Sheffield, the Bayelsa State Government and Niger Delta University in very clear terms wrote that they would not pay anything higher than what they would have paid to University of Essex where I was originally admitted. I relayed this to Mark and showed how disappointed I was because there was no way I could raise the difference of five thousand pounds (£5000.00) annually needed for studying in the University of Sheffield at the time. It was at that point Mark Osborn did the unusual. He wrote to the University of Sheffield, asking them to officially peg my tuition fee at the same amount Essex was charging while his laboratory defrayed the balance of five thousand (£5000.00) Pounds every year. That amount was meant to cover for my consumables which he made sure I got when I needed them for

my work. He did not only provide the consumables but made available to me funds I could use at will for the work. To paraphrase his words 'I am not only training you to have a PhD, I am also training you on how to effectively utilize research funds'. I am forever grateful to him.

Coming to the Niger Delta University, I must say I have enjoyed relating with all the Vice Chancellors, Prof. Buseri (the pioneer VC), Prof. Ikporikpo, Prof. Ogoni and now my digital VC, Prof. Samuel Gown Edoumiekumo. Though different in personality and approach, they have all impacted hugely on me. What I enjoyed most is the confidence they all had reposed in me at different times under different circumstances. I have had need to differ with them all at different times on different occasions, those differences never adversely affected how we related. I commend the great minds that have piloted the affairs of this great citadel of learning. In particular, I must thank my present Vice Chancellor, Professor Samuel G. Edoumiekumo. One thing you have impacted on me without knowing is that the best way to silence detractors and complainants is to prove your case, not by words of mouth but by the inarguable evidence of your service delivery. I am sure you would agree with me that even a blind person would easily confirm the massive and unparalleled infrastructural development that has accrued to the Niger Delta University when he assumed office. This reminds me of a scripture in the bible. Some people met Jesus and wanted to know if he was the expected Messiah or if they were to expect another. Jesus' response, like Prof. Edoumiekumo, was phenomenal. He responded, 'go tell them what you see; the lame walk, the blind have their sight restored, the deaf hear, the dumb speak etc' (Matt. 11:5). What a way to prove one's mettle?

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References

Abawi, G.S and Widmer T.L (2000). Impact of soil health management practices on soil borne pathogens, nematodes and root diseases of vegetable crops. *Appl. Soil Ecol.* 15:37-47

Adeyeye, O (2019). https://www.youtube. com/watch?v=3D 0trNUB-ME. Accessed 12th March, 2021

Ajumobi, F and Sessou, E (2021) Who is Afraid of DNA Testing https://www.vanguarddngr.com/2021/01/who-is-afraid-of-dna-testing/amp/.....)

Albert, B. (2003). DNA replication and recombination. *Nature*. 421:431-434

Albert, B. Johnson A, Lewis J, Raff M, Roberts K and Walter P (2002). Chromosomal DNA and its packaging in the chromatin fiber. In: (eds) Albert B, Johnson A, Lewis J, Raff M, Roberts K and Walter P. *Molecular Biology of the Cell,* 4th Edition, New York USA, Garland Science.

Allen, D. Ruan, C-H, King, B. and Ruan, K.H (2019). Recent advances and near future of insulin production and therapy. *Future Med. Chem*. 11(13): 1513-1517

Asita, A.O and **Etebu, E.** (1997). Toxic and mutagenic effects of extracts of some Nigerian dietary plants in the salmonella/mammalian microsome assay. *Niger Delta Biologia* 2(1): 28-34

Baltimore, D (1970). RNA-Dependent DNA polymerase in virions of RNA tumour viruses. *Nature*. 226:1209–1211

Benayoun, B.A and Veita, R.A (2009). A post-translational modification code for transcription factors: sorting through a sea of signals. *Trends in cell biol.* 19(5): 189-197

Bergseid M, Scott B, Mathur S, Nielson K, Shoemaker, D and Mathur, E (1991). A high fidelity thermostable DNA polymerase isolated from pyrococcus furiosus. *Strategies* **4:** 34-35

Bergthorsson, U and Ochman, H (1995). Heterogeneity of genome sizes among natural isolates of *Escherichia coli. J. Bacteriol*. 177 (20): 5784-5789

Bertani, G and Weigle, J.J (1953). Host controlled variation in bacterial viruses. *J. Bacteriol.* 65 113-121

Bhattacharjee, R.N (2015). *Fundamentals of Microbiology,* 1st Edition, India, Kalyani Publishers. 762pp

Black, D.L (2003). Mechanisms of alternative pre-messenger RNA *splicing. Ann. Rev. Biochem.* 72 (1):291-336. *Doi:10.1146/annurev.biochem. 72.121801.161721. PMID 12626338*

Blaser, M.J (2006). Who are we? Indigenous microbes and the ecology of human diseases. *EMBO Rep.* 7(10): 956-960

Briggs H (2021). Human cells grown in monkey embryos spark ethical debate.https://www.bbc.com/news/science-environment-56767517. Accessed April 16th 2021

Budgit Nigeria (2019). Cost of corruption: case of abandoned projects in Nigeria. https://medium.com/@BudgITng/cost-of-corruption-the-case-of-abandoned-projects-in-nigeria-14013b7e1ff3. Accessed 12th March, 2021

Centre for Disease Control (2020). CDC Diagnostic Tests for COVID-19. https://www.cdc.gov/coronavirus/2019-ncov/lab/testing.html. Accessed 1st March, 2021

Centre for Disease Control (2021). Understanding COVID-19 mRNA vaccines https://www.cdc.gov/coronavirus/2019-ncov/vaccines/different-vaccines/mrna.html. Accessed 8th May, 2021

Chang, A and Chan, L (1993). Clinical applications of Molecular Biology. *Biochemical Education.*21(1):3-15

Chien, A, Edgar D.B and Trela JM (1976). Deoxyribonucleic acid polymerase from the extreme thermophile Thermus aquaticus. *J. Bacteriol.* 174: 1550-1557.

Coffin, J.M and Fan, H (2016). Discovery of Reverse Transcriptase. *Annu. Rev. Virol*. 3: 29-51

Cohen, J (2019). Did CRISPR help-or-harm-the first-ever-gene edited babies? https://www.sciencemag.org/news/2019/08/ did-crispr-help-or-harm-first-ever-gene-edited-babies. Accessed 3rd March, 2021

Cooper, G.M and Hausman, R.E (2006) *The Cell: A Molecular Approach*, 4th Edition. ASM Press and Sunderland (Massachusetts): Sinauer Associate. 813 pages

Crick, F.H.C (1958). On protein synthesis. *Symp. Soc. Exp Biol. 12:138-168.* PMID: 13580867

Cryanoski, D. (2020). What CRISPR-Baby prison sentences mean for Research, *Nature*. 577: 1545-155

D'Alessio, V. (2019). We need to talk about CRISPR, Horizon: The EU Research and Innovation Magazine. https://horizon-magazine-eu/article/we-need-talk-about-crispr.html Accessed 3rd March, 2021

Darie, C.C. (2013). Post-Translational Modification (PTM) Proteomics: Challenges and Perspectives. *Mod. Chem. Appl. 1: e114. doi: 10.4172/2329-6798.1000e114*

Day, D.A. and Tuite, M.F (1998). Post-transcriptional gene regulatory mechanisms in eukaryotes: an overview. *J. Endocrinol.* 157: 361-371

Debus-Sherrill, S and Field, M.B (2019). Famillial DNA searching –an emerging forensic investigative tool. *Sci. and Justic.* 59**:** 20-28

diCenzo, G.C and Finan, T.M (2017). The divided bacterial genome: structure, function, and evolution. *Microbiol. Mol. Biol. Rev.* 81: e00019-17. https://doi.org/10.1128/MMBR.00019-17

Eme, O.I (2018). Inter-Security agency rivalry as an impediment to national counter terrorism strategy (NACTEST). AfriHeritage Research Working Paper 2018 003.https://media.africaportal.org/documents /inter-Security-Agency-Rivalry.pdf. Accessed on 13th March, 2021

Etebu, E. (1989). Antimicrobial activities of some plant extracts used locally as alcohol ("Kaikai") additives. BSc Thesis. Rivers State University of Science and Technology, Port Harcourt. 38pp

Etebu, E. (1997). *In vitro* studies on sporulation and sexual mating of *Mycosphaerella fijiensis* Morelet, causal agent of black sigatoka disease in bananas and plantains. MSc Thesis. Rivers State University of Science and Technology, Port Harcourt. 70pp

Etebu, E. (2008). Molecular detection and quantification of the pea footrot disease pathogen *(NectriaHaemotococca)* in agricultural soils: A potential model for disease prediction. PhD Thesis. The University of Sheffield, Sheffield, United Kingdom. 274pp

Etebu, E. (2012). Postharvest pathology and phytochemicals of *Irvingia gabonensis* (Aubry-Lecomte ex O'Rorke) fruits and wastes. *Agric. Sci. Res, J.* 2 (6): 285-294

Etebu, E. (2013a). Differences in fruit size, postharvest pathology and phytochemicals between *Irivingia gabonensis and Irvingia wombolu. Sust. Agric. Res.* 2 (1): 52-61

Etebu, E. (2013b). Potential panacea to the complexities of Polymerase chain reaction (PCR). *Adv. life sci. Technol.* 13: 53-59

Etebu, E. (2015). Agricultural soil health and pea footrot disease suppressiveness. In: Meghvansi MK and Varma A (Eds): *Organic Amendments and Soil Suppressiveness in Plant Disease Management.* Vol. 46 of the Series Soil Biology. Springer International Publishing Switzerland. Pp 125-145

Etebu, E. (2016). The principles, challenges and prospects of polymerase chain reaction (PCR) in Molecular biology. Paper presented at Humboldt Kolleg International Conference held between Oct 11-15, 2016 at Biodun Shobanjo Multi-Media Centre of Excellence, University of Lagos. Akoko, Lagos.

Etebu, E. (2019). Application of modern cell biology and genetics in Crime Investigation. A lecture delivered on 25th July, 2019 as part of Continuing Professional Development workshop organized by the Association of Medical Laboratory Scientist of Nigeria. Federal Medical Centre, Yenagoa Chapter, Bayelsa State, Nigeria held between 22-28th July, 2019

Etebu, E. and Oku I (2017). Quantification and inter-relationship between microbial load, disease, proximate composition and phytochemical content of postharvest *Irvingia* fruit waste. *Int. J. Agric. Earth Sci.* 3 (1): 19-34

Etebu, E. and Osborn, A.M (2009) Molecular assays reveal the presence and diversity of genes encoding pea footrot pathogenicity determinants in Nactria haematococca and in agricultural soils. *J. Appl. Microbiol.* 106 (5): 1629-1639

Etebu, E. and Osborn, A.M (2010) Molecular quantification of the pea footrot disease pathogen (*Nectriahaematococca*) in agricultural soils. *Phytoparasitica.* 38: 447-454

Etebu, E and Osborn, A.M (2011a) Molecular prediction of pea footrot disease in agricultural soils. *Asian J. Agric. Sci.* 3 (6): 417-426

Etebu, E and Osborn, A.M (2011b) Pea footrot disease depends on the combination of Pathogenicity genes in *Nectria heamatococca. Asian J. Agric. Sci.* 3 (3): 156-161

Etebu, E and Osborn, A.M (2011c) A potential model for pea footrot disease prediction. *Asian J. Agric. Sci.* 3 (3): 177-186

Etebu, E and Osborn, A.M (2011d) In Search of target gene(s) to quantify pea pathogenic *Nectria haematococca* in Agricultural Soils. *Curr. Res. J. Biol. Sci.* 3 (3) 195-208

Etebu, E and Osborn, A.M (2012a). A review of indicators of healthy agricultural soils with pea footrot disease suppression potentials. *Sust. Agric. Res.* 2 (1): 235-250

Etebu, E and Osborn, A.M (2012b). Molecular approach to plant fungal identification in agricultural soils. *Nig. J. Plt. Prot.* 26: 18-34

Etebu, E and Pondei, K (2013). The transformational role of Polymerase chain reaction (PCR) in environmental health research. *J. Nat. Sci. Res.* 3 (12): 23-29

Etebu, E. Pasberg-gauhl, C and Gauhl, F (2002) *In vitro* studies on sporulation and linear growth of *Mycosphaerella fijiensis*. *Niger Delta Biologia* 4 (1): 32-36

Etebu, E. Pasberg-gauhl C, Gauhl F and Daniel-Kalio, L.A (2003a) Preliminary studies on *In Vitro* stimulation of sexual mating among isolates of *Mycosphaerella fijiensis* Morelet, causal agent of black sigatoka disease in bananas and plantains. *Phytoparasitica* 31 (1): 69-75

Etebu, E. Pasberg-gauhl C, Gauhl F and Daniel-Kalio, L.A (2005). Effect of light and sealing patterns on sporulation and growth of *Mycosphaerella fijiensi*s. *InfoMusa* 14 (1): 24-25

Etebu, E. Tasie A.A and Daniel-Kalio, L.A (2003b). Post-harvest fungal quality of selected chewing sticks. *Oral Dis.* 9 (2): 95-98

Etebu, E. and Tungbulu, G (2015). Bacterial quality of post harvest *Irvingia gabonensis* (Aubry-Lecomte ex O'Rorke) fruit wastes. *Int. J. Appl. Microbiol. Biotechnol. Res.* 3: 96-103

Etebu, E and Tungbulu, G (2016) Effect of post harvest period on disease progression and proximate composition of Irvingia species fruit waste. *IOSR J. Environ. Sci., Toxico. Food Technol.* 10**:** 26-36

Etebu, E. Tungbulu, G and Ezenwaka, J (2016). Effect of post harvest period on disease progression, weight and vitamin content of Irvingia species fruit wastes. *Int. J. Agric. Inn. Res.* 5 (1): 98-104

Etebu, E. Torunana J.M.A and Aniso J (2018a). Effects of postharvest Irvingia fruit wastes on soil microbial diversity and physic-chemical properties. *Microbiol. Res. Int.* 6 (3): 26-39

Etebu, E. Torunana, J.M.A and Osaro B (2018b). Metagenomic analysis of fungal community associated with *Irvingia* species (African mango) fruit wastes. *Int. J. App. Microbiol. Biotechnol. Res. (IJAMBR)*. 6:78-86

Etebu, E. Torunana, J.M.A and Parker M (2018c). Metagenomic analysis of bacterial community associated with postharvest *Irvingia* species fruit wastes. *Microbiol. Res. Int.*. 6 (2): 7-15

Fakruddin, M.D and Mannan K.S.B (2013). Methods for analyzing diversity of microbial communities in natural environments. *Cey. J. Sci. (BiolSci)*. 42(1): 19-33.

Federal Government of Nigeria (2014). White Paper on the report of the Presidential Committee on Restructuring and Rationalization of Federal Government Parastatals. Commissions and Agencies. https://www.lawyard.ng /wp-content/uploads/2020/04/Steve-Oronsaye-Report.pdf. Accessed on 13th March, 2021

Frey, J (2007). Biological safety concepts of genetically modified live bacterial vaccines. *Vaccine* 25(30):5598-5605. doi: 10.1016/j.vaccine.2006.11.058

Gambari I.A (2008). The challenges of nations building: the case of Nigeria. A paper presented in the first year anniversary lecture of Mustapha of Akanbi Foundation on 7th February, 2008. http://www.mafng.org/anniversary/challenges_nation_building_nigeria.htm. Accessed 12th March, 2021

Garbeva, P. Van Veen JA and Van-Elsas, J.D (2004). Microbial Diversity in soil: Selection of microbial populations by plant and soil type and implications for disease suppressiveness. *Annu. Rev. Phytopathol.* 42: 243-270 Google Images. https://images.google.com

Govender, K. Naicker, T. Lin, J. Baijinath, S. Chuturgoon A.A, Abdul N.S, Docrat T. Kruger H.G and Govender T (2020). A novel and more efficient biosynthesis approach for human insulin production in *Escherichia coli* (E. coli). *AMB. Expr.* 10:43. https://doi.org/10.1186/s13568-020-00969-w

Guatelli, J.C Gingeras, T.R and Richman, D.D (1989). Nucelic acid amplification *in vitro*: Detection of sequences with low copy numbers and application to diagnosis of human immunodeficiency virus type 1 infection. *Clin. Microbiol. Rev.* 2(2): 217-226

Humbard, M.A and Maupin-Furlow, J.A (2013). Prokaryotic proteasomes: Nanocompartments of degradation. *J. Mol Microbiol. Biotechnol.* 23: 321-334. doi: 10.1159/000351348

Ikpeze, N. (2013). Fusion of anti-corruption agencies in Nigeria: A critical appraisal. *Afe Babalola University: J. Sust. Dev. Law and Policy.* 1(1): 148-167

Ishino, S and Ishino, Y. (2014). DNA polymerases as useful reagents for biotechnology – the history of developmental research in field. *Frontiers in Microbiol.*. 5(465):1-8

Ishino, Y. Shinagawa, H. Makino, K. Amemura, M and Nakata, A. (1987). Nucleotide sequence of the *iap* gene, Responsible for alkaline phosphatase isozyme conversion in *Escherichia coli,* and identification of the gen product: *J. Bacteriol.* 169: 5429-5433

Jacob, F and Monod, J (1961) Genetic regulatory mechanisms in the synthesis of proteins, *J. Mol. Biol.,* 3:318-356

Jeffreys, A. Wilson, V and Thein, SL (1985a). Hypervariable 'minisatellite' regions in human DNA. *Nature* 314:67-73. doi:10.1038/314067A0

Jeffreys, A. Wilson V and Thein, S.L (1985b). Individual-specific 'fingerprints' of human DNA. *Nature* 316:76-79. doi:10.1038/316076A0

Kapoor, N. Liang, W, Marbàn, E and Cho, H.C 2012. Direct conversion of quiescent cardiomyocytes pacemaker cells by expression of Tbx18. *Nature Biotechnol.* 31(1): 54-62. doi:10.1038/nbt.2465. PMC 3775583. PMID 2324 2162.

Khamsi, R (2005). Transgenic cows have udder success. *Nature*. doi:10.1038/news050328-14

Konrad-Adenauer, S. (2011). Concepts and principles of democratic governance and accountability. A guide for peer educator-s. https://www.kas.de/c/document _library/get_ file?uuid=56a283ae-50ff-0c9b-7179 954d05e0aa19 &groupId=252038. Accessed 12th March, 2021.

Lackner, D.H and Bàhler, J. (2008). Translational Control of Gene Expression: From transcripts to Transcriptomes. *Int. Rev. Cell and Mol. Biol.* 271:199-251

Lanese, N (2021). First genetically modified mosquitoes released in US. https://www.livescience.com/first-genetically-modified-mosquitoes-us.html. Accessed on 8th May, 2021

Lecker, S.H Goldberg, A.L and Mitch, W.E (2006). Protein degradation by the Ubiquitin-proteasome pathway in normal and disease states. *Am Soc. Nephrol.* 17:1807-1819. *doi: 10.1681/ASN.2006010083*

Lee, H. Zhang, Z and Krause, H.M (2019). Long noncoding RNAs and repetitive elements: junk or intimate evolutionary partners? *Trends in Genet.* 35 (12): 892-902 https://doi.org/10.1016/j.tig.2019.09.006

Lee, M.J and Yaffe, M.B (2016). Protein regulation in signal transduction, doi: 10.1101/cshperspect.a005918. http://cshperspectives.cshlp.org/Accessed 25th March, 2020

Lehman, I.R Bessman, M.J Simms, E.S and Kornberg A (1958). Enzymatic Synthesis of Deoxyribonucleic Acid. I. Preparation of Substrates and Partial Purification of Enzyme from *Escherichia coli. J. Biol. Chem.* 233(1): 163-170

Linares, D.M Ross, P and Stanton, C (2016). Beneficial microbes: The pharmacy in the gut. Bioengineer. 7(1): 11-20

Luria, S.E and Human M.L (1952) A non hereditary, host-induced variation of bacterial viruses. *J. Bacteriol.* 64:557-569

Maghari, B.M and Ardekani A.M, 2011. Genetically modified foods and social concerns. *Avicenna J. Med. Biotechnol.* 3(3): 109-117

Mathews M.B, Sonenberg, N and Hershey, J.W.B (2007). Origins and principles of Translational Control. In:*Translational Control in Biology and Medicine.* Cold Spring Harbor Laboratory Press 978087969767-9

Matthaei, J.H and Nirenberg, M.W (1961), Characteristics and stabilization of DNAase-sensitive protein synthesis in *E. coli extracts. Proceedings of the National Academy of Sciences of the United States of America,* 47 (10), 1580-1588. https://doi.org/10.1073/pnas.47.10.1580

McCartney, C (2010). The DNA revolution and forensic future. *Criminal Justice Matters.* 81(1): 26-27. DOI: 10.1080/09627251.2010.505397

Mojica, F.J, Diez-Villaseńor, C. Soria, E. and Juez, G. (2000). Biological significance of a family of regularly spaced repeats in the genomes of Archaea, Bacteria and mitochondria. *Mol. Microbiol.* 36(1):244-246. doi: 10.1046/j.1365-2958.2000.01838.x. PMID: 10760181

Mojica, F.J. Juez, G and Rodriguez-Valera. F. (1993). Transcription at different salinities of *Haloferax mediterranei* sequences adjacent to partially modified *pst*I sites: *Mol. Microbiol.* 9: 613-621.

Muñoz-López, M and García-Pérez, J.L (2010). DNA Transposons: Nature and Applications in Genomics. *Curr. Genomics.* 11: 115-128

Nawrat, A (2021) Novartis's SMA gene therapy Zolgensmato be available for NHS use. https://www/pharmaceutical-technology.com/features/cell-and-gene-therapy-skills-gaps-growing-sector/(Accessed April 16th 2021)

Newton, D. (2016). DNA Technology: *A Reference Handbook. 2nd Edition.* ABC-CLIO. 189pp. ISBN 9781440850486. https://books.google.com/books?id=ogypDQAAQBAJ&pg=PA189

OSCE (2021). Democratic governance. https://www.osce.org/odihr/democratic-governance. Accessed 12th March, 2021

Phillips, M.L (2008). Crime scene genetics: transforming forensic science through molecular technologies. *BioSci.* 58 (6): 484-489.

Piovesan, A. Pelleri M.C, Antonaros, F. Strippoli P. Caracausi, M and Vitale, L (2019). On the length, weight and GC content of the human genome. *BMC Res. Notes. 12:106. https://doi.org/10.1186/s13104-019-4137-z*

Poltronieri, P. Sun, B and Mallardo, M (2015). RNA Viruses: RNA roles in pathogenesis, coreplication and viral load. *Curr. Genomics.* 16: 327-335.

Portillo, M.C, Leff, J.W, Lauber C.L and Flerer, N (2013). Cell size distributions of soil bacteria and Archaeal taxa. *Appl. Environ. Microbiol.* 79 (24): 7610-7617

Pray, L.A (2008a) Discovery of DNA structure and function: Watson and Crick: *Nature Education* 1(1): 100

Pray, L.A (2008b). DNA replication and causes of mutation. *Nature Education,* 1(1): 214.

Prifti, E and Zucker, J.D, (2013). The new science of metagenomics and the challenges of its use in both developed and developing countries. hal-00821359. https://hal.inria.fr/hal-00821359. Accessed 11th March, 2021

Rao, S.R, Trivedi, S. Emmanuel, D. Merita, K and Hynniewta, M. (2010). DNA repetitive sequences types, distribution and function: A review. *J. Cell Mol. Biol.* 7(2):1-11

Reddy, M.K (2020). "Amino Acids" 2020 Encyclopedia Britannica. https://www.britannica.com/science/amino-acid. Accessed 23rd January, 2021.

Riley, M (1999). Correlates of smallest sizes for microorganism. Proceedings of a Workshop. National Academy of Science 21-25. http://www.nap.edu/catalog /9638.html. Accessed 6th March, 2021 Russell, PJ 2010 Genetics: A Molecular Approach, 3rd Edition.

Saiki, R, Gelfand, D, Stoffel, S, Scharf, S, Higuchi, R, Horn, G, Mullis, K and Erlich, H. (1988). Primer-directed enzymatic amplification of DNA with a thermostable DNA Polymerase. *Science* 239 (4839): 487-491

Singh, A. Jeena, LM and Rahangdale, S. (2019). Applications of molecular markers in livestock improvement: A Review. *European Journal of Biotechnology and Bioscience.* 7(3): 100-102

Smith, Y. (2019) DNA Replication and Repair. News-Medical. https:///www.news-medical.net/life-sciences/DNA-Replication-and-Repair.aspx. Accessed on March 4th, 2020

Todd, A. (1998). Revolutions, 1789-1917. Cambridge University Press, UK

Tugbulu, G. **Etebu, E** and Ezenwaka, J (2016). Effect of postharvest period on phytochemical content and brownish-black not disease of postharvest Irvingia species fruit wastes. *Int. J. Agric. Inn. Res.* 5 (1): 105-112.

Tutar, Y (2012). Pseudogens. Comparative Functional Genomics. Article ID 424526. doi:10.1155/2012/424526

Uddin, F. Rudin, C.M and Sen, T (2020). CRISPR gene therapy: Applications, limitations, and implications for the future. Frontiers in Oncology. 10:1-17 https://doi.org/10.3389/ fonc.2020.01387. Accessed 3rd March, 2021.

Verdier, J and Thompson, R.D (2008). Transcriptional regulation of storage protein synthesis during dicotyledon seed filling. *Plant Cell Physiol.* 49(9): 1263-1271

Voet, D. Voet, J and Pratt, C.W (2006). *Fundamentals of Biochemistry.* 2nd edition. John Wiley & Sons, New York, NY, USA

Vyas, S.P and Mehta, A. (2011) *Cell and Molecular Biology,* 1st Edition, CBS Publishers and Distributors PVT Limited PP 574

Wolpert, L (1995). Evolution of the cell theory. *Phil. Trans. R. Soc. Lond.* B349: 227-233 http://doi.org/10.1098/rstb .1995.0106

Zhao, L (2010). Genomics: The tale of our other genome. *Nature* 465(7300): 879-880.

40th Inaugural Lecturer

Professor Ebimieowei Etebu

B.Sc., M.Sc. (RSUST, Nigeria),
PhD (The Univ. of Sheffield, UK)
Professor of Agricultural and Molecular Microbiology
Department of Microbiology, Faculty of Science,

Citation of Professor Ebimieowei Etebu (Agricultural and Molecular Microbiologist)

Professor Ebimieowei Etebu, an indigene of Odi in Kolokuma/Opokuma Local Government Area of Bayelsa State, was born on 5th September, 1966 at Asamabiri to the family of Late Mr and Mrs Yelwa Etebu.

He completed his Primary school education in 1978 at Army Children's School, Alamala, Abeokuta. Thereafter he was sent to Odi by his father to attend the only Government Secondary School existing in his town at the time. His father who was a soldier at the time knew he would soon retire from the Nigerian Army, so Prof. Ebimieowei Etebu was sent back to his roots ahead of time.

Prof. Etebu was quite popular in his days of secondary school, especially for the different roles he featured in different drama episodes. He was the first and only Executive Senior Prefect of Government Secondary School Odi. He wrote his final O/Level exams in G.S.S. Odi in June 1983 but did not get credit scores in some of his core subjects to enable him further his education at the tertiary level. So he enrolled again for West African School Certificate O/Level exams at Government Secondary School Borokiri, Port Harcourt in 1984.

At this time, he passed all his registered subjects in one sitting, and got admitted into Rivers State University of Science and Technology (Now Rivers State University), Port Harcourt in 1985. In 1989 he bagged his Bachelor of Science degree in Applied Biology (Microbiology option), with Second class upper division, and was the best graduating student of his department that year.

He later worked as a Research Supervisor in the prestigious International Institute of Tropical Agriculture (IITA) in Onne, Rivers State from 1992 to 1996. During this period he was actively involved in various research experiments aimed at controlling different diseases affecting plantains and bananas.

In 1996, Prof. Etebu got employed into River State University (RSU) as a Graduate Assistant, and later bagged his Master's degree in Plant pathology from the same university in 1998. Meanwhile in 1997, Bayelsa State had been carved out from the then Rivers State which also led to the establishment of Niger Delta University (NDU) a few years later. Being the only Plant pathologist of Bayelsa State origin among the academic staff of RSU then, coupled with his experience in teaching genetics and other foundational courses in the Biological Sciences the Services of Prof. Etebu were in high demand by NDU, to kick start the Biological Sciences department in the Bayelsa State owned University, the Niger Delta University.

Owing to his unrelenting love to contribute to the development of his State, Prof. Etebu started lecturing in NDU with no extra pay or Allowance while he was still a staff of RSU. He jostled between RSU in Port Harcourt and NDU in Amassoma (Covering over 100 Km apart), teaching in both Institutions for over a year before the management of RSU reluctantly approved his Application for lateral transfer to NDU in October, 2003. That same year, the Bayelsa State Government awarded him a scholarship to study for his PhD degree in the United Kingdom in 2003.

Prof. Etebu gained admission into University of Essex, Colchester, United Kingdom in April 2004 but later transferred his studies to The University of Sheffield, Sheffield also in the United Kingdom, in 2005 where he successfully completed his studies in 2008. During his studies, he designed and validated molecular models that selectively detect and quantifies plant pathogens responsible for pea foot rot disease in agricultural soils without recourse to culture; the first of its kind in the world. He came up with a mathematical formula that would enable one to assess the risk of planting peas in any given agricultural soil, and the application of his predictive model would potentially enable the British agro-industry avoid a loss of about £25M annually.

Owing to his passion and desire to contribute his quota towards human capital development of his State and Country, Prof. Etebu returned to NDU almost immediately after his graduation from The University of Sheffield, UK, notwithstanding the readiness of his PhD Supervisor to further engage him.

Upon his return in 2008, Prof. Ebimieowei Etebu continued his lecturing job in NDU, and was promoted to the rank of Professor in Agricultural and Molecular Microbiology, effective 2017. By this promotion he became the one and only professor of Agricultural and Molecular Microbiology documented in any Nigerian University up to 2017 and possibly till date (NUC is yet to upload a more recent list of Professors in Nigerian University on their website for one to verify). He is the first professor of Kemenanabo Community in Odi. He is one of the three tenured pioneer staff of Biological Sciences department of NDU.

Prof. Etebu was the undergraduate Seminar Coordinator for the Biological sciences department as well as the Coordinator for the Faculty of Science. As seminar and project coordinator in his department, Prof. Etebu introduced the use of PowerPoint (Computer) for seminar presentations by Undergraduate final year students of the Biological Sciences department in NDU. At first even some of his colleagues disagreed and some even tried to turn students against him, but he stuck to his gun. Today, it is a delight to see the students of the department design and present seminars in PowerPoint.

Prof. Ebimieowei Etebu has numerous publications, mostly in International journals, to his credit. He is a Reviewer to several International Scientific journals. He has taught and still teaches several courses as a University Lecturer both at the undergraduate and postgraduate levels. Some of these are Molecular biology, Molecular ecology and bioinformatics, Basic techniques in Microbiology, Plant metabolism, Plant pathology, Biostatistics, General Microbiology, Mycology, Virology, General biology, Genetics, Environmental Microbiology, Soil Microbiology, Molecular biological techniques in Environmental biology, Microbial Genetics, Research Methods and Biostatistics etc

He has served the Niger Delta University as Director of General Studies from 2015 to date. As Director of General Studies, every single student of NDU, irrespective of the course studied must of necessity pass through the Unit he presides over on behalf of the Vice Chancellor. For this reason, he pilots the Unit with a high sense of fairness to all students and staff. He has thus formulated several policies which are

adopted for the smooth running of the Unit. One of such policies is the introduction of Computer Based Test Exams. This policy has, in no small ways, improved the assessment and compilation of students' results after exams. He has recently put together a student handbook on the operations of the General Studies Unit which would soon be published by the University Management.

Prof. Etebu is a man of many parts and versatility. Aside his doctoral degree, he has a certificate on Christian Counseling awarded by a reputable Organization in the UK. He also has a Post graduate diploma in Christian Theology from the Redeemed Bible College and also a Post graduate Diploma in Education awarded by the University of Port Harcourt.

Aside his lectureship in NDU, Prof. Etebu is a visiting adjunct Professor with Federal University Otuoke, Bayelsa State. He was recently nominated by the National University Commission as part of its Accreditation Teams to assess Microbiology programmes in two different Universities.

He is also a member of Bayelsa State Science and Technology Education Board. This Board is charged with formulation of policies for review and adoption by the Government of the day in the management and running of Science and Technical Education in Bayelsa State. He is also a member of an apolitical developmental organization (KOLGA DEVELOPMENT INITIATIVE, formerly, KOLGA FOCUS GROUP) of his Local Government Area of Bayelsa State where he heads the Agricultural subcommittee. The Agricultural Committee of this group is charged with the formulation of the Agricultural strategy and development

Blueprint/plan for the Kolokuma/Opokuma Local Government Area of Bayelsa State. Prof. Etebu once served as an Agricultural Advisor (non pensionable position) to Schlumberger, Gecko Prakla, and Consultant to Total Nigeria Plc. He was a member of a Technical Committee set up by the Bayelsa State Ministry of Education to plan and organize an Education Summit that would provide a 15 years educational roadmap for the State.

Prof. Etebu has won a few research grants as a lecturer with NDU. Part of funds obtained through such grants were utilized to kick start the setting up of a Molecular Biology Laboratory. Prof. Etebu is an astute guest Lecturer in both Scientific and non Scientific fora. He has delivered public lectures in different scientific fora both locally and internationally. As an Academician, Prof. Etebu has supervised over 150 students' research project, including Postgraduate and doctoral students.

Aside Academic and scientific research, Prof. Etebu plays very active roles in the church. He was the Coordinator of Sunday School in over 150 branches of his church before he left for his doctoral studies. On his return, He was saddled with the responsibility of training and development of manpower of his church in Bayelsa State, amongst several other roles and responsibilities. He currently serves as the Resident Pastor of the Headquarters branch of his Church in Akenfa, Yenagoa, Bayelsa State. He has published two Christian based books, “Constrained by Love” and “Echoes from heaven at Night”.

Prof. Ebimieowei Etebu, no doubt, has silently contributed a lot in the human capital development of Bayelsa State in particular, and humanity and society in general. The seemingly

silent and unassuming ways Prof. Etebu positively contributes to the growth of humanity, and Bayelsa state in particular, have not been unnoticed, and as such about a year ago he was conferred with the status of a Fellow of the Institute of Policy Management and Development in Nigeria.

Prof. Etebu is a member of several other Professional Bodies. Some of these are:

- Society of Microbiology, UK
- BioNet International, UK
- Nigerian society of plant protection, Nigeria
- Nigerian Society for Microbiology
- Science Association of Nigeria
- Nigerian Bioinformatics and Genomic Network
- International Society for Development and Sustainability, Japan
- Teachers' Registration Council

He is married to Mrs Ebimokemenimighan Etebu, and they are altogether blessed with five (5) Children, Pere, Tonye, Tari, Debz and Mercy.